

# STIC Search Report Biotech-Chem Library

**REM-1B69** 

## STIC Database Tracking Number: 179999

TO: Sheela Huff

Location: rem/3A15/3C18

Art Unit: 1643

Monday, February 27, 2006

Case Serial Number: 10/723872

96 Phone: (571) 272-4161

Vrietine Henele@wente we

From: Kristine Hensle

Kristine. Hensle@uspto.gov

**Location: Biotech-Chem Library** 

#### Search Notes

Examiner Huff,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle Librarian STIC Biotech/Chem Library (571)272-4161

> For spanning Search Notes





### STIC-Biotech/ChemLib

From:

Huff, Sheela

Sent:

Tuesday, February 21, 2006 5:32 AM

To: Subject: STIC-Biotech/ChemLib search request for 10723872

Please search and interference search SEQ ID NO. 12, 14, 16,18, 20, 22, 24 and 26. All are polypeptides.

Thanks-

Sheela Huff Art Unit 1643 571-272-0834 Remsen 3A15 mailbox Remsen 3C18 FEB 21 2005

Searcher:	_
Searcher Phone:	
Date Searcher Picked up:	
Date completed:	
Searcher Prep Time:	_
Online Time:	

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Type	Type of Search									
NA#	_ AA#:									
S/L: C	Oligomer:									
Encode/Tran	nsl:									
Structure #:	Text:									
Inventor:	Litigation:									

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endors and cost where applicable
STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other (Specify):



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OM protein - protein search, using sw model

February 23, 2006, 09:13:28; Search time 135.298 Seconds (without alignments) 457.897 Million cell updates/sec Run on:

Title: Perfect score:

US-10-723-872-12
755
1 MVLQTQVFISLLLWISGAYG......TVFYWYFDVWGRGTFVTVSS 141 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2443163 segs, 439378781 residues Searched:

2443163 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* geneseqp2005s:\* A\_Geneseq\_21;\*
11: geneseqp1980s:\*
2: geneseqp1990s:\*
4: geneseqp2000s:\*
6: geneseqp2001s:\*
5: geneseqp2028:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Aar70192 Humanized						_	Heavy	Heavy	Heavy	Heavy	Human		Adf71905 Hu3G8VH-1		Abp66590 Human RSV	Abp66588 Human RSV	Human				Ade35948 SYNAGIS a		Ade35944 SYNAGIS a
SUMMARIES		ΩI	AAR70192	AAY23770	AAY18117	AAR70191	AAY23769	AAY18125	AAR70190	AAY23768	AAY18121	AAY23780	AAY18122	ABP58289	ABG31445	ADF71905	ADF71908	ABP66590	ABP66588	ABP66586	ABU69451	ABU69453	ABU69449	ADE35948	ADE35946	ADE35944
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		Score	755	755	755	663	663	663	577	577	577	553	553	551	549.5	546.5	546.5	544.5	544.5	544.5	544.5	544.5	544.5	544.5	544.5	544.5
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ADW20090	ADW20086	ADW20088	AEB07072	AEB07068	AEB07070	ADF71910	ABP66409	AAE28064	ABU69272	ADE35767	ADI56929	ADT89252	ADW19909	AEB06891	ADF71916	ADF71912	ABP66405	AAE28060	ABU69268	ADE35763
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544.5	544.5	544.5	544.5	544.5	544.5	542.5	542.5	542.5	542.5	542.5	542.5	542.5	542.5	542.5	542.5	542.5	541.5	541.5	541.5	541.5
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Humanized antibody; antibody engineering; monoclonal antibody; MAb; interleukin-4; IL-4; allergy. 1. .19 /label= Sig\_peptide 51. .57 /label= CDR /note= "complementarity determining region" 72. .87
/label= CDR
/note= "complementarity determining region"
120. .130
/label= CDR
/note= "complementarity determining region" Humanized antibody 3B9 heavy chain. Location/Qualifiers AAR70192 standard; protein; 141 AA (revised)
(first entry) 25-MAR-2003 20-SEP-1995 Homo sapiens. WO9507301-A1 AAR70192; Key Peptide Region Region Region 

94WO-US010308. 93US-00117366. 93US-00136783. 07-SEP-1994; 07-SEP-1993; 14-OCT-1993; 16-MAR-1995

Sylvester DR; (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC. Gross MS, Holmes S,

WPI; 1995-123387/16. N-PSDB; AAQ83493.

Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from

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07-SEP-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                              A humanized antibody heavy chain variable region and signal sequence is given in AAR70192. The signal sequence is also provided in AAR70193. The CDR sequences of the construct are identical to the native CDRs of mouse anti-human IL-4 MAD 3B9 (AAR70198-200). (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heavy chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoslobulin E-mediated allergic reaction; allergic rintities; conjunctivitie; atopic dermatitie; atopic asthma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.
                                                                                                                                                                                                                                                                                                                                                                   TOTLILICIFSGFSLSTSGMGVSWIR
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high affinity mabs - useful in treatment of IL-4-mediated and IgB-
mediated allergic conditions.
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                                                                                                                                                                                                                                                                                  Length 141;
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100.0%; Pred. No. 1.2e-62;
iive 0; Mismatches 0;
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                                                                         Disclosure; Fig 4; 97pp; English
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93US-00136783.
94WO-US010308.
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N-PSDB; AAX85887.
                                                                                                                                                                                                                                                                                                      al Similarity
141; Conserv
                                                                                                                                                                                 anti-human IL-4 MP
correct PN field.)
                                                                                                                                                                                                                                              Sequence 141 AA;
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14-OCT-1993;
07-SEP-1994;
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Matches
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This sequence represents the heavy chain of the humanised 3B9 antibody of the invention. The antibody is a chimeric or humanised interleukin-4
The present sequence represents the heavy chain variable region of a humanised murine interleukin-4 (IL-4) antibody 3B9. The specification describes chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunos]obulin E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibody, interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease.
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0
                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 755; DB 2; Length 141; 100.0%; Pred. No. 1.2e-62; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tratment of allergic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 141; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                              Sequence 141 AA;
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QPSGKGLEWLAHIYWDDDKRYNPSLKSRLTISKDTSSNOVFLKITSVDTADTATYYCAR 120
                                                                                                              A human/mouse chimeric antibody heavy chain variable region was constructed (given in AAR70191) that contained the mouse anti-human IL-4 MAD 3B9 variable region including 3 CDRS (AAR70199-200) and a human antibody signal peptide (AAR70193). The construct was used for humanized antibody production. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New DNA molecules encoding recombinant antibodies useful for treating IL4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heavy chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin E-mediated allergic reaction; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic aethma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.
                    Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated and IgE-mediated allergic conditions.
                                                                                                                                                                                                                                                                                                                                             OPPGKGLEWLAHIYWDDDKRYNPSLKSRLTISKDTSRNQVVLTMTNMDPVDTATYYCARR
                                                                                                                                                                                                                                                                                                                              1 MVLQTQVFISLLLWISGAYGQVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIR
                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                              Length 141,
                                                                                                                                                                                                                                                                                            9; Indels
                                                                                                                                                                                                                                                            Score 663; DB 2;
Pred. No. 4.9e-54;
0; Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY23769 standard; protein; 141 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETVFYWYFDVWGRGTPVTVSS 141
                                                                                  Disclosure, Fig 3; 97pp; English
                                                                                                                                                                                                                                                            Query Match

Best Local Similarity 86.5%; Pr
Matches 122; Conservative 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ETVFYWYFDVWGAGTTVTVSS
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N-PSDB; AAX85886.
                                                                                                                                                                                                                                Sequence 141 AA;
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13-SEP-1999
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(IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft versus host disease
                                                                                                                                                                                                                                                                                                QPPGKGLEWLAHIYWDDDKRYNPSLKSRLTISKDTSRNOVVLIMTNMDPVDTATYYCARR 120
                                                                                                                                                                                                                                                                          OPPGKGLEWLAHIYWDDDKRYNPSLKSRLTISKDTSRNQVVLTMTNMDPVDTATYYCARR 120
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                                                                                                                                                                                                                              1 WVLQTQVFISLLIMISGAYGQVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIR
                                                                                                                                                                                                              1 MVLQTQVFISLLLWISGAYGQVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIR
                                                                                                                                                                               Gaps
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                                                                                                                                              Length 141;
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                                                                                                                                                                               Indels
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                                                                                                                                            100.0%; Score 755; DB 2;
100.0%; Pred. No. 1.2e-62;
iive 0; Mismatches 0;
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/label= Sig_peptide
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                                                                                                                                                                                                                                                                                                                                                            AAR70191 standard; protein; 141 AA
                                                                                                                                                                                                                                                                                                                                           ETVFYWYFDVWGRGTPVTVSS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric antibody 3B9 heavy chain.
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93US-00136783.
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/label= CDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
(first entry)
                                                                                                                                                             Best Local Similarity 100.
Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
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N-PSDB; AAQ83492.
                                                                                                                Sequence 141 AA;
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25-MAR-2003
20-SEP-1995
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the invention. The antibody is a chimeric or humanised interleukin-4 (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft versus host disease
                                                                                                                                                                                                                                                                                                                                                                                                       QPPGKGLEWLAHIYWDDDKRYNPSLKSRLTISKDTSRNQVVLTMTNMDPVDTATYYCARR 120
                                                                                                                                                                                                                                                                                                                                                                                                                        1 MVLQTQVFISLLLMISGAYGQVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIR
                                                     sequence represents the light chain of the chimeric 3B9 antibody
                                                                                                                                                                                                                                                                                                                               1 MVLQTQVFISLLLWISGAYGQVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIR
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                                                                                                                                                                                                                                                       87.8%; Score 663; DB 2; Length 141;
86.5%; Pred. No. 4.9e-54;
ive 10; Mismatches 9; Indels
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    1. .19
    /label= Sig_peptide
    50. .56
    /label= CDR

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETVFYWYFDVWGRGTPVTVSS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR70190 standard; protein; 140 AA
                 Example 5; Fig 3; 50pp; English.
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/label= CDR
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                                                                                                                                                                                                                                                                                           Matches 122, Conservative
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                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                    Sequence 141 AA;
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20-SEP-1995
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                                                              The present sequence represents the heavy chain variable region of murine/human interleukin-4 (IL-4) chimeric antibody 3B9. The specification describes chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin B-mediated allergic reactions e.g. allergic thinitis, conjunctivitis, atopic astuma, anaphylactic shock, rheumatoid arthritis, host-versus-graft disease and renal disease. They are also useful in the disquests of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans. (Updated on 17-OCT-2003 to standardise
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
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                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant IL4 antibodies useful for tratment of allergic rhinitis, atopic ashthma and anaphylactic shock.
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                                                                                                                                                                                                                                                                                                                                                  Length 141;
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                                                                                                                                                                                                                                                                                                                                              87.8%; Score 663; DB 2;
86.5%; Pred. No. 4.9e-54;
iive 10; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric 3B9 monoclonal antibody heavy chain.
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                                  Example 3; Fig 3; 50pp; English
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94WO-US010308.
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Matches 122; Conservative
-mediated conditions.
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N-PSDB; AAX79542.
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                            Sequence 141 AA;
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07-SEP-1994;
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Antibody, interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; gatt versus host disease.
                                                                                     interleukin-4 (IL-4) antibody 3B9. The sequences are used in the production chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, howersus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EWLAHIYWDDDKRYNPSLKSRLIISKDTSSNOVFLKITSVDTADTATYYCARRETVFYWY
                                                                                                                                                                                                                                                                                                                                                                                                                          7 SLILLIVPAYVLSQVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGL
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                                                                                                                                                                                                                                                                                                                                                                                                       10 SLLLWISGAY--GQVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIRQPPGKGL
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant IL4 antibodies useful for tratment of allergic rhinitis, atopic ashthma and anaphylactic shock.
                                                                        The present sequence represents the heavy chain variable region of
                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                             Length 140;
                                                                                                                                                                                                                                                                                                                                                                 13; Indels
                                                                                                                                                                                                                                                                                                                           76.4%; Score 577; DB 2; 81.3%; Pred. No. 5.4e-46; ive 10; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heavy chain sequence for murine 3B9 antibody
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CORP.
                                      English.
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93US-00136783.
94WO-US010308.
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                                                                                                                                                                                                                                                                                                                                                                 Matches 109; Conservative
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127 PDVWGAGTTVTVSS
                                    Fig 2; 50pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sylvester DR, Holmes
 conditions
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                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                           Sequence 140 AA;
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07-SEP-1994;
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                                    Example 3;
 -mediated
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                                                                                                                                                                                            hybridomas, which were screened for anti-IL-4 MAD secretion. Only clone 3B9 was positive. CDNA clones of the 3B9 light and heavy chains were cloned into pGEN7f+ and transformed into B. coli DHS-alpha. The clones were sequenced (AAQ83490-91), and used for antibody engineering. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heavy chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin E-mediated allergic reaction; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.
                                                                        from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EWLAHIYWDDDKRYNPSLKSRLTISKDTSRNQVVLTMTNMDPVDTATYYCARRETVFYWY
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                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                  Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived high affinity mAbs - useful in treatment of IL-4-mediated and IgE-mediated allergic conditions.
                                                                                                                                                                                                                                                                                                                                                                                    5;
                                                                                                                                                                             Spleen cells from mice immunized with human IL-4 were used to
                                                                                                                                                                                                                                                                                                                                                Length 140;
                                                                                                                                                                                                                                                                                                                                                                                  13; Indels
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                                                                                                                                                                                                                                                                                                                                            76.4%; Score 577; DB 2;
81.3%; Pred. No. 5.4e-46;
iive 10; Mismatches 13
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                                                                                                                                          Disclosure, Fig 2; 97pp; English.
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94WO-US010308.
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Best Local Similarity 81.3%
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               WPI; 1995-123387/16.
N-PSDB; AAQ83491.
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                                                                                                                                                                                                                                                                                                          Sequence 140 AA;
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                                                                                                                                                                                   invention
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Matches
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                               This sequence represents the heavy chain of the murine 3B9 antibody of the invention. The antibody is a chimeric or humanised interleukin-4 (ILA) monoclonal antibody for the treatment of immunoglobulin E (IgE) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic asthma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft versus host disease
                                                                                                                                                                                                                                                                                                                                                                                                                            127
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New DNA molecules encoding recombinant antibodies useful for treating IL4 -mediated conditions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Light chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; fimunosplobulin E-mediated allergic reaction; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic aesthma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy;
                                                                                                                                                                                                                                                                                                                                                               10 SLLLWISGAY -- GOVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIRQPPGKGL
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                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                 Length 140;
                                                                                                                                                                                                                                                                                                    13; Indels
                                                                                                                                                                                                                                                             76.4%; Score 577; DB 2; 81.3%; Pred. No. 5.4e-46; ive 10; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heavy chain variable region of 1g NEW.
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Claim 24; Fig 2; 50pp; English.
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FDVWGAGTTVTVSS 140
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Best Local Similarity
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14-OCT-1993;
07-SEP-1994;
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                          pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin Benediated allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host-versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess endoquetion through the measurement e.g. by BLISA of circulating endogenous IL-4 levels in humans. The present sequence represents the heavy chain variable region of Ig NEW, and is used in the course of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140
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The antibodies of the invention are used in therapeutic and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 YNPSLKSRLTISKDTSRNQVVLTMTNMDPVDTATYYCARRETVFYWYFDVMGRGTPVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIRQPPGKGLEWLAHIYWDDDKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant IL4 antibodies useful for tratment of allergic rhinitis, atopic ashthma and anaphylactic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.2%; Score 553; DB 2; Length 121; 81.8%; Pred. No. 8e-44; ive 12; Mismatches 10; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heavy chain sequence for humanised 3B9 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Col 65-66; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gross MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY18122 standard; protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM PLC. (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93US-00136783.
94WO-US010308.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93US-00117366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-370482/31.
N-PSDB; AAX79527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 121 AA;
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(JOHN/) JOHNSON L S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-SEP-1998;
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       OS field)
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mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft versus host disease
                                                                                                                                                                                                                                                                                                                                  140
                                                                                                                                                                                                                                                                                                                                                Monoclonal antibody, 10D5, complementarity determining region, CDR; mouse; human; humanised antibody, antibody, Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
                                                                                                                                                                                                                                                  80
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                                                                                                                                                                                                                                                                     YNPSLKSRLTISKDTSRNQVVLTMTNMDPVDTATYYCARRETVFYWYFDVWGRGTPVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "light chain variable region, claimed in Claim
                                                                                                                                                                                                                                               21 OVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIRQPPGKGLEWLAHIYWDDDKR
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20. .472
/label= Mature_protein
/note= "the mature light chain is claimed in Claim
                                                                                                                                                                                                          ô
                                                                                                                                                                  2; Length 121;
                                                                                                                                                                                                          10; Indels
                                                                                                                                                               73.2%; Score 553; DB 2;
81.8%; Pred. No. 8e-44;
                                                                                                                                                                                                     12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanised 10D5 antibody heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP58289 standard; protein; 472 AA.
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.= "CDR1"
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/note= "CDR2"
119. .131
/note= "CDR3"
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N-PSDB; ABZ24639, ABZ24641.
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                                                                                                                                                     Query Match
Best Local Similarity 81.8*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
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                                                                                                                          Sequence 121 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š 121
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Homo sapiens.
Chimeric.
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31-MAR-2003
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The present sequence is the protein sequence of the heavy chain of a humanised antibody of the present invention. In the variable portion, the complementarity determining regions (CDRs) originate from murine monoclonal antibody 10D5 and the framework region originates from human germline VH segment DP-28 and J segment JH4. Novel humanised antibodies of the invention have CDRs from 10D5 and human framework sequences. These humanised antibodies have binding affinitisms (affinity and epitope location) approximately the same as those of the mouse 10D5 antibody. The invention includes antibodies, single chain antibodies, and their framements, as well as nucleotide sequences, vectors, transformed host cells, and methods of using the humanised antibody to treat, prevent, alleviate, reverse or otherwise ameliorate symptoms and/or pathology associated with Down's syndrame, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral amyloid andjopathy, and to inhibit formation or reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human-murine chimeric antibody; humanised antibody; CDR; complementarity determining region; variable heavy chain; VH; variable light chain; VL; monoclonal antibody; MAb; RSV infection; respiratory syncytial virus infection; virucide; 1129 VH; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99
humanized 10D5 antibody, useful for the manufacture of a medicament treating Down's syndrome, clinical or pre-clinical Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 SFLLLIVPAYVLSQVTLKESGPVLVKPTETLTLTCTFSGFSLSTSGMGVSWIRQPPGKAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 SLLLWISGAY -- GOVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIRQPPGKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.0%; Score 551; DB 6; Length 472; 80.9%; Pred. No. 5.5e-43; ive 5; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence for humanised antibody 1129 VH.
                          for treating Down's syndrome, clinical disease or cerebral amyloid angiopathy.
                                                                                                           Disclosure; Page 13-15; 52pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ||:|| |||||
127 DAMDYWGQGTLVTVSS 142
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RESULT 15
ADF71908
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                                                                                                                                                                                                                                                                                                                                                                                                     AHIYWDDDKRYNPSLKSRLTISKDTSRNQVVLTMTNMDPVDTATYYCARRETVFYWYFDV 130
                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                         The present invention relates to a human-murine chimeric antibody comprising a human antibody containing at least one complementarity determining region (CDR) from each of the variable heavy (WH) and variable light (WH) Chains of a non-human, preferably murine, monoclonal antibody (MAD) against respiratory syncytial virus (RSV). The humanised antibody is useful for preventing or treating a respiratory syncytial virus infection. The antibody is also useful for diagnosing RSV infection. The antibody can be injected which is preferable to prior art treatment methods involving intravenous transfusions. The present
                                                                                                                                                                                                                                                                                                                                                                              69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anti-CD16A antibody; mouse; 3G8 antibody; humanised anti-CD16A antibody; immune response; haemostatic; antirheumatic; antiarthritic; dermatological; immunosuppressive; antihiflammatory; antianaemic; vasotropic; nephrotropic; neuroprotective; antipsoriatic; uropathic; ophthalmological; antiasthmatic; inflammatory response;
                                                                                                                                                                                                                                                                                                                                                              autoimmune disease; idiopathic thrombocytopenic purpura; rheumatoid arthritis; systemic lupus erythematosus; autoimmune haemolytic anaemis; scleroderma; autoimmune haemolytic anaemis; scleroderma; autoantibody trigged urticaria; pemphigus; vasculitis syndrome; systemic vasculitis; Goodpasture's syndrome; multiple sclerosis; psoriatic arthritis; ankylosing spondylitis; Sjogren's syndrome; Reiter's syndrome; Kowasaki's disease; polymyositis; dermatomyositis;
                                                                                                                                                                                                                                                                                                                                                   LLLWISGAYGQVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIRQPPGKGLEWL
                                               New human-murine chimeric antibody useful for preventing or treating respiratory syncytial viral (RSV) infection, contains at least one complementarity determining region from a murine antibody.
                                                                                                                                                                                                                                                                                                                          1; Gaps
                                                                                                                                                                                                                                                                                                 DB 5; Length 139;
                                                                                                                                                                                                                                                                                               Score 549.5; DB 5; Length :
Pred. No. 2e-43;
5; Mismatches 19; Indels
                                                                                                                                                                                                                                               sequence represents a human-murine chimeric antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hu3G8VH-1 amino acid sequence SEQ ID NO:104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADF71905 standard; protein; 118 AA.
                                                                                                  Example 7; Fig 9; 33pp; English.
                                                                                                                                                                                                                                                                                             72.8%;
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                                                                                                                                                                                                                                                                                                                          106; Conservative
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                        WPI; 2002-673988/72.
                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                       Sequence 139 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003101485-A1.
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Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-2004
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The present invention describes an anti-CD16A antibody (I) comprising a VH domain comprising complementarity determining regions (CDRs) derived from the mouse 3G8 antibody light chain or a humanised anti-CD16A derived from the mouse 3G8 antibody light chain or a humanised anti-CD16A antibody (II) that lacks effector function and comprises all six CDRs of mouse antibody 3G8. Also described is a method (MI) for reducting a deleterious immune response in a mammal in need of such reduction, which involves administering to the mammal a CD16A binding protein comprising an FC region derived from a human IgG heavy chain, where the FC region lacks effector function or is modified to reduce binding to an FC effector ligand. (I) and (II) have haemostatic, antirheumatic, antianamenic, vasotropic, nephrotropic, nephrotropic, nephrospic, nephrotropic, nephrotropic, nephrotropic, nephrospic, nephrospic, nephrotropic, nephrospic, ne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunoglobulin (IVIG) therapy e.g., allergic asthma. The present sequence is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                              Novel anti-CD16A antibody comprising complementarity determining regions derived from mouse 3G8 antibody and humanized anti-CD16A antibody that lacks effector function, useful for treating deleterious immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 QVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIRQPPGKGLEWLAHIYWDDDKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.4%; Score 546.5; DB 8;
86.0%; Pred. No. 3.2e-43;
ive 6; Mismatches 8;
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                                                                                                                                                                                                                  Tuaillon N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12; SEQ ID NO 104; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADF71908 standard; protein; 448 AA.
30-MAY-2002; 2002US-0384689P.
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Aatches 104; Conservative
                                                                                                                             (MACR-) MACROGENICS INC
                                                                                                                                                                                                                                                                                              WPI; 2004-042985/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 S 141
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                                                                                                                                                                                                                  Johnson LS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADF71908;
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dermatological; immunosuppressive; antiintlammatory; antianaemic; vacotropic; nephrotropic; neuroprotective; antiportatic; uropathic; ophthalmological; antiasthmatic; inflammatory response; autoimmune disease; idiopathic thrombocytopenic purpura; rheumatoid arthritis; systemic lupus erythematosus; autoimmune haemolytic anaemia; scleroderma; autoimmune haemolytic anaemia; scleroderma; autoimmune haemolytic anaemia; scleroderma; systemic vasculitis; Goodpasture's syndrome; multiple sclerosis; psoriatic arthritis; ankylosing spondylitis; Sjogren's syndrome; Reiter's syndrome; Kowasaki's disease; polymyositis; dermatomyositis; allergic asthma. antirheumatic; antiarthritic; response; haemostatic; immune 

Synthetic.

Mus sp.

Homo sapiens.

WO2003101485-A1

11-DEC-2003

29-MAY-2003; 2003WO-US017111.

30-MAY-2002; 2002US-0384689P 10-JAN-2003; 2003US-0439320P

(MACR-) MACROGENICS INC

Tuaillon N; Li H, Johnson LS, Huang L,

WPI; 2004-042985/04.

Novel anti-CD16A antibody comprising complementarity determining regions derived from mouse 3G8 antibody and humanized anti-CD16A antibody that lacks effector function, useful for treating deleterious immune response.

Disclosure; SEQ ID NO 107; 103pp; English

The present invention describes an anti-CD16A antibody (I) comprising a VH domain comprising complementarity determining regions (CDRs) derived from the mouse 3G8 antibody heavy chain and a VL domain comprising CDRs derived from the mouse 3G8 antibody light chain or a humanised anti-CD16A antibody (II) that lacks effector function and comprises all six CDRs of mouse antibody 3G8. Also described is a method (MI) for reduction, which involves administering to the mammal a CD16A binding protein comprising an Fc region derived from a human 1gG heavy chain, where the Fc region an Fc region derived from a human 1gG heavy chain, where the Fc region confirm thritic, dermatological, immunosuppressive, antiinflammatory, antianthritic, dermatological, immunosuppressive, antiinflammatory, antianaemic, vasotropic, nephrotropic, neuropachic, antiinflammatory, antianaemic, vasotropic, nephrotropic, neuropachic, antiinflammatory curopathic, ophthalmological and antiasthmatic activities. (I) or (II) is useful for reducing a deleterious immune response in a mammal which involves administering to the mammal (I) or (II). The deleterious immune disease such as idionathic thrombocutopenic minimum of is the particle of the particle o idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA), systemic lupus erythematosus (SLE), autoimmune haemolytic anaemia (AHA), scleroderma, autoantibody trigged urticaria, pemphigus, vasculitis syndrome, systemic vasculitis, Goodpasture's syndrome, multiple sclerosis (MS), psoriatic arthritis, anakylosing spondylitis, Sjogren's syndrome, Reiter's syndrome, Kowasaki's disease, polymyositis and dermatomyositis .mmunoglobulin (IVIG) therapy e.g., allergic asthma. The present sequence is used in the exemplification of the present invention. and also for treating diseases susceptible to treatment with intravenous

Sequence 448 AA;

21 QVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIRQPPGKGLEWLAHIYWDDDKR 80

72.4%; Score 546.5; DB 8; 86.0%; Pred. No. 1.4e-42; ive 6; Mismatches 8;

Gaps ë

Indels

Length 448;

ANTHONY STREET, CROSSING 81 YNPSLKSRLTISKDISRNQVVLTWINMDPVDTATYYCARRETVFYWYFDVWGRGTPVTVS 140 117 61 YNPALKSRLTISKDTSKOVOVLTWTNMDPVDTATYYCARINPAWFAY----WGQGTLVTVS 1 QVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVGWIRQPPGKALEWLAHIWWDDDKR S 141 S 118 118 141 ò d ઠ 셤

completed: February 23, 2006, 09:18:03 Job time : 137.298 secs Search

Query Match
Best Local Similarity 86.0°
Matches 104; Conservative

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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
                    Copyright
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OM protein - protein search, using sw model

February 23, 2006, 09:18:23 ; Search time 24.8824 Seconds (without alignments) 545.228 Million cell updates/sec Run on:

1 MVLQTQVFISLLLWISGAYG......TVFYWYFDVWGRGTPVTVSS 141 US-10-723-872-12 755 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_80:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARIES

SUMMARIES		3	2 Ig heavy chain V	Ig heavy	Ig heavy chain V-	Ig heavy	Ig heavy chain	Ig heavy chain	Ig heavy chain V	Ig heavy chain V-	Ig heavy chain V	9I	Ig heavy	Ig heavy	Ig heavy chain	Ig heavy	Ig heavy	gi	Ig heavy	Ig heavy	Ig heavy chain V	Ig heavy	Ig heavy	Ig heavy ch	Ig heavy	2 Ig variable	19 Ig heavy ch	11 Ig	12 Id heavy chain -
ß	a .	S3151	A49002	A36005	GTHUCO	PT017	S11740	S18555	8693	MHHO	GIHUHE	826465	S18556	G2HU	S26923	\$26924	S263	809959	MHHUOU	A49442	826922	GIHUDM	B2591	809711	831690	13778	13	8315	3
	DB	7						7																					
	Query Match Length	138	124	121	120	143	122	119	374	125	121	113	118	147	96	96	116	121	126	107	96	119	103	146	130	140	147	155	155
dp	Query Match		68.3	67.4	0.99	65.4	65.2	64.2	64.0	63.0	6.09		60.7					57.4				54.7				49.7		49.1	
	Score	523	15	509	ω	93	N	В	m	476	460	458.5	458	455	448	448	445.5	433	425.5	423	417	413	396	379	78	75	2	370.5	89
	Result No.		7	٣	4	2	9	7	œ	6	10	11	12	13	14			17	18	19	20	21	22	23	24	25	26	27	28

Ig heavy chain V region, rheumatoid factor RF antibody - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Abecies: Homo sapiens (man)
C;Accession: A49002
R;Stuber, F.; Lee, S.K.; Bridges Jr., S.L.; Koopman, W.J.; Schroeder, H.W.J.; Gaskin, F.Athritis Rheum. 35, 900-904, 1992
A;Title: A rheumatoid factor from a normal individual encoded by VH2 and V kappa II gene A;Reference number: A49002; WUID:92352481; PMID:1322670

A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-124 <STUJ
A;Cross-references: UNIPARC:UP10000176978; GB:M90808; NID:9185515; PIDN:AAA52989.1; PID
A;Experimental source: EBV-transformed lymphoblastoid cell line SSH23

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Ig gamma-2b chain	Ig heavy chain V r	Ig heavy chain pre	Ig heavy chain pre	Ig heavy chain pre	Ig heavy chain V r	Ig heavy chain pre	Ig heavy chain pre	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V r	5	Ig heavy chain pre	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V r
PC4155	S30534	A32456	A41287	PL0100	830530	G2MS14	S78055	S44114	S31676	820809	S54226	S78051	S44113	809710	846461
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231	130	139	139	135	123	144	145	129	137	122	141	135	121	146	78
48.7	48.5	48.4	48.3	47.2	47.0	47.0	47.0	47.0	46.9	46.8	46.8	46.7	46.6	46.6	46.5
368	366.5	365.5	365	356.5	355	355	355	354.5	354	353.5	353.5	352.5	352	351.5	351
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

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Ig heavy chain - human
Cispecies: Homo sapiens (man)
Cipate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
Cipates: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
Cipatession: 831813
Richastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
Submitted to the EMBL Data Library, December 1992
A; Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autc
                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPARC:UP100001160FA; EMBL:X69861; NID:g33084; PIDN:CAA49495.1; PIIC (S.Querfenanily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin homology cIMM> F;30-114/Domain: immunoglobulin homology cIMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 PGKGLEWLAHIYWDDDKRYNPSLKSRLTISKDTSRNQVVLTMTNMDPVDTATYYCARRE- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 PGKTLEWLALIYWDDDKRYSPSLKSRLTITKDTSQNQVVLTWTNMDPVDTATYYCAHRPG 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 LOTQVFISLLLWISGAYGQVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIRQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
69.3%; Score 523.5; DB 2; Length
Best Local Similarity 72.9%; Pred. No. 1.3e-39;
Matches 102; Conservative 13; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 -TVFYWYFDVWGRGTPVTVS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 IAVTGGNFDYWGQGTLVTVS 137
                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-138 < CHA>
                                                                                                                                                                                                                                         A; Accession: S31513
A; Status: preliminary
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Gaps

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Indels

Length 120;

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YNPSLKSRLTISKDISRNQVVLTMINMDPVDTATYYCARRETV--FYWYFDVWGRGTPVT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YMTSLETRLTISKDISRNOVVLI---MDPVDIATYYCARITVIPAPAGYMDVWGRGTPVT 117
                                                          A;Cross-references: UNIPROT: P01815; UNIPARC: UP1000012CEE9
C;Comment: This chain was isolated from an IgG1 myeloma protein.
C;Genetics:
C;Genetics:
A;Gene: GDB:IGHV@
A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 OVILRESGPALVKPIQILILICIFSGFSLSSTGMCVGWIRQPPGKGLEWLARIDWDDDKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 66.0%; Score 498.5; DB 1; Best Local Similarity 81.3%; Pred. No. 1.8e-37; Matches 100; Conservative 5; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 ---FDVWGRGTPVTVSS 141
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Matches 98; Conserv
                                             <PRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 VSS 141
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Ig heavy chain V region (M60) - human
C; Species: Howe sapiens (man)
C; Date: 21-Dec-1990 # sequence_revision 13-Sep-1991 #text_change 16-Dec-1998
C; Accession: A36005
R; Schroeder Jr., H.w.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A; Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene A; Reterence number: A36005; MUID: 90349571; PMID: 2117273
A; Accession: A36005
A; Status: preliminary
A; Mocession: A36005
A; Status: preliminary
A; Residues: 1-121 ASGNS
A; Accession: A36005
A; Status: Desiminary
A; Coss-references: UNIPARC: UPI0000176977; GB: M34027
C; Genetics:
A; Gene: GDB: IGHDY1
A; Cross-references: GDB: 118731; OMIM: 146910
A; Cross-references: GDB: 118731; OMIM: 146910
A; Muap position: 14432.33 - 14432.33
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 15-99/Domain: immunoglobulin homology < INMA>
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G1HUCO
IG heavy chain V-II region (Cor) - human (tentative sequence)
G1HUCO
IS pecies: Homo sapiens (man)
G1Species: Homo sapiens (man)
G1Species: A3-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
G1Species: A3-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
G1Species: B.M.; Hogg, N.M.
Biochem. J. 117, 641-660, 1970
Biochem. J. 117, 641-660, 1970
A;Reference number: A90250; MUID:70258837; PMID:5449120
A;Accession: A02089
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A;Note: sequence extracted from NCBI backbone (NCBIN:110261, NCBIP:110262) (S.byperfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-99/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                  Score 515.5; DB 2
Pred. No. 5.9e-39;
                                                                                                                                                 68.3%; sv. 78.2%; Pred. No. ... 12; Mismatches
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Matches 100; Conservative 5; Mismatches
                                                                                                                                                            Query Match
Best Local Similarity 78.2*
Matches 97; Conservative
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Ig heavy chain precursor V region (IdBS.7) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996
C;Accession: Pr0174
R;Perfetti, V.; Borden, P.; Tao, M.H.; Morrison, S.L.; Kabat, E.A.
A;Perfetti, V.; Specificity and variable region cDNA sequence of an isogeneic monoclonal antiid.
A;Reference number: Pr0174; MUID:91287738; PMID:1712074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EWLAHISWDDDNLYNPSLKSRLTISKDTSRNOVFLKITSVDTADTATYYCARRERGYGNY 126
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                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-143 < PRR>
A; Cross-real neues: UNIPARC: UP10000176976
A; Experimental source: strain BALB/c
C; Comment: IdBs.7 is an antibody to anti-alpha (1-6) dextran.
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heteroteramer; immunoglobulin
F;34-118/Domain: immunoglobulin homology < IMM>
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811740
18 heavy chain precursor V-D-J region - mouse (fragment)
C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65.4%; Score 493.5; DB 271.5%; Pred. No. 6.2e-37; ive 13; Mismatches 21
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Ig heavy chain V-II region (MCE) - human C; Species Homo sapiens (man) C; Species Homo sapiens (man) C; Species Homo sapiens (man) C; Species Homo val983 #sequence_revision 22-Nov-1983 #text_change 09-Jul-2004 C; Accession: A02092 R; Accession: A02092 R; Accession: A02092 R; Azin, A.; Kehoe, J.M.; Scheffel, C.; Erickson, B.W.; Litman, G.W. A; Tittle: Molecular basis for the temperature-dependent insolubility of cryoglobulins. X A; Reference number: A02092; MUID:81118242; PMID:6780622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 QPPGQALEWLALIFWDDDKRYSPSLRTRLTITKDTSKNQVVLTMTNVDPADTATYYCGYS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 ILCSTLLLLITIPSWV---LSQITLKESGPTLVKPTQTLTLTCTFSGFSLSKSGVGVMIR
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A;Gene: GDB:128528; OMIM:147070
A;Cross-references: GDB:128528; OMIM:147070
A;Map position: 14632.33-14632.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin; pyroglutamic acid
F;15-99/Domain: immunoglobulin homology <IMM>- Fils-99/Domain: ammunoglobulin homology <IMM-- Fils-99/Domain homology <IMM
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A,Rebidues: 1-15 cGER
A,Cross-references: UNIPROT:P01817; UNIPARC:UPI000012CEED
A,Note: this chain was derived from a monoclonal IgM cryoimmunoglobulin
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 «KHA»
A;Cross-references: UNIPARC:UPI0000176F24; EMBL:X81695
A;Cross-references: UNIPARC:UPI0000176F24; EMBL:X81695
R;Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: $72664
A;Accession: $72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140. (C',142-374 «KH2»
A;Cross-references: UNIPARC:UPI0000176F25; EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.0%; Score 483.5; DB 2; Length 374; 64.3%; Pred. No. 1.3e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : | ||||| ||1111
120 VEGYGQGYRFHSWGQGTLVTVSS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92; Conservative
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Matches 9
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                                        C; Accession: $11740
F; Hayakawa, K.; Carmarck, C.E.; Hyman, R.; Hardy, R.R.
submitted to the ENBL Data Library, May 1990
A; Description: Natural autoantibodies to thymocytes: Origin, VH genes, fine specificitie
A; Reference number: $11740
A; Reference number: $11740
A; Residues: 1-122 < EMBA
A; Residues: 1-122 < EMBA
A; Residues: 1-121 < EMBA
A; Cross-references: UNIPARC: UPI000011D0BS; EMBL: X53097; NID: G52368; PIDN: CAA37261.1; PID
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 22-106/Domain: immunoglobulin homology < IMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CiAccession: 818555
Rishin, E.K.; Mateuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H
Rishin, E.K.; Mateuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H
REGO J. 10, 31611-31645, 1991
A; Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A; Reference number: 818551; MUD:92037524; PMID:1935893
A; Accession: 818555
A; Molecule type: DNA
A; Residues: 1-119 <SHI>
C; Gross references: UNIPARC:UPI0000115FEF; EMBL:X62111; NID:g37839; PIDN:CAA44021.1; PIE
C; Genetics:
A; Introns: 16/1
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C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S63339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Bur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease. A;Reference number: S69339; MUID:95262687; PMID:7744049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Species: Homo sapiens (man)
Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 21-Jul-2000
            Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 QVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIRQPPGKGLEWLAHIYWDDDKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 YNPSLKSRLTISKDTSRNQVVLTMTNMDPVDTATYYCARRETVFYWYFDVWGRGT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <MAT>
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;Neywords: heterotetramer; immunoglobulin
;1-19/Domain: signal sequence #status predicted <SIG>
;20-119/Product: Ig heavy chain V region (VII-5) #status predicted ,34-118/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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80.0%; Pred. No. 6.4e-37;
ive 11; Mismatches 11
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Local Similarity 77.6%; Pred. No. 3.2e-36;
hes 90; Conservative 12; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          llarity 80.0%;
Conservative 1
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tes 92; Conserv
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Best Local S:
Matches 92
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Ig heavy chain V region precursor (VII-5b) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C;Accession: 818556
R;Shin, B.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; I BMBO J. 10, 3641-3645, 1991
A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: Cl. A;Reference number: $18551; MUID:92037524; PMID:1935893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: A02090
R;Takahashi, N.; Noma, T.; Honjo, T.
Proc. Natl. Acad. Sci. U.S.A. 81, 5194-5198, 1984
A;Title: Rearranged immunoglobulin heavy chain variable region (V-H) pseudogene that dell A;Reference number: A02090; MUID:84298107; PMID:6089186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPARC:UP10000115FEC; EMBL:X62108; NID:937840; PIDN:CAA44018.1; PID
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as Trp, TGG for residue 142
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A;Gene: GDB:ISB528; OMIM:147070
A;Gene: GDB:ISB528; OMIM:147070
A;Rup position: 14q32.33-14q32.33
A;Introns: 15/3
A;Introns: 15/3
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>F;20-147/Product: igneavy chain V-II region (Gess) #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Species: Homo sapiens (man)
C.Date: 17-Mar 1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ajintrons: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Styvords: heteroterramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-118/Product: Ig heavy chain V region (VII-5b) #status predicted <MAT>
F;34-116/Domain: immunoglobulin homology <IPM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 60.7%; Score 458; DB 2; Length 118; Best Local Similarity 75.9%; Pred. No. 7.2e-34; Matches 88; Conservative 10; Mismatches 14; Indels
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67.7%; Pred. No. 1.7e-33;
ive 10; Mismatches 25; Indels
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A,Molccule type: mRNA
A,Residues: 1-147 <1AAx
A,Cross-references: UNIPROT:P04438; UNIPARC:UPI000012CEF0
A,Note: the sequence was determined from the differentiated
A,Note: the authors translated the codon GGG for residue 16
as Ser, and CAG for residue 147 as Ser
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F;133-147/Region: J segment
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                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-118 <SHI>
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Best Local S:
Matches 90
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S26465
Ig heavy chain V region - mouse
C;Species: Wus musculus (house mouse)
C;Decies: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S26465
R;Kavaler, J.
submitted to the EMBL Data Library, April 1991
A;Reference number: S2645
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <KNA
A;Residues: 1-13 <KNA
A;Residues: UNIPARC:UPIO000115F69; EMBL:X59115; NID:g51928; PIDN:CAA41841.1; PIC
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;6-90/Domain: immunoglobulin homology <IMM>
                                   In heavy chain V-II region (He) - human
C;Species: Homo sapiens (man)
C;Species: O7-May-1881 #sequence_revision 07-May-1981 #text_change 09-Jul-2004
C;Accession: A02093
R;Cunningham, B.A.; Pflumm, M.N.; Rutishauser, U.; Edelman, G.M.
Proc. Natl. Acad. Sci. U.S.A. 64, 997-1003, 1969
A;Tille: Subgroups of amino acid sequences in the variable regions of immunoglobulin hea
A;Reference number: A02093
A;Molecule type: procein
A;Residues: 1-121 cCUN>
A;Coment: This gamma-1 chain was isolated from a myeloma protein.
C;Genetics:
A;Genetics:
A;Geneti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 QVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIRQPPGKGLEWLAH-IYWDDDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 60.9%; Score 460; DB 1; Length 12: Best Local Similarity 71.0%; Pred. No. 4.9e-34; Matches 88; Conservative 15; Mismatches 15; Indels
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11 LLLWI-SGAYGQVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIRQPPGKGLEW
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Length 147;
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Ig heavy chain V region (DP-28) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: $26924
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A;Title: The repertoire of human germine V(H) sequences reveals about fifty groups of V
A;Reference number: $26985, MUID: 93021117; PMID: 1404388
A;Accession: $25624
A;Accession: $25624
A;Accession: $26924
A;Accession: $26924
A;Residues: 1-96 <TOM>A;Residues: 1-96 <TOM
A;Residues: 1-98 <TOM
A;Residues: 1-98 <TOM
A;Resid
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Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
Ciscossion: S26923
Ritcher S26923
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of VARCession: S26923
A;Accession: S26923
A;Accession: S26923
A;Accession: S26923
A;Accession: S26923
A;Cosser-references: VIDIDARC: UPID0000116404; EMBL: Z12329; NID: g32875; PIDN: CAA78199.1; PIC
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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                                           69 LARIDWDDDKYYGTSLETRLTISKDTSKNOVVLKVTNMDPADTATYYCARMOVTMVREVM 128
70 LAHIYWDDDKRYNPSLKSRLTISKDTSRNQVVLTMTNMDPVDTATYYCARRETVFYW--- 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 QVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIRQPPGKGLEWLAHIYWDDDKR 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVILKESGPALVKPTQILTLICTFSGFSLSTSGMCVSWIRQPPGKALEWLALIDWDDDKY 60
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Pred. No. 4.5e-33;
4; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 YNPSLKSRLTISKDTSRNQVVLTMTNMDPVDTATYY 116
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Pred. No. 4.5e-33;
3; Mismatches 6
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Job time : 25.8824 secs
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Best Local Similarity 89.6%;
Matches 86; Conservative
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Best Local Similarity 90.6%;
Matches 87; Conservative
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129 ITSNAFDIWGQGT 141
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S26924
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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09U196 HUMAN
0569B3_RAT
0561M5_MOUSE
HV2B_HUMAN
HV2B_HUMAN
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HV2E_HUMAN
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Q58E54 MOUSE

G5VLR6—RAT

HV2A HUMAN

G043124 HUMAN

G043124 HUMAN

G05911 RAT

G10J1 RAT

G10J2 HUMAN

G10J3 HUMAN

G10J3 MOUSE

G59813 HUMAN

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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QS61MS;
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TISSUE=Spleen;
NCBI_TaxID=10116;
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                                                       Defens RAT PRELIMINARY; PRT; 617 AA.
0569B3;
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
10-MAY-2015 (TrEMBLrel. 30, Last annotation update)
11-MAY - 2015 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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Local Similarity 80.2%; Pred. No. 4.2e-44;
nes 97; Conservative 10; Mismatches 14; Indels
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ENEL, AFO35018; AAD56254.1; -; mRNA.
HSSP; P01820; 1A7N.
SNR; Q9U1.96; 1-121.
Ensembl; ENSG0000130076; Homo sapiens.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003596; Ig-v.
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124 WNAFDIWGQGTMVTVSS 140
                                                                                                                                                                                          125 YWYFDVWGRGTPVTVSS 141
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68 EWLAHIYWDDDKRYNPSLKSRLTISKDTSRNQVVLTMTNMDPVDTATYYCARRETV-FYW 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 SFLLLIVPAYVLSQVTLKESGPGILQPSQTLSLTCTFSGFSLSTYGMGVGWIRQPSGKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 SLLLWISGAY--GOVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIRQPPGKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APP-2005) to the EMBL/GenBank/DDBJ databases.

EMBL; BC09286; AAH92586.1; -; mRNA.

GO, GO.0003823; F.antigen binding; IEA.
InterPro; IPR003109; Ig.
InterPro; IPR003110; Ig-like.
InterPro; IPR003309; Ig.
InterPro; IPR003309; Ig.
InterPro; IPR00359; Ig.
InterPro; IPR003596; Ig.
InterPro; IPR003596; Ig.
InterPro; IPR003596; Ig.
InterPro; IPR00409; IG.
InterPro; IPR00409; IG.
InterPro; IPR00409; IG.
InterPro; IPR00409; IG.
InterPro; IRR0409; IG.
INTERPROSITE; PS00309; IG.
INTERPROSITE; PS003099; IG.
INTERPROSITE; PS00309; IG.
INTERPROSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (APR-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
10-MAY-2005 (TremBlrel. 30, Last annotation update)
Mame=LOC238447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.4%; Score 508.5; DB 2; 72.6%; Pred. No. 1.2e-42; ive 12; Mismatches 22;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVTLRESGPALVKPTQTLTLTCTFSGFSLSSTGMCVGWIRQPPGKGLEWLARIDWDDDKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 YNPSLKSRLTISKDISRNQVVLTMINMDPVDIATYYCARRETV--FYWYFDVWGRGTPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 QVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIRQPPGKGLEWLAHIYWDDDKR
                                                                                                                                                                                                            "The amino acid sequences of the Fd fragments of two human gamma-1
                                                                                                                                                                                                                                                                                               protein.
-!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
                                                                                                                                                                                                                              heavy chains.";
Biochem. J. 117:641-660(1970).
-!- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-like.
InterPro; IPR003596; IG_V.
SMART; SM0406; IGV; I.
PROSITE; PSS0835; IG_LIKE; I.
Direct protein sequencing; Glycoprotein; Immunoglobulin domain; Immunoglobulin V region; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.0%; Score 498.5; DB 1; Length 120; 81.3%; Pred. No. 2e-42; ive 5; Mismatches 13; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .2,
2e-42;
-hes 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyrrolidone carboxylic acid. N-linked (GlcNAc. . .).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 AA; 13226 MW; 158A8B29AE7EEB98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10 heavy chain V-II region MCE.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig-like.
                                                                                                                                                                     MEDLINE=70258837; PubMed=5449120;
  chain V-II region COR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                         Press E.M., Hogg N.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1
62
94
                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A02089; G1HUCO.
HSSP; P01820; 1A7N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                            [1]
PROTEIN SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1] T
PROTEIN SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 VSS 120
                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 VSS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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MOD RES
CARBOHYD
DISULFID
NON TER
SEQUENCE
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  g
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                                                                                                               TISSUB-Mammary tumor. WAP-TGF alpha model. 7 months old;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Astausberg R.L.; Feingold E.A.; Grouse L.H., Derge J.G.;

Altschul S.F.; Zeeberg B., Buschow K.H., Schaefer C.F.; Bhat N.K.;

Altschul S.F.; Zeeberg B., Buschow K.H., Schaefer C.F.; Bhat N.K.;

Hopkins R.F.; Jordan H., Moore T., Max S.I.; Wang J., Heileh F.;

Astachench L., Marusina K.F.; Farmer A.A.; Rubin G.M.; Hong L.,

Brownstein M.J.; Usdin T.B.; Toshiyuki S., Carninci P., Prange C.;

A Raha S.S., Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.;

Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;

Richards S., Worley K.C., Hale S., Garcia A.M.; Gay L.J.; Hulyk S.W.;

A Whiting M., Madan A.; Young A.C.; Shevchenko Y., Bouffard G.G.;

Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;

Butterfield Y.S.N.; Krzywinski M.I.; Skalaka U.; Smailus D.E.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 SLLLWISGAY - - GQVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIRQPPGKGL
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 66.4%; Score 501.5; DB 2; Length Best Local Similarity 72.3%; Pred. No. 4.8e-42; Matches 99; Conservative 12; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC093517, AAH93517.1; -; mRNA.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig. Ig.
InterPro; IPR003597; Ig. C1.
InterPro; IPR003506; Ig. MRC.
InterPro; IPR003506; Ig. WRC.
InterPro; IPR003596; Ig. V.
Pfam; PF07654; C1-8et; Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             485 AA; 52570 MW; E28F4BB70DAF828A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences."; -
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
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SMART; SM00407; IGc1; 3.
SMART; SM00406; IGC1; 3.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 YYAMDYWGQGTSVTVSS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                   Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Mix FVB/N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH MGC Project;
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21-JUL-1986 (
21-JUL-1986 (
10-MAY-2005 (
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RESULT 5 HV2B\_HUMAN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 YNPSLKSRLTISKDISRNQVVLTMTNMDPVDTATYYCARRETVFYWYFDVWGRGTPVTVS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YNPALKSRLTISKDTSSNQVFLKIASVDTADTATYYCAQINPAWPAY---WGGGTLVTVS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVTLXESGPGILQPSQTLSLTCSFSGFSLRTSGMGVGMIRQPSGKGLEWLAHIWWDDDKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 QVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIRQPPGKGLEWLAHIYWDDDKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cunningham B.A., Pflumm M.N., Rutishauser U., Edelman G.M.; Cunningham B.A., Pflumm M.N., Rutishauser U., Edelman G.M.; "Subgroups of amino acid sequences in the variable regions of immunoglobulin heavy chains."; Proc. Natl. Acad. Sci. U.S.A. (4:997-1003(1969).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
and FcgammaRIII (CD16) triggers effective lysis of lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                         1 1
118 118
118 AA; 12979 MW; F57BB07033742E99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.0%; Score 460.5; DB 2; 70.2%; Pred. No. 1.3e-38; tive 17; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A02093; GIHUHE.
HSSP; P01820; 1A7N.
GO; GO: 0005576; C: extracellular region; NAS.
GO; GO: 0003823; F: antigen binding; NAS.
GO; GO: 0006955; P: immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR00356; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 AA
                                                     Br. J. Haematol. 125:167-179(2004).
EMBL; AX173025; AA018227.1; -; mRNA.
HSSP; P01800; 1A7N.
SMR; OB1105; 1-118.
Ensembl; ENSMUSG0000057010; Mus musculus.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR007110; Ig-like.
InterPro; IPR005396; Ig-v.
SWART; SM00406; IGV:
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PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50835; IG LIKE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 70.28
Matches 85; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           Receptor.
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RAT TAKE THE CONTRIBUTION OF THE CONTRIBUTION 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                  This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 YNPSLKSRLTISKDISRNOVVLTMINMDPVDTATYYCARRETVFYWY-----FDVWGR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 OITLKESGPTLVKPTETLTLTCTPSGFSLSTSGVGVGWIRQRPGKALEWLAPINWDDDNR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annocation update)
Anti-human Fc gamma receptor III 3G8 gamma heavy chain variable region
                                                                                                                        cryoglobulins. X. The amino acid sequence of the heavy chain variable region of MCE.";
J. Immunol. 126:1212-1216(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 QVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIRQPPGKGLEWLAHIYWDDDKR
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DubMed=15059139; DOI=10.1111/j.1365-2141.2004.04893.x; Bruenke J., Fischer B., Barbin K., Schreiter K., Wachter Y., Mahr K., Titgemeyer F., Niederweis M., Peipp M., Zunino S.J., Repp R., Valerius T., Fey G.H.; Walerius T., Fey G.H.; "A recombinant bispecific single-chain Fv antibody against HLA class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                          Gerber-Jenson B., Kazin A., Kehoe J.M., Scheffel C., Brickson B.W.,
                                                                                                                                                                                                                                                           cryoimmunoglobulin.
-!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
                                                                                                                                                                                                                          -!- MISCELLANEOUS: This chain was derived from a monoclonal IgM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                       "Molecular basis for the temperature-dependent insolubility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.0%; Score 476; DB 1; Length 12771.9%; Pred. No. 3.9e-40; ... wiematches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pyrrolidone carboxylic acid
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PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region; Pyrrolidone carboxylic acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO: 0005576; C: extracellular region; NAS. GO: 00013823; F: antigen binding; NAS. GO: 0006955; P: immune response; NAS. InterPro; IPR007110; IG-11ke.
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MEDLINE=81118242; PubMed=6780622;
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92; Conservative
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Q811US;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTLVTVSS 125
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Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; P01820; 1A7N.
P01817; 1-125.
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REDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

REDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

REDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

REDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Liacher R.D., Colling F.S., Magner L., Shenmen C.M., Schuler G.D.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rab S., Loquellano M.B., Roaldo M.F., Casavant T.L., Scheetz T.E.,

Rah S.S., Loquellano M.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Roals S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Nillalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Richards S., Worley M., Sodergen B.J., Lu X., Gibbs R.A.,

Richards A., Youchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Retreffield Y.S., N. Krzywinski M.I., Skalska U., Smailus D.E.,

Ruberteffield Y.S., N. Krzywinski M.I., Skalska U., Smailus D.E.,

Ruberteffield Y.S., N. Krzywinski M.I.; Skalska U., Smailus D.E.,

Rubenertic A., Schein J.E., Jones S.J.M., Marra M.A.;

Redenertion and initial analysis of more than 15,000 full-length human
                                                                                                           69 LARIDWDDDKYYGTSLETRLTISKDTSKNQVVLKVTNMDPADTATYYCARMQVTMVREVM 128
                          9 LLLTVPSGVLSQVNLRESGPALVKATHTLTLTCTFSGLSVNTRGMSVSWIRQPPGKALEW
                                                                                  70 LAHIYWDDDKRYNPSLKSRLTISKDTSRNQVVLTMTNMDPVDTATYYCARRETVFYW---
  11 LLLWI-SGAYGQVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIRQPPGKGLEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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InterPro; IPR003006; Ig-like.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003596; Ig-WHC.
InterPro; IPR003596; Ig-WHC.
InterPro; IPR00409; IG; 3.
SWART; SW00409; IG; 3.
SWART; SW00406; IGv; 1.
PR05ITE; PS00299; IG MHC; UNXCWN 2.
PR05ITE; PS00290; IG MHC; UNXCWN 2.
SEQUENCE 485 AA; 52383 MW; 44087147CE49A50B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH MGC Project;
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO92065; AAH92065.1; -; mRNA.
GO; GO:0003823; F:antigen binding; IEA.
                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Pred. No. 2.5e-36;
                                                                                                                                                                                                                                                                                                                      485 AA
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STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                   127 ----YFDVWGRGT 135
                                                                                                                                                                                                             129 ITSNAFDIWGQGT 141
                                                                                                                                                                                                                                                                                                                    QSBES4_MOUSE PRELIMINARY;
QSBES4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
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NUCLEOTIDE SEQUENCE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                      21 QVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIRQPPGKGLEWLAH-IYWDDDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                            60.9%; Score 460; DB 1; Length 121; larity 71.0%; Pred. No. 1.6e-38; Conservative 15; Mismatches 15; Indels
                                                            Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PSS0835; IG LIKE; 1.
[mmunoglobulin domain; Immunoglobulin V region; Signal.
                                                                              121 AA; 13483 MW; 88A5082C273753B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16323 MW; FCBCDB3D00FB6666 CRC64;
                    Immunoglobulin V region, Pyrrolidone carboxylic acid.
DOMAIN 1 120 Ig-like.
Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
IIG heavy chain V-II region SESS precursor.
Homo sapiens (Human).
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J segment.
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Direct protein sequencing;
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Best Local Similarity 67.7
Matches 90; Conservative
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PROSITE; PS50835; IG LIN
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HSSP; P01820; 1G7I.
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133
147
147 AA;
                                                                                                                                          Query Match
Best Local Similarity
Matches 88; Conserv
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58.5%; Score 442; DB 2; Length 487; 64.2%; Pred. No. 5.1e-36; ive 19; Mismatches 24; Indels
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                              128 F---DVWGRGTPVTVSS 141
                                                                                                                                                                                                                                                                                                                                                              126 FHALDNWGPGTSVTVSS 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-2005 (TrEMBLrel. 29, 01-FEB-2005 (TrEMBLrel. 29, 01-FEB-2005 (TrEMBLrel. 29,
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LFDYWGQGVMVTVSS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 65.2% datches 88; Conservative
                                                     88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OSVLR6 RAT PRELIMINARY;
QSVLR6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116,
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  Query Match
Best Local (
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                                                     Matches
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WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausher R.D., Collins F.S., Wagner L., Schaefer C.F., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenco L., Marusina K.R., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M.J. Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Brownstein M.J., Workernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahesley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Brownstein A.M. Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                              EWLAHIYWDDDKRYNPSLKSRLTISKDTSRNQVVLTMTNMDPVDTATYYCARRETVFYWY 127
                                                                             7 SFLLLIVPAYVLSQVTLXESGPGILQPSQTLSLTCSFSGFSLSTYGIGVGWIRQPSGKGL 66
                                                SLLLWISGAY -- GQVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIRQPPGKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Mutidae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (WAR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC092066; AAH92066.1; -; mENA.
CO; GO:003823; F:antigen binding; IEA.
InterPro; IPR003110; Ig-like.
InterPro; IPR0031006; Ig-MrC.
InterPro; IPR003006; Ig-MrC.
InterPro; IPR003596; Ig-V.
F Ffam; PF07644; Cl-set; Z.
SMART; SM00409; IG; 3.
SMART; SM00409; IG; Mr; UNKNOWN 2.
SROUENCE 487 AA; 52616 MW; 835B85363A764CFI CRC64;
  27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
  18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                           FDVWGRGTPVTVSS 141
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NIH MGC Project;
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Q58E53;
  87; Conservative
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10.885 MUS T
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68 EWLAHIYWDDDKRYNPSLKSRLTISKDTSRNQVVLTMTNMDPVDTATYYCARRETVFYWY 127
                                                                                                                                                                                       68 EWLAHIYWDDDKRYNPSLKSRLTISKDTSRNQVVLTMTNMDPVDTATYYCARR-ETVFYW 126
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                                                                                 7 SFLLLIVPAYVLSQVTLKESGPGILQPSQTLSLTCSVSGFSLTTFGLGVGWIRQPSGKGL
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                                                     10 SLLLWISGAY--GQVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIRQPPGKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukamalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Rattus.
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Gaps
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xoami, X. Yamakita S., Irino T., Osaka M.;

Koami, Y. Yamakita S., Irino T., Osaka M.;

Koami, Y. Yamakita S., Irino T., Osaka M.;

Koami, CCT-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AVIS8661; AAO17784.1; -; mRNA.

SNR; Q5VLR6; 251-460.

R Q5; G0:003823; F:antigen binding; IEA.

R InterPro; IPR003110; Ig-1ike.

R InterPro; IPR003599; Ig cl.

R InterPro; IPR003599; Ig cl.

R InterPro; IPR003599; Ig cl.

R InterPro; IPR003596; Ig v.

R SNART; SN00409; IG, 3.

R SNART; SN00409; IG cl. 3.

R SNART; SN00409; IG cl. 3.

R SNART; SN00409; IG LIKE; 4.

R PROSITE; PS50835; IG LIKE; 4.

R PROSITE; PS50835; IG LIKE; 4.

R PROSITE; PS60835; IG LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.1%; Score 438.5; DB 2; Length 65.2%; Pred. No. 1.1e-35; ive 16; Mismatches 28; Indels
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P01814;
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-!- MISCELLANEOUS: This chain was obtained from IgG1 isolated from the serum of a patient with hypergammaglobulinemia.
-!- SIMILARITY: Contains 1 Ig-like (Immunoglobulin-like) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 TLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIRQPPGKGLEWLAHIYWDDDKRYN
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                                                             Borretzen M., Natvig J.B., Thompson K.M.;
"Heterogenous RF structures between and within healthy individuals
mot related to HLA DRB1*40401.";
Mol. Immunol. 0:0-0(1997).
EMB1. APGS8802; AAB88534.1; -; mRNA.
HSSP; PO1820; LGTI.
SWR; O43234; 1-96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Press E.M., Hogg N.M.; "The amino acid sequences of the Fd fragments of two human gamma-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 422; DB 2; Lengu...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 AA; 10748 MW; DDC0BF47B9AA812D CRC64;
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SMART, SMO0406, IG LIKE, 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 PSLKSRLTISKDTSRNQVVLTMTNMDPVDTATYYCAR 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TSLKSRLTISKDTSKSQVVLTMTNMDPMDTATYYCAR
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tive 10; Mismatches
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GO; GO:0005576; C:extracellular region;
GO; GO:0003823; P:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
                                                                                                                                                                                                                                                          Ensembl; ENSG0000196662; Homo sapiens.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=70258837; PubMed=5449120;
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        [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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10-MAY-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                           Science 182:287-291(1973).
-!- MISCELLANEOUS: This mu chain was isolated from a Waldenstrom's
                                                                                                                                                                                                                                                                                                                                                                               human IgM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IRR003555, ---
SMART; SM00406; IGV; 1.-
PROSITE; PS50835; IG LIKE; 1.
PROSITE; Ps50835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region; Pyrrolidone carboxylic acid.
I 113
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                            Putnam F.W., Florent G., Paul C., Shinoda T., Shimizu A., "Complete amino acid sequence of the Mu heavy chain of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-GCT-2003 (TrEMBLrel. 25, Last annotation update)
Rheumatoid factor RF-ET13 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.4%; Score 425.5; DB 1 67.5%; Pred. No. 5.1e-35;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Ig heavy chain V-II region OU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005576; C:extracellular region; NAS. GO; GO:0003823; F:antigen binding; NAS. GO; GO:000555; P:immune response; NAS. InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Mismatches
                                                                                                                                                                                                                                                                                                               MEDLINE=74005511; Pubmed=4742735;
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043234;
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1es 85; Conservative
                                                                                                                     Homo sapiens (Human)
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HSSP; P01820; 1A7N.
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126 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            macroglobulin.
                                                                                                                                                                                                                                                                                          PROTEIN SEQUENCE.
                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                    immunoglobulin.
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SEQUENCE
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Matches

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Search completed: February 23, 2006, 09:23:05 Job time : 155.441 secs

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Humanized antibody; antibody engineering; monoclonal antibody; MAb;
interleukin-4; IL-4; allergy.
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/note= "complementarity determining region"
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AAY43749
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|abel= Sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR75355 standard; protein; 131 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Humanized antibody 3B9 light chain.
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93US-00136783.
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|label= CDR
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/label= CDR
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14-OCT-1993;
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20-SEP-1995
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Ada47339
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Ada847332
Adg8442
Adg8845
Adg8945
Adg89964
Adg89996
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                        GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from

Sylvester DR;

WPI; 1995-123387/16. N-PSDB; AAQ73986.

Antibody Antibody Human vlk Hu3G8VL-1

ADP88443 AEB13680 ADF71899

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Gaps

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ö 5;

Length 131; Indels

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The present sequence represents the light chain variable region of a humanised murine interleukin-4 (IL-4) antibody 3B9. The specification describes chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis, atopic archma, anaphylactic shock, rheumatoid archritis, versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans
                                                                                                                                                                                                                                                                                                                          QKPGQPPKLLIYAASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSNEDPPR 120
                                                                                                                                                                                                                                                                                                                                           61 QKPGQPPKLLIYAASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSNEDPPR 120
                                                                                                                                                                                                                                                                                       1 MGWSCIILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMNWYQ
                                                                                                                                                                                                                                                                     1 MGWSCIILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMNWYQ
                                                                                                                                                                                                            100.0%; Score 687; DB 2;
100.0%; Pred. No. 5.7e-42;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              atopic ashthma and anaphylactic shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY18118 standard; protein; 131 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gross
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SMIK ) SMITHKLINE BEECHAM PLC. (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 16; Fig 5; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93US-00117366.
93US-00136783.
94WO-US010308.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   FGGGTKVEIKR 131
                                                                                                                                                                                                                                                                                                                                                                                                 Holmes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAX79517
                                                                                                                                                                                   Sequence 131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-SEP-1993;
14-OCT-1993;
07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1995;
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                                                                                                                                                                                                                                                                                                              QKPGQPPKLLIYAASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSNEDPPR 120
                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA molecules encoding recombinant antibodies useful for treating IL4
                                                                 A humanized antibody light chain variable region and signal sequence is given in AAR75355. The signal sequence is also provided in AAR70194. The sequences of the first 2 CDRs are identical to mouse anti-human IL-4 MAb 3B9 light chain CDRs (given in AAR70195-96), but the third (AAR70201) differs by a single amino acid from the native mouse CDR (AAR70197). (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Light chain variable region; interleukin-4; IL-4; antibody 389; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin E-mediated allergic reaction; allergic rintities; conjunctivitis; atopic dermatitis; atopic aethma; anaphylactic short; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.
                                                                                                                                                                                                                                                                       QKPGQPPKLLIYAASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSNEDPPR
                                                                                                                                                                                                                                                     1 MGWSCIILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMNWYQ
                                                                                                                                                                                                                              Gaps
high affinity mAbs - useful in treatment of IL-4-mediated and IgE-
mediated allergic conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Light chain variable region of humanised murine IL-4 antibody 3B9
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                                                                                                                                                                                               Score 687; DB 2; Length 131;
Pred. No. 5.7e-42;
                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY23771 standard; protein; 131 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gross
                                          Disclosure; Fig 5; 97pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
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                                                                                                                                                                                               100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                           Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                    131
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                                                                                                                                                                                                                                                                                                                                                                   FGGGTKVEIKR
                                                                                                                                                                                                                                                                                                                                                                                              FGGGTKVEIKR
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                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                                     Sequence 131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus sp.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1995;
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07-SEP-1994;
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Antibody, interleukin-4, IL4; immunoglobulin E; IgE mediated disease; allargic disorder; allargic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the light chain of the humanised 389 antibody of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant IL4 antibodies useful for tratment of allergic rhinitis,
Light chain sequence for humanised 3B9 antibody.
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       (IL4) monoclonal antibody for the treatment of immunoglobulin E (1gE) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft versus host disease
                                                                                                                                                                                         QKPGQPPKLLIYAASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSNEDPPR 120
                                                                                                                                         9
                                                                                                                                                  A humanized antibody light chain variable region and signal sequence is given in AAR75355. The signal sequence is also provided in AAR70194. The sequences of the 3 CDRs are identical to mouse anti-human IL-4 MAb 3B9 light chain CDRs (given in AAR70195-97). (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                     1 MGWSCIILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMNWYQ
                                                                                                                     Gaps
  humanised interleukin-4
                                                                                                                                                                                                                                                                                                                                                                              Humanized antibody; antibody engineering; monoclonal antibody; MAb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric and humanised IL-4 monoclonal antibodies (mabs), derived high affinity mabs - useful in treatment of IL-4-mediated and IgE-mediated allergic conditions.
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                                                                                               100.0%; Score 687; DB 2; Length 131; 100.0%; Pred. No. 5.7e-42; ive 0; Mismatches 0; Indels (
                                                                                                                   ;
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The antibody is a chimeric or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Page 71-72; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DR;
                                                                                                                                                                                                                                                                                                                                                           Humanized antibody 3B9 light chain.
                                                                                                                                                                                                                                                                                        AAR70202 standard; protein; 131 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sylvester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93US-00117366.
93US-00136783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94WO-US010308
                                                                                                                                                                                                                                                                                                                                                                                         interleukin-4; IL-4; allergy
                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
                                                                                           Query Match
Best Local Similarity 100.
Matches 131; Conservative
                                                                                                                                                                                                                                 121 FGGGTKVEIKR 131
                                                                                                                                                                                                                     FGGGTKVEIKR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gross MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-123387/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAQ83520
                                                                              Sequence 131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 131 AA
                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                               WO9507301-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-SEP-1994;
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                                                                                                                                                                                                                                                                                                                             25-MAR-2003
20-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAR-1995.
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                                                                                                                                                                                                                  QKPGQPPKLLIYAASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSNEDPR 120
                                                                                                                                                                                                                                              encoding recombinant antibodies useful for treating IL4
                                                                                                              9
                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Light chain variable region; interleukin-4; IL-4; antibody 389; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin E-mediated allergic reaction; allergic rintities; conjunctivitis; atopic dermatitis; atopic aethma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.
                                                                                                                                                1 MGWSCIILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMWYQ
                                                                                                            MGWSCIILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMNWYQ
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Light chain variable region of humanised murine IL-4 antibody 3B9.
                                                    ;
0
     Length 131;
                                                    Indels
99.1%; Score 681; DB 2;
99.2%; Pred. No. 1.5e-41;
ive 0; Mismatches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gross MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY23779 standard; protein; 131 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
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93US-00136783.
94WO-US010308.
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  Query Match
Best Local Similarity 99.2
Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                           131
                                                                                                                                                                                                                                                                                                                                                                          121 FGGGTKVEIKR 131
                                                                                                                                                                                                                                                                                                                   FGGGTKVEIKR
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mediated conditions
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Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1995;
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14-OCT-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Holmes SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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WO2002102853-A2
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19-OCT-2001; 2
18-APR-2002; 2
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-APR-2002;
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Ringler D,
                                                                                                                                                                                                                                                ADA47339;
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                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
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                                                                                                                                    OKPGOPPKILIYAASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSNEDPPR 120
                                                                                                                                                    Antibody, interleukin-4, IL4; immunoglobulin E; IgE mediated disease; allargic disorder, allargic thinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease.
                                                                                                          9
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                                                                                              MGWSCIILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMNWYQ
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant IL4 antibodies useful for tratment of allergic rhinitis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.1%; Score 681; DB 2; Length 131; 99.2%; Pred. No. 1.5e-41; ive 0; Mismatches 1; Indels
                         Length 131;
                         Score 681; DB 2; Length 13
Pred. No. 1.5e-41;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                       Light chain sequence for humanised 3B9 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              atopic ashthma and anaphylactic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Col 59-62; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gross MS;
                                                                                                                                                                                                                                                                                       AAY18126 standard; protein; 131 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SMIK ) SMITHKLINE BEECHAM PLC. (SMIK ) SMITHKLINE BEECHAM CORP.
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94WO-US010308.
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                           99.18;
                                       99.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.2
Matches 130; Conservative
                                                    Matches 130; Conservative
                                                                                                                                                                                            FGGGTKVEIKR 131
                                                                                                                                                                                                                    FGGGTKVEIKR 131
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                         Query Match
Best Local Similarity
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 Sequence 131
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                                                                                                                                                                                                                                                                                                                                            11-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-SEP-1993;
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07-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
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The invention relates to a method for treating a primate to induce tolerance to at least one antigen. The method of the invention comprises administering at least one compound which when in a primary mixed lymphocyte reaction in vitro reduces the amount of CD4+ CD25+ cells produced. The preferred compound is a humanised antibody or its fragment, that does not bind to the Fc receptor, and includes CDRs that are free of
                                                        OKPGOPPKLLIYAASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSNEDPPR 120
                                                                       61 QKPGQPPKLLIYAASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSNEDPPT 120
                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating a primate to induce tolerance to at least one antigen, useful for inhibiting graft rejection or treating an autoimmune disease, comprises administering a TRX1 antibody to reduce the amount of CD4+CD25+ cells produced.
             1 MGWSCIILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMNWYQ
MGWSCIILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMNWYQ
                                                                                                                                                                                                                                                                                                                                  Antibody; TRX1; immunosuppressive; immunomodulator; vaccine; antigen; graft rejection; autoimmune disease; humanised.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kornaga
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                                                                                                                                                                                                                                                                                                       TRX1 light chain amino acid sequence #SEQ ID 14
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(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
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Winsor-Hines D;
                                                                                                                                                                                                                                                                                                                                                                                                                          1. .20
/label= leader peptide
                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                   ADA47339 standard; protein; 238 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 30; Fig 2C; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 2001GB-00022724.
; 2001US-0345194P.
; 2002US-0373470P.
; 2002US-0373471P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  44. .58
/label= CDR
74. .80
/label= CDR
113. .121
/label= CDR
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                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                 121 FGGGTKVEIKR 131
                                                                                                                                        121 FGGTKVEIKR 131
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Cobbold S,
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Contracting the metals to give

125 126

99

Gaps

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administering at least one compound which when in a primary mixed lymphocyte reaction in vitro reduces the amount of CD4+ CD25+ cells produced. The preferred compound is a humanised antibody or its fragment, that does not bind to the Fc receptor, and includes CDRs that are free of a glycosylation site. The method of the invention is useful for inducing ameliorating or reducing an immune response to an antigen. The antibody is useful for manufacturing an emdicament for inducing tolerance to an antigen (possibly in the form of a vaccine), for inhibiting an immune response, for inhibiting an immune response, for inhibiting an autoin of a graft (such as an organ) in a human patient, and for treating an autoimmune disease. The current sequence represents the TRX1 light chain.
  to at least one antigen. The method of the invention comprises
                                                                                                                                                                                                                                                                                                                                                             67 PPKLLIYVASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQOSLQDPPTFGGGT
                                                                                                                                                                                                                                                                                                      PPKLL1YAASNLESGVPDRFSGSGSGTDFTLT1SSLQAEDVAVYYCQQSNEDPPRFGGGT
                                                                                                                                                                                                                                                                                      6 IILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMNWYQQKPGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunosuppressive; immunomodulator; vaccine; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating a primate to induce tolerance to at least one antigen, usefu for inhibiting graft rejection or treating an autoimmune disease, comprises administering a TRX1 antibody to reduce the amount of CD4+
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                                                                                                                                                                                                                                238;
                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                      Score 572.5; DB 6;
Pred. No. 1.7e-33;
7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     graft rejection, autoimmune disease; humanised.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ISIS-) ISIS INNOVATION LTD.
(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRX1 light chain encoding DNA #SEQ ID 12.
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Winsor-Hines D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADA47338 standard; protein; 238 AA.
                                                                                                                                                                                                                                                            4;
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20-SEP-2001; 2001GB-00022724.
19-OCT-2001; 2001US-0345194P.
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                                                                                                                                                                                                                                                           Matches 112; Conservative
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Cobbold 8
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                                                                                                                                                                                                                                                                                                                                                                                                                            KVEIKR 132
                                                                                                                                                                                                                                                                                                                                                                                                       KVEIKR 131
                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                    Sequence 238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibody; TRX1;
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Ringler D,
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(TOLE-)
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             tolerance to at least one antigen, specifically for inhibiting, ameliorating or reducing an immune response to an antigen. The antibody is useful for manufacturing a medicament for inducing tolerance to an antigen (possibly in the form of a vaccine), for inhibiting an immune response, for inhibiting the response and of a graft (such as an organ) in a human patient, and for treating an autoimmune disease. The current sequence represents the TRX1 light chain amino acid sequence.
                                                                                                                                                                                                                                                                                      PPKLLIYAASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSNEDPRFGGGT 125
                                                                                                                                                                                                                   65
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 glycosylation site. The method of the invention is useful for inducing
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                                                                                                                                                                                                                                10 VLLLWVPGSTG---DIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMMWYQQKPGQ
                                                                                                                                                                                                                 6 IILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMNWYQQKPGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRX1; immunosuppressive; immunomodulator; vaccine; antigen; ection; autoimmune disease; humanised.
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method for treating a primate to induce
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                                                                                                                                                         Length 238;
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                                                                                                                                                                                     Indels
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                                                                                                                                                       Score 572.5; DB 6;
Pred. No. 1.7e-33;
4; Mismatches 7;
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(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD
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Winsor-Hines D;
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2001US-0345194P.
2002US-0373470P.
                                                                                                                                                         83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                    Query Match
Best Local Similarity 88.9
Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD25+ cells produced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waldmann Cobbold
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N-PSDB; ADA47329.
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(TOLE-) TOLERRX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                graft rejection;
                                                                                                                             Sequence 238 AA;
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19-OCT-2001; 2
18-APR-2002; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibody;
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18-APR-2002; 2002US-0373471P
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                                                                       Ringler D,
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                                                             Frewin M,
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                                     The invention relates to a method for treating a primate to induce to at least one antigen. The method of the invention comprises administering at least one compound which when in a primary mixed lymphocyte reaction in vitro reduces the amount of CD4+ CD25+ cells produced. The preferred compound is a humanised antibody or its fragment, that does not bind to the Fc receptor, and includes CD8s that are free of a glycosylation site. The method of the invention is useful for inducing ameliorating or reducing an immune response to an antigen. The antibody is useful for manufacturing a medicament for inducing tolerance to an antigen (possibly in the form of a vaccine), for inhibiting an immune response, for inhibiting the rejection of a graft (such as an organ) in a human patient, and for treating an autoimmune disease. The current sequence represents the TRX1 light chain.
                                                                                                                                                                                                                                                                                                    PPKILLIYAASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSNEDPPRFGGGT 125
                                                                                                                                                                                                                                                                                                               67 PPKLLIYVASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSLQDPPTFGGGT 126
                                                                                                                                                                                                                                                            65
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                                                                                                                                                                                                                                                                        10 VLLLWVPGSTG---DIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMMYQQKPGQ
                                                                                                                                                                                                                                                            6 IILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMNWYQQKPGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibody; TRX1; immunosuppressive; immunomodulator; vaccine; antigen; graft rejection; autoimmune disease; humanised.
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                        3;
                                                                                                                                                                                                                    Length 238;
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                  Score 572.5; DB 6;
Pred. No. 1.7e-33;
4; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .20
/label= leader peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                 ADA47332 standard; protein; 238 AA.
                    Claim 29; Fig 2A; 131pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001GB-00014517.
2001GB-00022724.
2001US-0345194P.
2002US-0373470P.
                                                                                                                                                                                                                   83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44. .58
/label= CDR
74. .80
/label= CDR
113. .121
/label= CDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRX1 light chain #SEQ ID 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                              Best Local Similarity 88.9
Matches 112; Conservative
CD25+ cells produced.
                                                                                                                                                                                                                                                                                                                                            KVEIKR 131
                                                                                                                                                                                                                                                                                                                                                               KVEIKR 132
                                                                                                                                                                                                Sequence 238 AA;
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20-SEP-2001;
19-OCT-2001;
18-APR-2002;
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                                                                                                                                                                                                                    Query Match
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The invention relates to a method for treating a primate to induce tolerance to at least one antigen. The method of the invention comprises administering at least one compound which when in a primary mixed lymphocyte reaction in vitro reduces the amount of CD4+ CD2+ cells produced. The preferred compound is a humanised antibody or its fragment, that does not bind to the Fc receptor, and includes CDRs that are free of a glycosylation site. The method of the invention is useful for inducing tolerance to at least one antigen, specifically for inhibiting, amoliorating or reducing an immune response to an antigen. The antibody is useful for manufacturing a medicament for inducing tolerance to an antigen (possibly in the form of a vaccine), for inhibiting an immune craponse, for inhibiting an immune craponse, for inhibiting an immune craponse, for inhibiting an autoimmune disease. The current sequence represents the TRX1 light chain amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 PPKLLIYAASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSNEDPPRFGGGT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 PPKLLIYVASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSLQDPPTFGGGT 126
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                                                                                                                                                                                                                                                                                   Treating a primate to induce tolerance to at least one antigen, useful for inhibiting graft rejection or treating an autoimmune disease, comprises administering a TRX1 antibody to reduce the amount of CD4+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 ILLFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMNWYQQKPGQ
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                                                                                                                              Kornaga
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Pred. No. 1.7e-33;
4; Mismatches 7; Indels
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                                                                                                                                 Rao
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      1 LTD.
TECH SERVICES LTD.
                                                                                                                          Gorman S, Hale
Winsor-Hines D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 27; Fig 1C; 131pp; English.
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(ISIS-) ISIS INNOVATION (UYCA-) UNIV CAMBRIDGE 1
                                                                                                                                 μ̈́ς
                                                                                                                          Waldmann Cobbold
                                                                                                                                                                                                                                                                                                                                                                             CD25+ cells produced
                                   (UYCA-) UNIV CAMBKIL (TOLE-) TOLERRX INC.
                                                                                                                                                                                                                        WPI; 2003-175228/17.
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Treating a primate to induce tolerance to at least one antigen comprises administering at least one anti-CD4 antibody or its fragment in an initial dose of at least 40 mg/kg and at least one compound that inhibits CD8+ T cells.
                                                                                                                                                                        The present invention relates to a process of treating a primate to induce tolerance to at least one antigen, which comprises administering to the primate at least one anti-CD4 antibody or lis fragment in an initial dose of at least 40 mg/Kg and at least one compound that inhibits CD8+ T cells, where the anti-CD4 antibody or its fragment is present in the primate when the antigen is present in the primate. The method is useful in treating a primate to induce tolerance to at least one foreign antigen to prevent transplant rejection. The present sequence is an antibody fragment used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating a primate to induce tolerance to at least one antigen comprises administering at least one anti-CD4 antibody or its fragment in an initial dose of at least 40 mg/kg and at least one compound that inhibits CD8+ T cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunosuppressive; transplant rejection; antigen tolerance; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 572.5; DB 8; Length 238;
Pred. No. 1.7e-33;
4; Mismatches 7; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRX1 light chain with leader sequence SEQ ID NO: 27.
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1.7e-33;
7;
                                                                                                                                     Disclosure; SEQ ID NO 19; 113pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP88450 standard; protein; 238 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                   83.3%;
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  N-PSDB; ADP88441, ADP88440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 112; Conservative
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N-PSDB; ADP88448.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                            Sequence 238 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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ADP88450
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                                                                                                                                                                                                                                                                                                          The present invention relates to a process of treating a primate to induce tolerance to at least one antigen, which comprises administering to the primate at least one anti-CD4 antibody or its fragment in an initial dose of at least 40 mg/Kg and at least one compound that inhibits CD8+ T cells, where the anti-CD4 antibody or its fragment is present in
                                                                                                                                                                        Treating a primate to induce tolerance to at least one antigen comprises administering at least one anti-CD4 antibody or its fragment in an initial dose of at least 40 mg/kg and at least one compound that inhibits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPKLLIYVASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSLQDPPTFGGGT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPKLLIYAASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSNEDPRFGGGT 125
                                                                                                                                                                                                                                                                                                                                                                                                                 the primate when the antigen is present in the primate. The method is useful in treating a primate to induce tolerance to at least one foreign antigen to prevent transplant rejection. The present sequence is an antibody fragment used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 572.5; DB 8;
Pred. No. 1.7e-33;
4; Mismatches 7;
                                                                                                                                                                                                                                                                       Example 3; SEQ ID NO 11; 113pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ringler DJ;
                                                                            Ringler DJ
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09-DEC-2002; 2002US-0431839P
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                                                                                                                                     N-PSDB; ADP88433, ADP88432.
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                                     TOLERRX INC
                                                                                                                 2004-468712/44
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Matches 112; Conserv
                                                                          Windsor-Hines D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 238 AA;
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6 6 6

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Gaps

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Length Indels

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PPKLLIYAASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSNEDPPRFGGGT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primate, tolerance, antigen, mixed lymphocyte reaction, MLR; CD4+; CD25+; IL-2; IL-4; IL-12; immune response, graft rejection; immunosuppressive; antirheumatic; antiarthritic; antidiabetic; neuroprotective; antiinflammatory; antiallergic; antimatic; cytostatic; antimicrobial; transplant; graft-versus-host disease; autoimmune disease; inflammation; allergy; asthma; cancer; infection; humanised; TRX1; light.
 the primate when the antigen is present in the primate. The method is mesful in treating a primate to induce tolerance to at least one foreign antigen to prevent transplant rejection. The present sequence is an antibody fragment used in the exemplification of the invention.
                                                                                                                                                                                                                    67 PPKLLIYVASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSLQDPPTFGGGT
                                                                                                                                                                                                6 IILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMNWYQQKPGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complementarity determining region 3
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/label= Framework region 1
44 .58
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label= Complementarity determining
                                                                                                               Score 572.5; DB 8;
Pred. No. 1.7e-33;
7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Light chain of a humanised TRX1 antibody #3.
                                                                                                                                                             4; Mismatches
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/label= Framework region
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'label= Constant region
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                                                                                                                         83.3%;
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(ISIS-) ISIS INNOVATION LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .121
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                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                         KVEIKR
                                                                                         Sequence 238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004067554-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
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                                                                                                                            Query Match
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                               The present invention relates to a process of treating a primate to induce tolerance to at least one antigen, which comprises administering to the primate at least one anti-CD4 antibody or its fragment in an initial dose of at least 40 mg/Kg and at least one compound that inhibits CD8+ T cells, where the anti-CD4 antibody or its fragment is present in the primate when the antigen is present in the primate. The method is useful in treating a primate to induce tolerance to at least one foreign antigen to prevent transplant rejection. The present sequence is an antibody fragment used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                      1,
                                                                                                                                                                                                                                                                                                                                                                                           125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a process of treating a primate to induce tolerance to at least one antigen, which comprises administering to the primate at least one anti-CD4 antibody or its fragment in an initial dose of at least 40 mg/kg and at least one compound that inhibits CD8+ T cells, where the anti-CD4 antibody or its fragment is present in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating a primate to induce tolerance to at least one antigen comprises administering at least one anti-CD4 antibody or its fragment in an initial dose of at least 40 mg/kg and at least one compound that inhibits
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                                                                                                                                                                                                                                                                                                                                          6 IILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMNWYQQKPGQ
                                                                                                                                                                                                                                                                                                                                                                                           PPKLLIYAASNLESGVPDRFSGSGGTDFTLTISSLQAEDVAVYYCQQSNEDPRFGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunosuppressive; transplant rejection; antigen tolerance; antibody;
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                      3,
                                                                                                                                                                                                                                                   Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibody TRX1 light chain with leader sequence SEQ ID NO: 3.
                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                  Score 572.5; DB 8;
Pred. No. 1.7e-33;
                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 3; 113pp; English.
SEQ ID NO 27; 113pp; English
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                                                                                                                                                                                                                                                83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-DEC-2003; 2003WO-US039165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-DEC-2002; 2002US-0431839P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                    Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-468712/44.
N-PSDB; ADP88424.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               KVEIKR 131
                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Windsor-Hines D,
                                                                                                                                                                                                                 Sequence 238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2004052398-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified.
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                                                                                                                                                                                                                                                   Query Match
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RESULT 14

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(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
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Rao P, Kornaga T; Gorman S, Hale G, Winsor-Hines D; Waldmann H, Cobbold S, Frewin M, W Ringler D,

2004-580970/56

N-PSDB; ADQ87971

Inducing tolerance to an antigen comprises administering a CD4 antibody alone or in combination with other compounds that induce tolerance against one or more antigens.

Claim 11; Fig 3A; 85pp; English

The invention relates to a novel method for treating a primate to induce to at least one antigen. The method comprises administering a compound, or a combination of compounds, that induces tolerance against one or more antigens. The compounds that induces tolerance against compound, or a combination of compounds, that induces tolerance against come or more antigens. The compound or the combination being in a primary mixed lymphocyte reaction and that compounds in the primary mixed lymphocyte reactions and that in least one of a primary and secondary mixed lymphocyte reactions, and the amount of a primary and secondary mixed lymphocyte reactions.

The compound of a primary and secondary mixed lymphocyte reactions and the amount of a primary and secondary mixed lymphocyte reaction. The compound or the combination being administered in an amount and for a time so as to induce tolerance against the antigen, the compound or the combination being present in the specification; a composition of the same epitope as the humanised primate when the antigen is present in the primate. The linvention further comprises: an antibody given in the specification; a composition of a primate the inhibiting and immune response in a patient; inhibiting an immune response in a patient or for antibody and a pharmaceutical carrier; inducing tolerance on an antigen in a patient; inhibiting on immune to a serient in a patient or for a composition of at least two compounds for use in inducing tolerance. The compositions of the invention have the following activities: immuneouppressive, antitheumatic, antiarthritic, and antimicrobial. The composition and methods activities: immuneouppressive, antitheumatic, antiarthritic, and antimicrobial. The composition and methods activities: immuneouppressive, antitheumatic, antiarthritic, and antimicrobial. The composition or readence of artiarthritis, diabetes or multiple selection, gaterone representing or multiple selection of a humanised TRXI allergy, asthma, cancer or infections. These may also be 

Sequence 238 AA;

3; Gaps Query Match 83.3%; Score 572.5; DB 8; Length 238; Best Local Similarity 88.9%; Pred. No. 1.7e-33; Matches 112; Conservative 4; Mismatches 7; Indels 3

66 PPKILLIYAASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSNEDPPRFGGGT 125 10 VLLLWVPGSTG---DIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMWYQQKPGQ 66 6 IILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMNWYQQKPGQ 셤 ઠ

67 PPKLLIYVASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYCQQSLQDPPTFGGGT 126

KVEIKR 131 126

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KVEIKR 132 127 Search completed: February 23, 2006, 09:18:04 Job time : 126.702 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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- protein search, using sw model OM protein

February 23, 2006, 09:18:23 ; Search time 23.1176 Seconds (without alignments) 545.228 Million cell updates/sec Run on:

US-10-723-872-14 687 Title: Perfect score:

1 MGWSCIILFLVATATGVHSD.......QQSNEDPPRFGGGTKVEIKR 131 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
-	502.5	73.1	131	7	PH1226	Ig kappa chain pre
7	499	72.6	112	7	S19971	chain
٣	493	71.8	111	П	KVMS43	kappa
4	492		111	Н	KVMS83	
ഹ	489	71.2	111	٦	KVMS08	Ig kappa chain V r
9	486	70.7	111	г	KVMS69	
7	478	9.69	134	٦	K4HU17	
ω	476.5	69.4	133	ч	K4HUJI	chain
0	476	69.3	111	П	KVMSC1	chain
10	475	69.1	112	7	S19976	
11	468.5	68.2	110	н	KVMS10	
12	465	67.7	113	7	S34003	
13	464	67.5	112	7	S19972	Ig kappa chain V r
14	463		134	7	849531	anti-Sm antibody V
12	462	67.2	111	-1	KVMS37	Ig kappa chain V r
16	462	67.2	124	7	S40364	Ig kappa chain - h
17	459	φ	113	~	S30523	Ig kappa chain V r
18	457.5	9.99	131	-	KVMSM6	Ig kappa chain pre
19	457	66.5	113	~	830520	Ig kappa chain V r
20	457	66.5	114	~	K4HULN	Ig kappa chain V-I
21	455	ė.	115	7	863596	Ig kappa chain V r
22	451	•	111	~	996608	Iq kappa chain V-J
23	450	65.5	114	7	S44116	Ig kappa chain V-J
24	450	65.5	129	~	S40347	Iq kappa chain - h
25	449	65.4	113	~	S34002	Iq kappa chain V r
56	444	64.6	111	7	D45722	anti-glycoprotein
	443	64.5	114	~	S44119	Ig kappa chain V-J
28		64.3	120	~	S51147	
53	440.5	64.1	138	~	A53261	Ig kappa chain pre

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chain V r								in V r	chain V r	in V r	chain V r	chain - h	chain V r	chain pre
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S26344 S46373	KVMS32	KVMS40	809965	KVMS84	S26343	840329	K4HU	A56169	B49047	KVMS75	KVMS85	840317	KVMS80	806084
01	4 1	ч	~	Н	7	N	Н	7	7	-	-1	~	Н	7
107	132	111	111	111	107	129	121	210	108	111	111	129	111	240
64.0	63.7													61.4
440	437.5	436	435	434	433	433	430	428	425	425	424	423	422	422
30	35	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 PH1226	
Ig kappa chain precursor V region (M-T310) - mouse (fragment)	
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000	
C;Accession: PH1226 R:Weissenhorn W : Schener W : Kaluza R : Schwirzke M : Beiter C : Rlieger D : Lenn	Tons
Anticoccurrent 2.1, 271-278, 1992	71127
A, Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and or	nd or

A;Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and or A;Reference number: PH1224; MUID: 93077041; PMID:1446824
A;Reference number: PH1226
A;Residue: PH1226
A;Molecule type: mRNA
A;Residues: 1-131 <MEI.
A;Residues: 1-131 <MEI.
A;Cross-references: UNIPARC: UPI00001153EE; GB:S50265; NID:g260765; PIDN:AAB24320.1; PID
A;Note: this mouse sequence was hybridized and fused with a human constant region gene C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-131/Product: Ig light chain V region #status predicted <MAT>
F;36-114/Domain: immunoglobulin homology <IMM>

Gaps 3; Query Match 73.1%; Score 502.5; DB 2; Length 131; Best Local Similarity 76.0%; Pred. No. 5.7e-35; Matches 95; Conservative 13; Mismatches 14; Indels 3

65 10 VLLLWVPGSTG---DIVLTQSPASLPMSLGQRATISCKASQSLDYDGDSYMWYQQKPGQ 66 6 IILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMNWYQQKPGQ ઠ 셤 66 PPKLLIYAASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSNEDPPRFGGGT 125 셤 ઠે

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RESULT S19971

A; Reference number: S19963

A;Accession: S19971 A;Molecule type: mRNA A;Residues: 1-112 <WEI> A;Cross-references: UNIPARC:UP10000116030; EMBL:X65091; NID:g52288; PIDN:CAA46219.1; PID

Mon Feb 27 09:28:10 2006

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71.8%;
83.8%;
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                                                                                                                                                                                                                                                                                                                                                 93; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein A; Residues: 1-111 <WEI>
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
     A; Residues: 10-99 < MOO>
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                 Matches
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Ig Kappa chain V region (FG7043) - mouse (Iragment)

C.Species Mas manaculus (house mouse)

C.Species (1-5ep-1914 Heaquence_revision of -6ep-1914 Heat.

C.Date: 0.-5ep-1914 Heaquence_revision of -6ep-1914 Heat.

C.Date: 0.-5ep-1914 Heaquence_revision of -6ep-1914 Heat.

C.Date: 0.-5ep-1914 Heaquence_revision of -6ep-1914

R.Mengert W. i. Genmaltan. L.; Loh, E.; Schilling, J.; Hood, L.

A.Firelet Heatrangement of genetic information may produce immunoglobulin diversity.

A.Recenter uniber: A92304; WUID:79073182; PMID:103003

A.Recenter uniber: A92304; WUID:79073182; PMID:103003

A.Recenter uniber: A92304; WUID:79073182; PMID:103003

A.Recenter uniber: A92304; MUID:79073182; PMID:1030002A100

R.Rocalder I.-11 - Walls

A.Recenter uniber: S2104; MUID:94009207; PMID:7651608

A.Recenter uniber: S2104; MUID:94009207; PMID:7651608

A.Recenter uniber: S2107; MUID:94009207; PMID:7651608

A.Recenter uniber: S2107; MUID:94009207; PMID:7651608

A.Recenter uniber: S2108; MUID:94009207; PMID:7651608

A.Recenter uniber: UNIPARC:UPIO000116552; EMBL:225448; NID:9407836; PIDN:CAA80933.1; PI
A.Recenter uniber: S2108; MUID:9400931.1; PI
A.Recenter uniber: S2108

A.Recenter uniber: UNIPARC:UPIO00011655E; EMBL:225446; NID:9407834; PIDN:CAA80933.1; PI
A.Recenter uniber: UNIPARC:UPIO00011655E; EMBL:225422; NID:9407834; PIDN:CAA80933.1; PI
A.Recenter uniber: UNIPARC:UPIO00011655E; EMBL:225422; NID:9407834;
A; Experimental source: clone M-T310
A; Accession: S19973
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Cross-references: UNIPARC: UPI0000116030; EMBL:X65092; NID:g52292; PIDN:CAA46220.1; PIL
A; Experimental source: M-T404
C; Superfamaily: immunoglobulin V region; immunoglobulin homology
C; Keywords: hetezoterramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology < IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSNEDPPRFGGGTKVEIKR 131
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                                                                                                                                                                                                                                                                                         Length 112;
                                                                                                                                                                                                                                                                                      ch 72.6%; Score 499; DB 2; Length 11
1 Similarity 82.1%; Pred. No. 9.6e-35;
92; Conservative 10; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          kappa chain V region (PC7043) - mouse (fragment)
                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 92; Conserv
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A; Molecule type: DNA
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A,Cross-references: UNIPARC:UP1000011655C; EMBL:225454; NID:g407842; PIDN:CAA80941.1; PJ A;Note: V-kappa-21B; anti-collagen
C,Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa-18 to immunoglobulin heterotetramer subunit sulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>
F;23-92/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P01666; UNIPARC:UPI000002A101
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kag hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
E;16-94/Domain: immunoglobulin homology < IMM>
F;23-92/Disulfide bonds: #status predicted
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A,Residues: 1-111 cMEI. ARET.
A,Cross-references: UNIPROT:P01667, UNIPARC:UPI000002A102
C,Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ....... kearrangement of genetic information may produce immunoglobulin diversity. A;Reference number: A93204; MUID:79073152; PMID:103003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig kappa chain V region (PC7183) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: BO1937, A01937
E;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMMYYQQKPGQPPKLLIYAASNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 DIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES
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Pred. No. 3.6e-34;
8; Mismatches 11
                                                                                                                                                                                                                                                                                                                 Pred. No. 3e-34;
7; Mismatches
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8

63 99

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C;Accession: A01904
R;Klobeck, H.G.; Bornkamm, G.W.; Combriato, G.; Mocikat, R.; Pohlenz, H.D.; Zachau, H.G.
Nucleic Acids Res. 13, 6515-6529, 1985
A;Title: Subgroup IV of human immunoglobulin K light chains is encoded by a single germ!
A;Reference number: A93589; MUID:86041853; PMID:2997712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kar ani disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GB:Z00022; GB:X51570; NID:93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GOPPKLLIYAASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSNEDPPRFGG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 GQPPKLLIYCASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYNLPWTFGQ 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 IILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSVDYDGD--SYMNWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 IILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSVDYDGD--SYMNWYQQKP
      chain V-IV region (B17) #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-133 <KLO>
A;Cross-references: UNIPROT:P06313; UNIPARC:UPI000012E165; GB:Z00
A;Note: the sequence was determined from the differentiated gene
                                                                                                                                                                                                                                                                                                                                       DB 1; Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                 21; Indels
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                                                                                                                                                                                                                                                                                                                                       Score 478; DB 1;
Pred. No. 6.3e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 476.5; DB | Pred. No. 8.4e-33
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                                                                                                                                                                                                                                                                                                                                                                                                 9; Mismatches
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F;21-134/Product: Ig kappa chain V-IV region (F;21-43/Region: framework 1
F;36-116/Domain: immunoglobulin homology <IMM>F;44-60/Region: complementarity-determining 1
F;76-17/Region: framework 2
F;76-82/Region: complementarity-determining 2
F;83-114/Region: framework 3
                                                                                                                                                                                                           F:115-121/Region: complementarity-determining F:122-134/Region: framework 4 F:43-114/Disulfide bonds: #status predicted
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F;61-75/Region: framework 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GDB:119341; OMIM:146980
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                                                                                                                                                                                                                                                                                                                                    69.68;
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127 GTKVEIKR 134
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                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Introns: 17/1
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                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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C; Species: A01905
R; Marsh, Roll 1965
R; Mucleic Acids Res. 13, 651-6544, 1985
A; Title: Detection of a unique human WappaIV germline gene by a cloned cDNA probe.
A; Reference number: A01905; MUID:86041854; PMID:2997713
A; Recession: A01905
A; Rolcous: L-134 cMRA
A; Residues: 1-134 cMRA
A; Residues: UNIPARC:UPI000017370A
A; Roce: the sequence was determinated from the differentiated gene
A; Note: the authors translated the codon TGC for residue 76 as Trp
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin | mmunoglobulin | mmunoglobulin |
F;1-20/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Whis musculus (house).

C; Species: Whis musculus (house).

C; Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004

C; Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004

C; Date: 30-Jun-1993

R; Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.

R; Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.

Nature 276, 785-799, 1978

A; Title: Rearrangement of genetic information may produce immunoglobulin diversity.

A; Reference number: A93204; MUID:79073152; PMID:103003

A; Accession: B01937

A; Residues: 1-111 < WEI>
A; Residues: 1-111 < WEI>
A; Residues: 1-111 < WEI>
A; Residues: London and accessive and a graph and igh, the subunits associate into la C; Superfamily: immunoglobulin wellongy immunoglobulin homology

C; Superfamily: immunoglobulin homology without a status predicted

F; 23-92/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                     1 DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMMYQQXQXPQQPPKLLIYTASNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIVLTQSPASLAVSLGQRATISCKASQSVDXDGDSYMNWYQQKPGQPPKVLIFAASNLES
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                                                                                                                                                       Length 111,
      C; Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Indels
                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 70.7%; Score 486; DB 1; Best Local Similarity 82.0%; Pred. No. 1.1e-33; Matches 91; Conservative 9; Mismatches 11;
                                                                                                                                                    Score 489; DB 1;
Pred. No. 6.4e-34;
7; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kappa chain precursor V-IV region (B17) - human
                              C; Keywords: heterotetramer; immunoglobulin F;16-94/Domain: immunoglobulin homology <IMM>F;23-92/Disulfide bonds: #status predicted
                                                                                                                                                 Query Match
Best Local Similarity 82.9%;
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [g kappa chain V region (PC7769)
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A;Tille: Rearrangement of genetic information may produce immunoglobulin diversity.

A;Reference number: A93204; MUID:79073152; PMID:103003

A;Reference number: A93204; MUID:79073152; PMID:103003

A;Accession: D01937

A;Residues: 1-110 (WEI>
A;Cross-references: UNIPROT;P01668; UNIPARC;UP100002A103

A;Cross-references: UniPROT;P01668; UNIPARC;UP100002A103

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into 1e C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;16-94/Domain: immunoglobulin homology cIMM>

F;23-92/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIVMTOSPDSLAVSLGERATINCKSSOSVLYSSNNKNYLAWYOOKAGOPPKLLIYWASTR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig kappa chain V region - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000 C;Accession: S34003 R;Mariette, X.; Tsapis, A.; Brouet, J.C. Bur. J. Immunol. 23, 846-851, 1993 A;Title: Nucleotidic sequence analysis of the variable domains of four human A;Reference number: S34001; MUID:93209281; PMID:7681398
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C;Species: Mus musculus (house mouse)
C;Date: 06-Peb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
                                                         CiSpecies: Mus musculus (house mouse)
CiDate: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
CiAccession: D01937, A01937
RiWeigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIVLTQSPASLAVSLGQRATISCKASQSLDYDGDSYMMYQQKPGQPPKLLIYAASNLES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSNEDPPRFGGGTKVEIK 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Pred. No. 6.4e-32;
4; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 468.5; DB 1
Pred. No. 3.2e-32;
8; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: UNIPARC: UPI0000176CCA
                              Ig kappa chain V region (PC7210) - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.7%;
illarity 83.2%;
Conservative 4
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81.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-113 < MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Best Local S
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S19972
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                                                                                                                                                                                                                     C;Species: Was musculus (house mouse)
C;Species: Was musculus (house mouse)
C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 09-Jul-2004
C;Accession: A01936
R;McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A;Title: Mechanisms of antibody diversity: multiple genes encode structurally related mc A;Reference number: A93822; MUID:79012520; PMID:99744
A;Accession: A01936
A;Molecule type: protein
A;Residues: 1-111 AMCK.
A;Cromser. Ferences: UNIPROT:P01664; UNIPARC:UPI000002A0FF
C;Comment: This chain was isolated from a myeloma protein.
A;Residues: 1-11 AMCK.
A;Cromser. An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C;Complex: An immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer
F;16-94/Domain: immunoglobulin homology <IMM>F;23-92/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
$1976
Ig kappa chain V region (M-T413) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
R;Weissenhorn, W.; Riethmueller, G.; Weiss, B.M.; Rieber, E.P.
A;Description: Structural characterization of CD4 mAb.
A;Reference number: S19976
A;Reference number: S19976
A;Residues: 1-112 <WEI>
A;Residues: 1-112 <WEI>
A;Residues: 1-112 <WEI>
A;Residues: 1-112 <WEI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <INM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 111;
                                                                                                                                                                                                  Ig kappa chain V region (CBPC 101) - mouse (tentative sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 476; DB 1; Length 11
Pred. No. 7.7e-33;
8; Mismatches 13; Indels
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ilarity 79.5%; Pred. No. 9.4e-33;
Conservative 11; Mismatches 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 81.1%;
Matches 90; Conservative
                                                   GTKVEIKR 133
GTKVEIKR 131
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Best Local Similarity
Matches 89; Conserv
124
                                                      126
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Search completed: February 23, 2006, 09:23:58 Job time: 24:1176 secs
                        A; Molecule type: protein A; Residues: 1-111 <WEI>
                                                                                                                                                                                                                                   A,Accession: A93822
A,Molecule type: protein
A,Residues: 1-111 <MCK>
                                                                                                                                                                                                               A; Contents: T111
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             When the second of the EMBL Data Library, March 1992

Submitted to the EMBL Data Library, March 1992

Submitted to the EMBL Data Library, March 1992

Appearation: Structural characterization of CD4 mAb.

Appearation: S19972

A; Accession: S19972

A; Regidues: 1-12 < WEI>
A; Residues: 1-12 < WEI>
A; Cross-references: UNIPARC: UPI0000116032; EMBL: X65094; NID: 952290; PIDN: CAA46222.1; PID C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology < INM>
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A;Residues: 1-134 <MAH>
A;Crose-references: UNIPARC:UPIO0001166FE; EMBL:Z46347; NID:g560841; PIDN:CAA86466.1;
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;36-116/Domain: immunoglobulin homology <IMM>
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R; Weigert, M.; Gatmaitan, L.; Loh, B.; Schilling, J.; Hood, L. Nature 276, 785-790, 1978  
A; Title: Rearrangement of genetic information may produce immunoglobulin diversity. A; Reference number: A93204; MuID: 79073152; PMID: 103003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: S49531
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48797
A;Accession: S49531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Homo sapiens (man)
Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                     67.5%; Score 464; DB 2; Length 112; 78.6%; Pred. No. 7.7e-32;
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;; Pred. No. 1.1e-31;
10; Mismatches 22;
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Best Local Similarity 73.4%;
Matches 94; Conservative 1
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Best Local Similarity 78.6*
Matches 88; Conservative
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Accession: S19972
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A,Cross-references: UNIPROT:P01660; UNIPARC:UP1000002A0FB
R;McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. US.A. 75, 3913-3917, 1978
A;Title: Mechanisms of antibody diversity: multiple genes encode structurally related markeference number: A93822; MUID:79012520; PMID:99744
                                                                                                                                                                                                                                                                                                                                  A.Cross-references: UNIPARC:UPI000002A0FB
C.Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap circomplex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into l. C;Superfamily: immunoglobulin V region; immunoglobulin homology
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; Pred. No. 1.1e-31;
14; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Kejwords: heterotetramer
F;16-94/Domain: immunoglobulin homology <IMM>
F;23-92/Disulfide bonds: #status predicted
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Best Local Similarity 78.4%
Matches 87; Conservative
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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February 23, 2006, 09:13:48; Search time 142.559 Seconds (without alignments) 648.323 Million cell updates/sec Run on:

US-10-723-872-14 687 score: Perfect Title:

1 MGWSCIILFLVATATGVHSD......QQSNEDPPRFGGGTKVEIKR 131 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2166443 segs, 705528306 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: uniprot\_sprot:\*
2: uniprot\_trembl:\* UniProt 05.80:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	P01665 mus musculu	P01666 mus musculu	P01667 mus musculu	P01669 mus musculu	P06313 homo sapien	P01664 mus musculu	Q811u6 mus musculu	P06314 homo sapien	P01668 mus musculu	P01660 mus musculu	P01625 homo sapien	P01661 mus musculu	anw	P01663 mus musculu	P01658 mus musculu	P01672 mus musculu	P01670 mus musculu	៣18 ព	P06312 homo sapien	៣៤៩ ព	P01656 mus musculu	P01671 mus musculu	P01673 mus musculu	Q66js7 mus musculu	P01655 mus musculu	P01654 mus musculu	P03977 mus musculu	homod	homo	Q52164 mus musculu	Q96sa9 homo sapien
	;	TD	KV3M MOUSE	KV3N MOUSE	KV3O MOUSE	KV3Q MOUSE	KV4B HUMAN	KV3L_MOUSE	Q811V6 MOUSE	KV4C HUMAN	KV3P MOUSE	KV3H_MOUSE	KV4A HUMAN	KV3 I MOUSE	KV3J_MOUSE	KV3K_MOUSE	KV3F MOUSE	KV3T MOUSE	KV3R_MOUSE	Q920E9 MOUSE	KV40 HUMAN	KV3G_MOUSE	KV3C_MOUSE	KV3S_MOUSE	KV3U_MOUSE	Q66JS7 MOUSE	KV3B MOUSE	KV3A MOUSE	KV3D MOUSE	Q6PIH7 HUMAN	KV1M HUMAN	Q52L64 MOUSE	Q96SA9_HUMAN
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ф	Query	Match	71.8	71.6	71.2	70.7	69.4	69.3	69.1	69.1	68.2	67.2	67.2	9.99	65.5	64.3	63.7	63.5	63.2	63.0	62.6	62.4	61.9	61.9	61.7	61.6	61.5	61.4	60.1	60.1	59.7	59.4	59.3
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## ALIGNMENTS

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MEDIJNE=94009207; PubMed=7691608;
MO J.A., Bona C.A., Holmdahl R.;
Wariable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen.";
Eur. J. Immunol. 23:2503-2510(1993).
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STRUCTURE BY NMR OF 1-111.
STRUCTURE BY NMR OF 1-111.
MEDLINE=20264305; PubMed=10801487; DOI=10.1016/S0969-2126(00)00119-2;
Tugarinov V., Zvi A., Levy R., Hayek Y., Matsushita S., Anglister J.;
"NMR structure of an anti-gpl20 antibody complex with a V3 peptide
reveals a surface important for co-receptor binding.";
Structure 8:385-395(2000).
                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
15 Asppa chain V-III region PC 7043.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Eurchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN SEQUENCE.
MEDLINE-79073152; PubMed=103003;
Weigert M., Garmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
       111 AA
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Ensembl; ENSWUSGO000053225; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003296; Ig_v.
SMART; SM00406; IGV; 1.
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EMBL; Z25446; CAA80933.1; -; mRNA.
EMBL; Z25450; CAA80935.1; -; mRNA.
EMBL; Z25450; CAA80937.1; -; mRNA.
EMBL; Z25452; CAA80937.1; -; mRNA.
EMBL; Z25454; CAA80931.1; -; mRNA.
EMBL; Z25454; CAA80941.1; -; mRNA.
EMBL; Z25458; CAA80945.1; -; mRNA.
       PRT;
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Nature 276:785-790(1978).
       STANDARD;
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PDB; 1QNZ; NMR; L=1
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P01665;
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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                                                              Complementarity-determining-1. Framework-2.
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Complementarity-determining-1.
Framework-2.
Complementarity-determining-2.
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Complementarity-determining-3.
Framework-4.
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                                                                                                                                                                                                                                           Score 493; DB 1;
Pred. No. 4.8e-41;
7; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
18 kappa chain V-III region PC 7183.
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SMR; P01665; 1QNZ.
SMR; P01665; 1-111.
SMR; P01665; 1-111.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003596; Ig_v.
SMART; SM0406; IG_v.
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin do Immunoglobulin V region.
                                                                                                                                                                        By similarity.
                                                                                                                      Framework-3.
                                                   Framework-1
                                                                                                                                                                                                          12002 MW;
                                                                                                                                                                                                                                                            83.88;
                                                                                                                                                                                                                                             71.8%;
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                                                                                                                                                                                                                                                            Local Similarity 83.8
nes 93; Conservative
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                                mmunoglobulin V region
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KV3N MOUSE
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                          DIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES
                                                                                                                                                 Mammalia; Eutheria; Euzrhontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Musinae; Mus. NCBI_TaxID=10090;
                                                                                    Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=79073152; PubMed=103003; Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; Rearrangement of genetic information may produce immunoglobulin
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                                     71.6%; Score 492; DB 1; Length 111; 82.9%; Pred. No. 6e-41; ive 8; Mismatches 11; Indels
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Complementarity-determining-3.
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ches 12; Indels
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111 AA; 11952 MW; 2058BB50CE306D31 CRC64;
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InterPro; IPR007110; Ig-like.
InterPro; IPR03596; Ig_v.
SMART; SM00406; IGv; 1.
PROSTIF; PSSO35; IG_IKE; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
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                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
19 kappa chain V-III region PC 6308.
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sive 7; Mismatches
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                                                                                92; Conservative
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                                     Query Match
Best Local Similarity
Matches 92; Conserv
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SMR; P01667; 1-111
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P01667;
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   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GOPPKLLIYAASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQOSNEDPPRFGG
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                            MEDLINE=86041853; PubMed=2997712;
Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.
                                                                                                                                                        Zachau H.G.;
Subgroup IV of human immunoglobulin K light chains is encoded by
single germline gene.";
Nucleic Acids Res. 13:6515-6529(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.4%; Score 476.5; DB 1; Length 133; ilarity 75.8%; Pred. No. 2.6e-39; Conservative 10; Mismatches 18; Indels 3
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Complementarity-determining-1.
Framework-2.
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Pramework-4.
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ID KV3L MOUSE

AC P01664;

DT 21-JUL-1986. (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE 19 kappa chain V-III region CBPC 101.
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SMR, P06313, 21-133.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:006855; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                    EMBL; Z00022; CAA77317.1; -; Genomic_DNA PIR; A01904; K4HUJI.
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PROSITE; PS50835; IG LIKE; 1.
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                                                     NCBI_TaxID=9606;
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Local Sim.
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                                                                                                                                                                                                 Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Muridae; Mus
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MEDLINE=79073152; PubMed=103003;
Weigert M., Gatmaltan L., Loh B., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDPWTFGSGTKLEIK 111
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Complementarity-determining-1.
Framework-2.
Complementarity-determining-2.
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Pred. No. 2.4e-40;
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PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
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01-JAN-1988 (Rel. 06, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Homo sapiens (Human).
                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MXY-2005 (Rel. 47, Last annotation update)
1G kappa chain V-III region PC 7769.
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9; Mismatches
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SMR; P01669; 1-111.
Smembl; BNSWIGG0000053225; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-V.
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l Similarity 82.0%;
91; Conservative
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                                                                                           STANDARD;
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                                                                                                                                                                                               This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation-the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Anti-human Fc gamma receptor III 3G8 kappa light chain variable region
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                                                                           McKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinee; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bruenke J., Fischer B., Barbin K., Schreiter K., Wachter Y., Mahr K., Titgemeyer F., Niederweis M., Peipp M., Zunino S.J., Repp R., Valerius T., Fey G.H.; M., Pey G.H.; M., Pey G.H.; Is a tecombinant bispecific single-chain FV antibody against HLA class II and FcgammaRIII (CD16) triggers effective lysis of lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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Complementarity-determining-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50815; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
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                                                                                                                                                                                                                                                                                                                                                                             Ensembl; ENSMUSGG0000053225; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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                                                            MEDLINE=79012520; Pubmed=99744;
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Q811U6;
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Mus musculus (Mouse)
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HSSP; P01665; 1QNZ.
SMR; P01664; 1-111.
NCBI_TaxID=10090;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=86041854; PubMed=2997713;
Marsh P., Mills F., Gould H.;
"Detection of a unique human V kappa IV germline gene by a cloned cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 IVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLESG
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HSSP; P01655; 11vVB.
SMR; P06314; 21-134
GO; GO:000557; C:extracellular region; NAS.
GO; GO:0005823; F:antigen binding; NAS.
GO; GO:000585; P:immune response; NAS.
InterPro; IPR00559; I=1ke.
InterPro; IPR00559; Ig_v.
SMART; SM00406; IG_v.
PROSITR; PSS0835; IG_LKE; 1.
Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                            69.1%; Score 475; DB 2; Length 11
79.3%; Pred. No. 2.9e-39;
ive 10; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                   111 111
111 AA; 12101 MW; CEDECEE157F2C94A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1988 (Rel. 06, Created)
01-APR-1988 (Rel. 07, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
14 Kappa chain V-IV region BI7 precursor.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 AA
                                                                     SMR; O811U6; 1-111.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR001110; Ig-like.
InterPro; IPR001596; Ig.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 13:6531-6544(1985).
Br. J. Haematol. 125:167-179(2004).
EMBL; AY173024; AAO18226.1; -; mRNA.
HSSP; P01665; 1QNZ.
                                                                                                                                                                                SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                 88; Conservative
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                                                                                                                     1 DIVLTQSPASLAVSLGQRATISCKASQSLDYDGDSYMMYQQKPGQPPKLLIYAASNLES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=79012520; PubMed=99744;
McKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally
                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
-!- MISCELLANEOUS: The PC 3741 and TEPC 111 sequences are identical.
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurogna:
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN SEQUENCE (PC 3741).
MEDLINE=79073152; PubMed=103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                       80 GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSNEDPPRFGGGTKVEIK 130
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Framework-2.
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Framework-3.
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   110 AA; 11950 MW; 69F1A5CE886B1249 CRC64;
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                                    DB 1;
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; Pred. No. 5.8e-38;
14; Mismatches 10;
                                   Score 468.5; DB 1
Pred. No. 1.3e-38;
3; Mismatches 12
                                                                                                                                                                                                                                                                                                                         10-MAY-2005 (Rel. 01, Last sequence update) Ig kappa chain V-III region PC 3741/TEPC 111. Bukaryota: Materyota: Materyota
                                                                                                                                                                                                                                                                                        111 AA
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Ensembl; ENSWINGS00000060064; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
PROSITE; PSS0935; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin of Immunoglobulin V region.
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01, Last seq
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                                 Query Match
Best Local Similarity 81.1%;
Matches 90; Conservative
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PROTEIN SEQUENCE (TEPC 111)
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Best Local Similarity 78.4
Matches 87; Conservative
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                                                                                                                                                                                                                                                                                                                         67 GQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYCQQYYNLPWTFGQ 126
                                                                                                                                                                                                                                                                                                    GOPPKLLIYAASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSNEDPRFGG 123
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                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                      Gaps
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                               Complementarity-determining-2. Framework-3. Complementarity-determining-3.
                                                                                                                                                                  Length 134;
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Framework-4.
Complementarity-determining-1.
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                                                                                                                                   6413A22FD0738832 CRC64;
                                                                                                                                                                 Score 475; DB 1; L. Pred. No. 3.7e-39; 9; Mismatches 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
RAPPA chain V-III region PC 7210.
Mus musculus (Mouse).
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                     Framework-2
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MEDLINE=79073152; PubMed=103003;
                                                                                                                               14966 MW;
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InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
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Direct protein sequencing; Im
Immunoglobulin V region.
                                                                                                                                                                 ch 69.1%;
| Similarity 75.0%;
96; Conservative
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SMR; P01668; 1-110
                                                                                                                                   134 AA;
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                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
              DIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES
                                 Schneider M., Hilschmann N.;
"The primary structure of a monoclonic immunoglobulin-L-chain of subgroup IV of the kappa type (Bence-Jones protein Len).";
Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
                                                                                  3D-structure, Bence-Jones protein, Direct protein sequencing, Immunoglobulin domain, Immunoglobulin V region.
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Complementarity-determining-3.
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PDB; 1EEQ; X-ray; A/B=1-114.
PDB; 1EKG; X-ray; A/B=1-114.
PDB; 1EKG; X-ray; A-1-114.
PDB; 1EKG; X-ray; G=1-114.
PDB; 2LVE; X-ray; G=1-114.
PDB; 3LVE; X-ray; G=1-114.
PDB; 3LVE; X-ray; G=1-114.
PDB; 5LVE; X-ray; A/B=1-114.
PDB; 5LVE; X-ray; A/B=1-11
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01-OCT-1996 (Rel. 34, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
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                                                                                                                                                                                                                                                                                                   Ig kappa chain V-IV region Len. Homo sapiens (Human).
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MEDLINE=78235887; PubMed=98179;

MEDLINE=78235887; PubMed=98179;

MEDLINE=7825887; PubMed=98179;

MEDLINE=7825881; PubMed=98179;

Puratiant Y. Schechter 1.;

Variable and constant regions of immunoglobulin light chain

precursors: implications on the organization and controlled expression of immunoglobulin genes.";

Biochemistry 17:2392-2400(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNSKNYLAWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=79012520; PubMed=99744;
MCKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 DIVMTQSPDSLAVSLGERATINCKASQSVDYDGDS--YMNWYQQKPGQPPKLLIYAASNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSNEDPPRFGGGTKVEIKR 131
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7
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                                                                                                                                                                                                                                                                                                                                        12640 MW; 0647F1D17F236485 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kappa chains with limited sequence differences.";
Biochemistry 12:760-771(1973).
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21-JUL-1986 (Rel. 01, Last sequence update)
10-WAY-2005 (Rel. 47, Last annotation update)
1g kappa chain V-III region MOPC 63 precursor.
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MEDLINE=73140225; PubMed=4691517;
MCKean D.J., Potter M., Hood L.E.;
Mouse immunoglobulin chains. Pattern
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 114 AA:
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10-MAY-2005
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as long as its content is in no way modified and this statement is
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McKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions."; Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
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-!- MISCELLANEOUS: The ABPC22 and PC9241 sequences are identical.
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Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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Framework-1.
Complementarity-determining-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ,16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 457.5; DB 1;
; Pred. No. 2e-37;
17; Mismatches 16;
                                                                                                                                                                                         Direct protein sequencing; Immunoglobulin domain, Immunoglobulin V region; Signal.
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21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Ilg kappa chain V-III region ABPC 22/PC 9245.
Mus musculus (Mouse).
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SMR; P01661; 21-131.
Ensembl; ENSMUSG0000060064; Mus
                                                                                                                     InterPro; IPR007110; Ig-like.
InterPro; IPR001359; Ig v.
SMART; SM00406; IGv; 1.
PROSITE; PS50815; IG_LIKE; 1.
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Muroidea, Muridae, Murinae, Mus.
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"Rearrangement of genetic information may produce immunoglobulin
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                                                                                                                                                                                                                                                                                                  Immunoglobulin domain;
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14; Mismatches
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By similarity.
                                                                                                                                                                  Ensembl; ENSMUSSO000060064; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
PROSITE; PS50815; IG_LIKE; 1.
Direct procein sequencing; Immunoglobulin
Immunoglobulin V region.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                   Framework-1.
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                                                                                                                                                                                                                                                                                                                                                                                                    Framework-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.5%;
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SMR; P01662; 1-111,
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SMR; P01663; 1-111.
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[mmunoglobulin V region; Signal.

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMES outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDITINE-78255887; PubMed=98179;
Burstein Y., Schechter I.;
Burstein Y., Schechter I.;
Primary structures of N-terminal extra peptide segments linked to the variable and constant regions of immunoglobulin light chain precursors; implications on the organization and controlled expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IG-v.
PROSITE; PS50815; IG_LIKE; 1.
Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISCELLANBOUS: The partial sequence of the C region of this Bence-Jones protein was also determined. It differs from that reported for mouse MOPC 21 only in the transposition of two nearby
                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
1g kappa chain V-III region MOPC 321 precursor.
Mus musculus (Mouse).
Bukaryota; Merazoa; Chordata, Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Euarchontcoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Mus.
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"Mouse immunoglobulin chains. Partial amino acid sequence of a kappa
                                                                                                                                                                                                                                                                                            GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSNEDPPRFGGGTKVEIK 130
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Complementarity-determining-1.
Framework-2.
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Biochemistry 17:2392-2400(1978)
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Immunoglobulin V region
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SMR; P01658; 21-132
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62.7%; Pred. No. 1.9e-35;
ive 27; Mismatches 17
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| 2023   | 0823   | 7059   | 9853  | 7914  | 7233<br>19852  | 9926   | 7211   | 7218   
   | 3684   | 3678   | 8538  | 8536   | 3688   
   | 3682   | 3683   | 9887   | 3693   | 1897   | 7166   
   | 6943   | 0652   | 0688   | 1919   | 1903  
  | 7724  | 3680  | 6140  | 6773  | 7439   
   | 9886   | 5662   | 0030   | 4211   | 9597  | 9895                                   |
| Ady2   | Aay5<br>Aay5                                   | Abrs   | Aanb<br>Aau9  | Adje  | Adg3<br>Aau9   | Aao2<br>Adj8   | Adg3   | Adq3   
   | Adq3<br>Aeb1   | Aeb1   | Aaol  | Aayy   | Aar/<br>Aeb1   
   | Aeb1<br>Aeb1                                   | Aeb1   | Adwo<br>Adw7   | Adwo<br>Aeb1   | Adf7<br>Abo2   | Abo2<br>Adf7   
   | Aab7   | Adwo   | Adwo   | Adf.   | Adf7  
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   | 3682<br>3689                                   | 3683<br>5654   | 0690<br>9887   | 0691<br>3693   | 1897<br>7167   | 7166<br>1899   
   | 5943<br>7030   | 0652   | 0688<br>0688   | 6161   | 1903<br>1920  
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                                                                                                                                                                                                                                                    Chimeric antibody, humanized antibody, antibody engineering, monoclonal antibody; MAb; interleukin-4; IL-4; allergy; CDR; complementarity determining region.
                                                                                                                                                                      ALIGNMENTS
                 ADY28825
ADY28849
ADZ81895
AEB09552
                                         AAR15442
AAR95947
ABB79731
AAR74967
                                                                AAR28668
AAW01143
AAW44168
AAU76130
AAU76121
AAU76131
AAW03723
                                                                                                             AAW01525
AAW24989
                                                                                                                        AAR74966
AAW19578
AEB48772
                                                                                                                                         ABG60106
                                                                                                                                                     ADS07227
                                                                                                                                                                                                                                                                                                                                                           Gross MS, Sylvester DR;
                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 54; 97pp; English.
                                                                                                                                                                                                  AAR70195 standard; protein; 15 AA
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                                                                                                                                                                                                                                                                                                                         93US-00117366.
93US-00136783.
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                                                                                                                                                                                                                              (first entry)
 MAb 3B9 light chain CDR.
                                                                                                                                                                                                                         (revised)
                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-123387/16.
 WO9507301-A1
                                                                                                                                                                                                                                                                                                              07-SEP-1994;
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                                                                                                                                                                                                                        25-MAR-2003
20-SEP-1995
                                                                                                                                                                                                                                                                                                   16-MAR-1995
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 AAR70195;
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3B9 was positive. CDNA clones of the 3B9 light and heavy chains were cloned into pGEM7f+ and transformed into E. coli DH5-alpha. A light chain consolation was sequenced (AAQ83490) that encoded the protein given in AAR70189. 3 CDRs (AAR70195-97) were identified. (Updated on 25-MAR-2003 to correct PN field.)
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to evaluate drugs in animal models and to treat Fas-associated diseases
e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HFETA, monoclonal antibody, mouse, Fas; humanised antibody; apoptosis; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomernlar nephritis; complementarity determing region; CDR.
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                                                                                                                                                                                                                                                                                            Length 15;
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                                                                                                                                                                                                                                                                                     100.0%; Score 79; DB 2; 1 100.0%; Pred. No. 4.2e-06;
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                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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97JP-00169088.
97JP-00276064.
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(first entry)
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                  Sequence 15 AA;
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15-MAR-1999
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08-OCT-1997;
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             evaluate, in animal models, treatments of diseases that involve Fas/Fas autoimmune disease (e.g. systemic lupus errthematosus, including autoimmune disease (e.g. systemic lupus errthematosus, Hashimoto a disease, e.g. systemic lupus errthematosus, Hashimoto and sisease, scleroderma, Goodpasture syndrome, pernicious anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myosclerosis, myapthy, glomenular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed). (Updated on 25-MAR-2003 to correct DR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New DNA molecules encoding recombinant antibodies useful for treating IL4-mediated conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Light chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin E-mediated allergic reaction; allergic rhinitis; conjunctivitis; atopic dermeltis; atopic dermeltis; atopic dermeltis; antopic assethma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a complementarity determining region (CDR) of the light chain variable region of murine interleukhar4 (IL-4) antibody 3B9. The specification describes chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin B-mediated allorgic reactions e.g. allergic rhintis, conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,
                                                                                                                                                                                                                                                                                                                           Gaps
inhibiting Fas-induced apoptosis in normal cells. They are used to
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                                                                                                                                                                                                                                                                                    Length 15;
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                                                                                                                                                                                                                                                                                  Score 79; DB 2; L. Pred. No. 4.2e-06; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY23772 standard; peptide; 15 AA.
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94WO-US010308.
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ilarity 100.0%;
Conservative 0
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N-PSDB; AAX85889.
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Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                               Sequence 15 AA;
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07-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a light chain complementarity determining region (CDR) from an antibody of the invention. The antibody is a chimeric or humanised interleukin-4 (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgB) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft
rheumatoid arthritis, host-vergus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans
                                                                                                                                     Gaps
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                                                                                                    100.0%; Score 79; DB 2; I
100.0%; Pred. No. 4.2e-06;
iive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                Light chain CDR for hIL-4 specific antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant IL4 antibodies useful for atopic ashthma and anaphylactic shock.
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                                                                                                                                                                                                                                                                        AAY18114 standard; peptide; 15 AA.
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CORP.
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93US-00136783.
94WO-US010308.
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SMITHKLINE BEECHAM
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                                                                                                                                  Conservative
                                                                                    Query Match
Best Local Similarity
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14-OCT-1993;
07-SEP-1994;
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                                                                         Sequence 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                      AAY18114;
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                                                                                                                                                                                                                                            RESULT 4
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Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dematological; immunoumpressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; hepatotropic; humanized; addison's disease; systemic lupus erythematosus; sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, which is useful for the lymphocytes from cells to be used in bone marrow transplantation of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived complementarity determining region CDR-1 protein fragment which is used to illustrate the method of the invention
                                                                                                              Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells.
                                                                  Murine CD4/CD34 recognizing antibody light chain CDR-1 region #1.
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100.0%; Pred. No. 4.2e-06;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                            99WO-JP002711.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ASAH ) ASAHI KASEI KOGYO KK.
(ASAH ) ASAHI MEDICAL CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                             98JP-00159957
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                                                                                                                                                                                           CDR-1; light chain; murine.
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                        31-MAR-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                               24-MAY-1999;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autolmmune diseases, contains anti-Fas antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFE7A, or a humanised version of HFE7A containing identical CDRs (complementarity determining regions) to antibody HFE7A. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulomephritis, aplactic anaemia (pammyelophthiais), hepatitis, AIDS and organ graft rejection. Sequences AAB14744-B14746 represent CDRs 1-3 of the light chain of the murine anti-human Fas monoclonal antibody HFE7A, which is produced by hybridoma HFE7A (FERM-BP-5828)
                                                                                                                                                                                                                                                                                                                                                 Anti-Fas antibody, monoclonal antibody HFE7A, FERM-BP-5828, murine, complementarity determining region, CDR, human Fas; Fas ligand; apoptosis modulator; programmed cell death, autoimmune disease, allergy, atteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 79; DB 3; Length 15; 100.0%; Pred. No. 4.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                          Mouse anti-Fas antibody HPE7A light chain CDR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; Page 65; 139pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY51136 standard; protein; 15 AA.
                                                                                                                                                                  AAB14744 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99JP-00278301
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KASQSVDYDGDSYMN 15
                                            KASOSVDYDGDSYMN 15
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                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SANY ) SANKYO CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-485645/43.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JP2000169393-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            light chain.
                                                                                                                                                                                                                                                           24-NOV-2000
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Gaps

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AAY51136;

AAYS1136 ID AAYS XX AC AAYS RESULT 6

Best Loca Matches

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Length 15; Indels " All contracts that were lift

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Antibody 4H5 L chain variable region CDR1 fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel humanized anti-Fas antibody-like

molecule (1) that, induces apoptosis in cells with an abnormal Fas/Fas

ligand system, by binding to Fas on the cell surface, and prevents

candiand sits ligand. The products of the invention have anti-inflammatory,

anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,

canti-anemic, nephrotropic, anti-allergic, anti-arthritic, antiviral,

antiarteriosclerctic, cardiant and hepatropic activity. (1) induce

apoptosis by binding to cell surface Fas or inhibit it by competitive

inhibition of ligand binding. (1) are used to treat and/or prevent

diseases associated with the Fas/Fas ligand system, especially systemic

clupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft

versus host disease, slorgen's syndrome, pernicious or hypoplastic

canemia, Addison's disease, sclercderm, docdpasture syndrome, Crohn's

disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,

multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin

dependent diabetes mellitus, allorsy, arteriosclerosis, myocarditis,

cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral

(B, C or D) or alcoholic), and transplant rejection. (I) selectively

inhibit apoptosis in normal cells but selectively induce it in abnormal

cells. They bind to both human and murine selectively induce it in abnormal her artive site of Fas, i.e. they mimic

the next induced the selective in the active site of Fas, i.e. they mimic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "MALLINE ALBERGE MODGESS. (1) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a murine anti-Fas antibody peptide fragment described in the method of the invention
                                                                                                                                                                                                                                                                                                       New humanized anti-Fas antibody, useful for treating or preventing e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
            insulin dependent diabetes mellitus, arteriosclerosis, myocarditis; cardiomyopathy, glomerulonephritis, hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                     inflammatory or autoimmune disease, induces apoptosis selectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                           Takahashi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 79; DB 3; Length 15; 100.0%; Pred. No. 4.2e-06;
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                                                                                                                                                                                                                                                           Haruyama H, Nakahara K, Tamaki I,
                                                                                                                                                                                                                                                                                                                                                     cells with abnormal Fas-Fas ligand systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 98; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY59259 standard; peptide; 15 AA.
                                                                                                                                                    99EP-00307711
                                                                                                                                                                                 98JP-00276881
                                                                                                                                                                                               98JP-00276882
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hes 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15 AA;
                                                                                                                                                                                                                           (SANY ) SANKYO
                                                            Mus musculus
                                                                                                                                                 29-SEP-1999;
                                                                                                                                                                                 10-SEP-1998;
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                                                                                      EP990663-A2
                                                                                                                                                                                                                                                           Serizawa N,
                                                                                                                      05-APR-2000
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Matches
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The invention provides an antibody having affinity to CD4 antigen. The anti-buman CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. Sequences AAY59259-61 represent the complementarity determining region (CDR)-1, -2 and CDR-3 fragments in the L chain variable region of the antibody respectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drug for preventing or treating e.g. autoimmune disease or allergy, comprises humanized anti-Fas antibody.
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Local Similarity 100.0%; Pred. No. 4.2e-06;
les 15; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   An antibody and the nucleic acid coding the antibody
CD4 antigen; anti-human; antibody; 4H5; drug; CDR; complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB74909 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 14; 25pp; Japanese.
                                                                                                                                                                                                                                                     98JP-00163034.
                                                                                                                                                                                                                                                                                                               98JP-00163034
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                                                                                                                                         JP11332563-A.
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KASQSVDYDGDSYMN 15
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Local S...
15;
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Matches
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AAR66143
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                         The invention relates to a preventive or treating agent for diseases caused by abnormality in the FasFras ligand system containing, as the active component, an antibody having a light chain subunit and a heavy chain subunit and an activity of combining specifically with mammalian Fas and an activity of inducing apoptosis in a cell expressing Fas. The agent has antiallergic, immunosuppressive and apoptotic activity and is used for preventing and treating autoimmune diseases, allergy, atopy and others. The present sequence is that of a peptide useful to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a preventive or treating agent for diseases caused by abnormality in Fas/Fas ligand system containing as the active component an antibody having as the light chain subunit a polygeptide containing residues 1-218 of one of 3, 239 residue amino acid sequences, or residues 1-451 of one of 3, 470 residue amino acid sequences, all fully defined in the specification and having an activity of combining apecifically with mammalian Fas and an activity of inducing apportes is a cell expressing Fas. The agent has immunosuppressive and antiallergic activity and is used for preventing and treating autoimmune diseases, allergy, at acpy and others. The present sequence is that of a peptide,
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drug containing humanized anti-Fas antibody, used for preventing and treating autoimmune diseases, allergy, and atopy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, mouse; humanised anti-Pas antibody, Fas/Fas ligand,
light chain subunit; apoptosis; immunosuppressive; antiallergic;
autoimmune disease; allergy; atopic.
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                                                                                                                                                                                      100.0%; Score 79; DB 5; Length 15; 100.0%; Pred. No. 4.2e-06;
                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        Humanised anti-Fas antibody related peptide SEQ ID NO 29
 Example 6 (preparatory); Page 26; 154pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6 (Preparatory); Page 26; 194pp; Japanese.
                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                    ABB74863 standard; peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                   15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         allergy, atopy and other
useful to the invention
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR86140-R66146 are peptides complementary to the variable region of the CD-4 antibody, these peptides are fixed onto a claimed nonwoven fabric (average fibre dia. of 1-30 microns) coated with keto-alkyl halide functional groups. This material can be used as a filter for CD-4 positive cells in a medical treatment involving the extra-corporeal circulation of blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Material for collecting cells positive for CD-4 antibody - comprises nonwoven fabric having keto-alkyl halide functional gp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                       CD-4 antibody variable region; complementary peptide; extra-corporeal blood circulation; cell filter material
                                                                                                                                                                                                                                     CD-4 antibody variable region complementary peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine derived protein fragment #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY51140 standard; protein; 103 AA.
                                                                                                                AAR66143 standard; peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 6; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          93JP-00057206
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                                                                                                                                                                                           (first entry)
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1 KASQSVDYDGDSYMN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1994-346316/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TOYM ) TOYOBO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9961629-A1
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mineral will and objection

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Chemokine; scFV; CD4 antibody; human immunodeficiency virus; HIV; RANTES; pharmaceutical; infection; acquired immune deficiency syndrome; AIDS; inflammatory; autoimmune disease; gene therapy; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a chemokine construct comprising scFV anti-CD4 and a RANTES chemokine or their fragments. Sequences of the invention are useful for preparing a pharmaceutical composition for treating human immunodeficiency virus (HIV) -infection or acquired immune deficiency syndrome (AIDS) or inflammatory and/or autoimmune diseases. They are used as vaccines and in gene therapy. The present sequence is MT413 modified VL protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chemokine,
 The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents the L chain variable region of the antibody 4H5.
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New chemokine construct comprising scFV anti-CD4 and a RANTES chemokinseful for the preparing a composition for treating HIV-infection or inflammatory or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                            ö
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                                                                                                                                  100.0%; Score 79; DB 3; Length 103; 100.0%; Pred. No. 3.6e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 105;
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100.0%; Pred. No. 3.7e-05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 19; 109pp; English.
                                                                                                                                                                                                                                                                                                                                              AAE37732 standard; protein; 105 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-DEC-2002; 2002WO-EP014683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-DEC-2001; 2001EP-00130746
                                                                                                                                                                                                             1 KASQSVDYDGDSYMN 15
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                                                                                                                                                                                                                                               16 KASQSVDYDGDSYMN 30
                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MT413 modified VL protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 KASQSVDYDGDSYMN
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schloendorff
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                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAD56804
                                                                                              Sequence 103 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 105 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003054017-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                         06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                   AAE37732;
                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine.
                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                                                                                          RESULT 14
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   88888
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                                                                                                                                                                                                                                                                                                                                                                                                                                             for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lymphocytes from cells to be used in bone marrow transplantation, the detection of leukenic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used to illustrate
                                                                                                                                                                                                                                                                                  Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells.
                                                                                                                                                                                                                                                                                                                                                                                                 differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for collection of hematopoietic undifferentiated cells, elimination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel device (I) for separating cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 79; DB 3; Length 103; Pred. No. 3.6e-05; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody and the nucleic acid coding the antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD4 antigen; anti-human; antibody; 4H5; drug.
                                                                                                                                                                                       Soka T, Morimoto I, Miyamura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibody 4H5 L chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Page 15-16; 25pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY59263 standard; protein; 103 AA.
                                                                                                                                                                                                                                                                                                                                            Claim 22; Page 79; 111pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.08;
                                     99WO-JP002711
                                                                         98JP-00159957
98JP-00163023
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                                                                                                                                KASEI KOGYO KK
                                                                                                                                                    MEDICAL CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KASOSVDYDGDSYMN 15
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Best Local Similarity 100.
Matches 15, Conservative
                                                                                                                                                                                                                             WPI; 2000-086720/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 103 AA;
                                                                                                                                (ASAH ) ASAHI
(ASAH ) ASAHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP11332563-A
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                                     24-MAY-1999;
                                                                         25-MAY-1998;
26-MAY-1998;
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02-DEC-1999
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                                                                                                                                                                                       Ono M,
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RESULT 15

AAR33309

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This sequence represents the light chain amino acid sequence of a mouse anti-human immunoglobulin E (IgE) antibody. The invention relates to a bispecific antibody that binds specifically to IgE when IgE is bound to its low affinity receptor (FCEL), but does not bind to IgE, when IgE is bound to its high affinity receptor (FCEH). The bispecific antibody comprises an IgE-binding arm with human framework residues of a recipient human antibody and donor murine CR (complementarity determining region) residues, but with at least one human antibodies work by displacing murine residue. The antibody also comprises an FV that is specific for a predetermined antigen other than IgE. The antibodies work by displacing bound IgE from its receptor, or via competitive inhibition of its binding. The bispecific antibodies are used for diagnosis, treatment and prevention of allergy and other IgE-mediated diseases, also, when it mmobilised, for the isolation of FCEL from cells (for research or therapy). The bispecific antibodies of the invention do not cause granulation or release of histamine from mast cells
                                                                                                                                                                                                                                                                                New bispecific antibodies, useful for treating immunoglobulin B-mediated disease, binds to IgE, but only when on the low affinity receptor, and to an antigen other than IgE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 79; DB 3; I
100.0%; Pred. No. 3.7e-05;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP90541 standard; protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 2; 48pp; English.
                                                                                        92WO-US006860.
94US-00185899.
95US-00405617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89EP-00101583
                                                    95US-00466151.
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                                                                                                                                                                                                          Presta LG, Jardieu PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
                                                                                                                                                                    (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised
                                                                                                                                                                                                                                             WPI; 2000-269913/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-1988;
                                                      06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                            14-AUG-1992;
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                                                                                                                               15-MAR-1995;
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                 14-MAR-2000
                                                                                                             26-JAN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibodies capable of binding FCEL-bound IgE but which are substantially incapable of binding FCEH-bound IgE or inducing histamine release from mast cells or basophils, comprise a human Kabat CDR domain into which has been substituted a positionally analogous residue from a Kabat CDR domain of the murine anti-hulgE antibodies MAEL1, MAEL3, MAELS or MAEL7. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                        Antibody; high affinity; FCEH; low affinity; FCEL; IgE receptor; histamine; mast cell; basophil; Kabat; CDR; murine; MAE11; MAE13; MAE15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin B; IgB; anti-human IgB; bispecific antibody; FCEL; FCEH; low affinity binding receptor; high affinity binding receptor; allergy; diagnosis; treatment; histamine release; prevent; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptide(s) binding to specific Fc epsilon receptors - act as IgE antagonists; useful for treating and preventing IgE-mediated disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Light chain amino acid sequence of mouse antibody MaE15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 79; DB 2; I 100.0%; Pred. No. 3.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                     AAR33309 standard; protein; 106 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Fig 2; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              92WO-US006860
                                                                                                                                                                                                                                                                                                                                                                                                                                    91US-00744768
92US-00879495
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                                                                                                             (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Presta LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-094004/11.
                                                                                                                                                                    MaE15 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e.g. allergies.
                                                                                                                                                                                                                                                                                                                      WO9304173-A1
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07-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US6037453-A.
                                                                                                             25-MAR-2003
                                                                                                                               05-JUL-1993
                                                                                                                                                                                                                                                                                                                                                           04-MAR-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jardieu PM,
                                                                                                                                                                                                                                                                                  Synthetic.
                                                                        AAR33309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY85197,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Matches

RESULT 16 AAY85197

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Gaps

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Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV. The heavy and light chain variable regions from these antibodies were sequenced (AAR55120-R55123). The murine anti-HIV CDRs were introduced into human framework regions to construct chimeric antibodies (AAR55124-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse-human chimeric anti-HIV antibody heavy and light chains - and recombinant antibody consisting of the H- and L-chains, useful in AIDS
been substituted a positionally analogous residue from a Kabat CD of the murine anti-huigE antibodies MAE11, MAE13, MAE15 or MAE17. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                            Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;
human immunodeficiency virus; variable region; VH chain; murine
                                                                                                                            ö
                                                                                               Length 111;
                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                               Mouse anti-HIV mu5.5 light chain variable region.
                                                                                            Score 79; DB 2;
Pred. No. 3.9e-05;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KAGA-) ZH KAGAKU KESSEI-RYOHO KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Fig 4; 22pp; Japanese.
                                                                                                                                                                                                                                                                 AAR55123 standard; protein; 111
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0
                                                                                          Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative 0
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/label= CDR2
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/label= CDR3
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/label= FR2
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/label= FR3
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/label= FR1
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/label= FR4
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                                                                                                                                                         1 KASQSVDYDGDSYMN
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                                                               Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ65554
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                                                                                                                                                                                                                                                                                                                                27-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP06125783-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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                                                                                                                                                                                                                                                                                                  AAR55123;
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                                                                                                                                                                                                                                                    AAR55123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody; high affinity; PCEH; low affinity; FCEL; IgE receptor; histamine; mast cell; basophil; Kabat; CDR; murine; MAE11; MAE13; MAE15; MAE17.
                                                                                                                                                                                                                                              The sequence is an L chain variable region from an immunoglobulin with anti-HIV neutralising activity. See AAN90491-3, and AAN90495. (Updated c25-WAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to correct OS field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptide(s) binding to specific Fc epsilon receptors - act as IgE antagonists; useful for treating and preventing IgE-mediated disorders e.g. allergies.
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                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                      Chimeric anti-human immune virus antibodies - contg. mouse variable regions and human constant regions for diagnosis, treatment and
                                                               Matsushita S, Hattori
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                                                                                                                                                                                                                                                                                                                                                            Score 79; DB 1; Length 111;
Pred. No. 3.9e-05;
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                                                             Tokiyoshi S,
                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                SERO THERAPEUTIC RES INS.
                                                                                                          WPI; 1989-229050/32.
N-PSDB; AAN90491, AAN90492, AAN90493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR33305 standard; protein; 111 AA.
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                                                                                                                                                                                                                  Claim 5; Page 15; 33pp; English.
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                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                             Kimachi K,
   88JP-00171385
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92US-00879495
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1993-094004/11.
                                                                                                                                                                      regions and human c
prevention of AIDS.
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MaE11 light chain.
                                                             Eda Y,
                                                                                                                                                                                                                                                                                                                               Sequence 111 AA;
                             (KAGA ) CHEMO
 08-JUL-1988;
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07-MAY-1992;
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                                                                            Takatsuki K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
05-JUL-1993
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                                                               Maeda
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Length 111;

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The recombinant antibody light chain has neutralising activity against HIV. Chimeric antibodies comprising both mouse and human sequences are useful in the treatment/prevention of AIDS caused by HIV. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                           Antibody; heavy chain; light chain; human immunodeficiency virus; HIV; acquired immune deficiency syndrome; AIDS: treatment; prophylaxis; Mus musculus; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant chimeric anti HIV antibody - useful for the treatment
          R55127). (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Osatomi K,
                                                  100.0%; Score 79; DB 2; L
100.0%; Pred. No. 3.9e-05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                        Anti HIV antibody light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             102. .111
/label= Framework region 4.
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|abel= Framework region 1.
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                                                                                                                                                                                                                                                                                                                                                                             19. .53
'label= Framework region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KAGA ) CHEMO SERO THERAPEUTIC RES INST.
                                                                                                                                                                                                                                                                                                                         location/Qualifiers
                                                                                                                                                                  AAR60302 standard; protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                     61. .92
/label= Framework
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93WO-JP000039.
                                                                                                                                                                                                                                                                                                                                                                                                 54. .60
/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                   CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= CDR3
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                                                                                            1 KASQSVDYDGDSYMN 15
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                                                                                                                                                                                                                      (first entry)
                                                                                                          24 KASOSVDYDGDSYMN
                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          .101
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/label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1994-249145/30.
N-PSDB; AAQ70372.
                                                            Local Similarity
les 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prevention of HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 111 AA;
                                Sequence 111 AA;
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                                                                                                                                                                                                                                                                                                      Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JAN-1993;
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09-MAR-1995
                                                                                                                                                                                       AAR60302;
                                                     Query Match
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Region
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                                                               Best Loc
Matches
                                                                                                                                               RESULT 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV. The heavy and light chain variable regions from these antibodies were sequenced (AAR55120-R55123). The murine anti-HIV CDRs were introduced into human framework regions to construct chimeric antibodies (AAR55124-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse-human chimeric anti-HIV antibody heavy and light chains - and recombinant antibody consisting of the H- and L-chains, useful in AIDS
                                Gaps
                                                                                                                                                                                                 Mouse-human chimeric anti-HIV mu5.5-derived light chain V region.
                                                                                                                                                                                                                    Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;
human immunodeficiency virus; variable region; VL chain; murine;
                                .;
0
         100.0%; Score 79; DB 2; Length 111; 100.0%; Pred. No. 3.9e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KAGA-) ZH KAGAKU KESSEI-RYOHO KENKYUSHO.
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                                                                                                                        AAR55127 standard; protein; 111 AA.
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                                                                                                                                                                                                                                                                                                           "murine"
                                                                                                                                                                                                                                                                                                                                                                                                                      "murine"
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/note= "human"
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/label= CDR3
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/label= CDR2
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|abel= FR2
                                                  1 KASOSVDYDGDSYMN 15
                                                               24 KASQSVDYDGDSYMN 38
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|abel= FR3
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(first entry)
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Ouery Match
Best Local Similarity 100...
Local 15, Conservative
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                                                                                                                                                                                                                                           chimeric; humanised
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                                                                                                                                                                                                                                                             Mus musculus.
                                                                                                                                                                                                                                                                        Homo sapiens.
Chimeric.
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30-JAN-1995
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                                                                                                                                               AAR55127;
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                                                                                                    RESULT 20
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Tokiyoshi S;

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The specification describes chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin E-mediated allergic reactions e.g. allergic thinitis, conjunctivitis, atopic astima, anaphylactic shock, rheumatoid arthritis, host-versus-graft disease and renal disease. They are also useful in the disagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans. The present sequence represents the light chain variable region of Ig REI, and is used in the course of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New DNA molecules encoding recombinant antibodies useful for treating IL4
                                                                                                                                                                                                                                                                                      Light chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin E-mediated allergic reaction; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 79; DB 2; Length 111; 100.0%; Pred. No. 3.9e-05; ive 0; Mismatches 0; Indels
                                      Score 79; DB 2; Length 111;
Pred. No. 3.9e-05;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                 Light chain variable region of Ig REI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Col 69-70; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gross MS;
                                                                                                                                                                                   AAY23781 standard; protein; 111 AA
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                                      ch
1 Similarity 100.0%; P.
15; Conservative 0;
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93US-00136783.
94WO-US010308.
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                                                                                           1 KASQSVDYDGDSYMN 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SMIK ) SMITHKLINE BEECHAM (SMIK ) SMITHKLINE BEECHAM
                                                                                                                                                                                                                                       (first entry)
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                                                                                                        24 KASQSVDYDGDSYMN
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                                      Query Match
Best Local Similarity
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                Sequence 111 AA;
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14-OCT-1993;
07-SEP-1994;
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                                                                                                                                                                                                                                                                          Antibody; heavy chain; light chain; human immunodeficiency virus; HIV; acquired immune deficiency syndrome; AIDS: treatment; prophylaxis; Mus musculus; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant chimeric anti HIV antibody - useful for the treatment and
                            Gaps
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/label= CDR1.
/note= "Mouse derived amino acid sequence."
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| Alabel = CDR3.
| Anotes = "Mouse derived amino acid sequence."
| 102. .11
| Alabel = Framework region 4.
100.0%; Score 79; DB 2; Length 111; 100.0%; Pred. No. 3.9e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "Mouse derived amino acid sequence."
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                                                                                                                                                                                                                                                                                                                                                                                                 .. .23
'label= Framework region 1.

    .92
    /label= Framework region 3.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KAGA ) CHEMO SERO THERAPEUTIC RES INST.
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                                                                                                                                          AAR60306 standard, protein; 111 AA.
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                                                   1 KASQSVDYDGDSYMN 15
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(revised)
(first entry)
                                                                         24 KASQSVDYDGDSYMN
                           Conservative
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/label=
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              Similarity
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                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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25-MAR-2003
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              Best Loca
Matches
                                                                                                                RESULT 22
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SMITHKLINE BEECHAM PLC. SMITHKLINE BEECHAM CORP.
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93US-00136783.
94WO-US010308.
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94US-00185899.
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ses 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 111 AA;
                                                                                                                                                                                                      Sylvester DR,
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                                                                                                         07-JUN-1995;
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26-JAN-1994;
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07-SEP-1994;
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                                                                USS914110-A.
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                                            Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            part of a method to improve the affinity of anti-igs antibodies such as each and e27 antibodies can be used for reducing or preventing Igs mediated production of histamine in a mammal. They can be used for treating a disorder mediated by Igs such as hypersensitivity, actor, asthma, allergic rhinitis, conjunctivitis, hay fever, eczema, anaphylactic shock and urticaria. The antibodies can also be used for affinity purification, detection and diagnosis
                                                                                                                                                                                                                                                                                                                                                                          Improving affinity of polypeptides, particularly anti-IgE antibodies - by identifying aspartyl residues which undergo isomerisation and substituting alternative residues and screening for affinity against the
                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence is that of the variable light chain of MaEll. It was used as
                                                                                                                                                 Variable light chain; IgB; antibody; anti-IgB; reduction; prevention; histemine; production, hypersensitivity; allergen; anaphylaxis; atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever; eczema; anaphylactic shock; urticaria.
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                                                                                                                             Mus musculus anti-IgE MaE11 variable light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 79; DB 2; I 100.0%; Pred. No. 3.9e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Light chain sequence for humanised 3B9 antibody,
                                                                                                                                                                                                                                                                                                                                  Lowe J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 87-88; 129pp; English.
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                                                               AAW95650 standard; protein; 111 AA
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KASQSVDYDGDSYMN 38
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                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-106057/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 111 AA;
                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                          WO9901556-A2
                                                                                                                                                                                                                                                                    30-JUN-1998;
                                                                                                                                                                                                                                                                                        02-JUL-1997;
                                                                                                         08-JUN-1999
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                                                                                    AAW95650;
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allergic disorder, allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the light chain of the humanised 3B9 antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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100.0%; Pred. No. 3.9e-05;
iive 0; Mismatches 0;
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differentiation describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hemacopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions
                                              Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or CD34 and their use for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                              Disclosure; Page 97-98; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 95; 111pp; Japanese.
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(ASAH ) ASAHI MEDICAL CO LID
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  N-PSDB; AAZ44232.
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 111 AA;
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                                              Devices
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                                                                                                                                                                                                                                                                                                                            anti-human immunoglobuling E (195) antibody. The invention relates to a bispecific antibody that binds specifically to IgE when IgE is bound to its low affinity receptor (FCEL), but does not bind to IgE, when IgE is bound to its low affinity receptor (FCEH). The bispecific antibody comprises an IgE-binding arm with human framework residues of a recipient human antibody and donor murine CDR (complementarity determining region) residues, but with at least one human CDR residue replacing the analogous murine residue. The antibody also comprises an FV that is specific for a murine residue, the antibody also comprises an FV that is specific for bound IgE from its receptor, or via competitive inhibition of its bingecific antibodies are used for diagnosis, treatment and prevention of allergy and other IgE-mediated diseases, also, when the isolation of FCE from cells (for research or therapy). The bispecific antibodies of the invention do not cause granulation or release of histamine from mast cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                        New bispecific antibodies, useful for treating immunoglobulin E-mediated disease, binds to IgE, but only when on the low affinity receptor, and to an antigen other than IgE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cluster differentiation, cell separation, antibody, CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine.
                                                                                                                                                                                                                                                                                                              This sequence represents the light chain amino acid sequence of a mouse
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Pred. No. 3.9e-05;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY51146 standard; protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine derived protein fragment #8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; ~~
Best Local Similarity 100.0%; Pr
Matches 15; Conservative 0;
                                                                                                                                                                                                                                                                Claim 1; Fig 2; 48pp; English.
95US-00405617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-JP002711
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MEDICAL CO LTD
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                                                                                       Jardien PM:
                                           (GETH ) GENENTECH INC
                                                                                                                               WPI; 2000-269913/23
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15-MAR-1995;
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26-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-DEC-1999
                                                                                       Presta LG,
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Sequence 111 AA;
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                                                                            30-JUN-1998;
                                           US6172213-B1
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                                                            09-JAN-2001.
                                                                                                                              Lowman HB,
                           Synthetic.
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for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used to illustrate the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                             The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents a L chain fragment of the antibody 4H5.
                                                                   Gaps
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                                                 Score 79; DB 3; Length 111;
Pred. No. 3.9e-05;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                            An antibody and the nucleic acid coding the antibody
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                                                                                                                                                                                                                  CD4 antigen; anti-human; antibody; 4H5; drug
                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 22-23; 25pp; Japanese.
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                                                                                                                                              AAY59267 standard; protein; 111 AA
                                                 100.0%; Sc
100.0%; Pr
tive 0;
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                                                                                                                                                                                                 Antibody 4H5 L chain fragment
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                                                                                   1 KASQSVDYDGDSYMN 15
                                                                                                    24 KASQSVDYDGDSYMN 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                               Query Match
Best Local Similarity 100.
Matches 15; Conservative
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                                  Sequence 111 AA;
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Matches
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This invention relates to a nucleotide sequence encoding an antibody with improved anti-IgE antibody activity. The antibody has improved action due to a process comprising, a) identifying aspartyl residues prone to isomerisation in unimproved anti-IgE (immunoglobulin E) antibody; b) substituting alternative residues to create candidate molecules, and c) selecting those candidate molecules which display affinity against the target molecule. Use of the antibody results in antiasthmatic; antiallergic; ophthalmological; dermatological and antiinflammatory antiallergic; ophthalmological; dermatological and antiinflammatory antiallergic ophthalmological; conjunctivitis, eczema, urticaria and food allergies. The mutant antibodies produced by the above mentioned to nucleic acids may also be used as affinity purification agents and in diagnostic assays for detecting the expression of an antigen of interest in specific cell, tissues or serum. Amino acid sequences AAB76935.

AAB76960 represent fragments of anti-IgE antibodies of the invention. Polymucleotide sequence AAF69253 repression plasmid used in the generation of affinity improved anti-IgE antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding anti-immunoglobulin E antibody with improved properties, produced by substituting aspartyl residues in unimproved immunoglobulin E prone to isomerization by other residues by affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-IgB antibody; immunosuppressive agent; IgB-mediated disorder; therapy; atopic allergy; anaphylactic hypersensitivity; asthma; allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy; murine; MaEll; variable light chain domain; VL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine anti-human IgE mAb MaEll variable light chain domain (VL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC
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المحرار والمحروب المعاشلة المحروب والمحرار

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The present invention relates to a method for treating an IgB-mediated disorder. The method involves administering a therapeutical amount of an anti-IgB antibody or its IgB binding fragment. The invention is useful for treating an IgB-mediated disorder e.g. asthma, allergic rhinitis, eczema, urticaria, food allergies and hypersensitivity e.g. anaphylactic hypersensitivity. The present sequence is the murine MaB11 light chain variable region protein.
                                            Treating an IgB-mediated disorder, e.g. asthma, allergic rhinitis, eczema, urticaria, food allergies, or hypersensitivity, by administering an anti-IgB antibody or its antigen-binding fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antibody or its antigen-binding fragment specific to a vertebrate high mobility group box (HMGB) A box that inhibits release of a proinflammatory cytokine from a cell treated with HMGB protein, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High mobility group box; HMGB1; monoclonal antibody; antibody therapy sepsis; antibacterial immunosuppressive; graft rejection; arthritis; antiarthritic; asthma; antiarthritic; lupus erythematosus; antiinflammatory; inflammation; dermatological; respiratory distress syndrome; respiratory-gen.; psoriasis; antipsoriatic; chronic obstructive pulmonary disease; peritonitis; burns; vulnerary ischemia; vasotropic; Behcets disease; garaft versus host disease; inflammatory bowel disease; gastrointestinal-gen.; multiple sclerosis neuroprotective; cachexis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anabolic; infection; musculoskeletal disease; immune disorder
                                                                                                                                                                                                                                                                                             Length 111;
                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                          Score 79; DB 9; 1
Pred. No. 3.9e-05;
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                                                                                                          Example 2; SEQ ID NO 5; 92pp; English
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Best Local Similarity 100.0%;
Matches 15; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry
                                                                                                                                                                                                                                                                                                                                                        KASQSVDYDGDSYMN
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                   WPI; 2005-038757/04
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                                                                                                                                                                                                                                                               Sequence 111 AA;
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Rattus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chemotherapy, IgE-mediated disorder; asthma; allergic rhinitis; eczema; urticaria; food allergy; hypersensitivity; anaphylactic hypersensitivity; antiasthmatic; antiallergic; dermatological; antibacterial; immune disorder; inflammation; ard disease; ince disease; throat disease; respiratory disease; antiinflammatory; dermatological disease;
                                                                                                                                                                                                                            New composition of an improved anti-1gE antibody or IgE binding fragment, useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma, conjunctivitis, eczema, urticaria or food allergies.
                                                                                                                                                                                                                                                                                                                  The invention relates to therapeutic compositions comprising anti-IgE antibody or IgE binding fragment in combination with an adjunct immunosuppressive agent. The composition is useful for treating IgE-mediated disorders. The disorders include atopic allergy associated with anaphylactic hypersensitivity as athma, allergic rhinitis and conjunctivitis, eczema, urticaria and food allergies. The present sequence is murine anti-human IgE mAD MAE11 variable light chain domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 79; DB 8; L
Pred. No. 3.9e-05;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine MaE11 light chain variable region protein.
                                                                                                                                                                    Lowe J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lowe J;
                                                                                                                                                                                                                                                                                        Example 2; SEQ ID NO 5; 89pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jardieu PM,
                                                                                                                                                                    Jardieu PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADW00648 standard; protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUL-1997; 97US-0051554P.
30-JUN-1998; 98US-00109207.
17-NOV-2000; 2000US-00716028.
                                                            17-NOV-2000; 2000US-00716028
                                                                                        97US-0051554P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAR-2004; 2004US-00791619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KASQSVDYDGDSYMN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KASOSVDYDGDSYMN 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.v.
Best Local Similarity 100.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunosuppressive; antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                    Presta LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Presta LG,
                                                                                                                                   (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC
                                                                                                                                                                                               WPI; 2004-326922/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2004259077-A1.
                                                                                        02-JUL-1997;
US6723833-B1
                                                                                                       30-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-MAR-2005
                              20-APR-2004
                                                                                                                                                                   Lowman HB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lowman HB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADW00648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 32
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The invention provides antibodies, or thear antigen-binding fragments, that bind to a vertebrate high mobility group box (EMGE) polypeptide, to methods of detecting and/or identifying an agent that binds to an HMGB polypeptide, methods of treating a condition in a subject characterized by activation of an inflammatory cytokine cascade, and methods of detecting an HMGB polypeptide in a sample. The antibody (or antigenbinding fragment) binds to a vertebrate HMGB hox but does not specifically bind to non-A box epitopes of HMGB, and inhibits release of a proinflammatory cytokine from a vertebrate cell treated with an HMGB captodin. A method of treating a condition characterized by activation of an inflammatory cytokine cascade comprises administering an antibody of the invention, or its antigen-binding fragment. The condition is selected temperatory distress syndrome, chronic obstructive pulmonary disease, psoriasis, pancreatitis, peritonitis, burns, ischemia, Behcet's disease, graft versus host disease, inflammatory bowel disease, multiple sclerosis and cachexia, especially sepsis, anthiritis, or lupus. The present sequence is that of the A box of human HMGB1. An identical
                                                                                                                                                                                                                                                                                                                                                                  ö
               or their antigen-binding fragments,
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human x mouse modified anti-HIV antibody Light chain RLO.5beta.
                                                                                                                                                                                                                                                                                                                                     Length 111;
                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                    Score 79; DB 9; 1
Pred. No. 3.9e-05;
                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heavy; light; CDR; HIV; AIDS; REI; 0.5beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR24575 standard; protein; 112 AA.
               invention provides antibodies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KAGA ) KAGAKU OYOBI KESSEI RYOHO.
                                                                                                                                                                                                                                                                                                                                    100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54. .60
/label= CDR2
61. .92
/label= FR3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24. .38
/label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39. .53
/label= FR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93. .101
/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                           1 KASQSVDYDGDSYMN 15
                                                                                                                                                                                                                                                                                                                                                                                                          24 KASQSVDYDGDSYMN 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ...23
|abel= FR1
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/label= FR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1992-212765/26
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                       Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP04141095-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-OCT-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-MAY-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR24575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibody; DC-SIGN; dendritic cell-specific ICAM-3 grabbing non-integrin; cancer; neoplasm; cytostatic; inflammation; antinflammatory; ectoparasite infection; antiparasitic; infection; viral infection; bacterial infection; antibacterial; virucide; autoimmune disease; immunosuppressive; immune discráer; allergy; antiallergic; immunotherapy; transplant rejection; humanized antibody; single chain antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel antibody capable of binding or recognizing human dendritic cell-
specific intercellular adhesion molecule-3 grabbing non-integrin receptor
on cell, useful for treating cancer, and viral and bacterial infections.
                                                                                                                                  CDRs are mouse monoclonal antibody 0.5beta derived sequences. The anti-
HIV modified antibody can be used for the prophylaxis and treatment of
          New recombinant modified anti-HIV antibodies - comprise human x mouse modified antibody H and L chains.
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                 framework regions (FR) are derived from the human antibody REI.
                                                                                                                                                                           AIDS. Specific examples of the H chain are given in AAR24556-58 and AAR24560-62. A specific example of the L chain is given in AAR24575
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                                                                                                                                                                                                                                                                            Score 79; DB 2; Length 112;
Pred. No. 4e-05;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human DC-SIGN antibody, light chain, SEQ ID NO:44.
                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 5; SEQ ID NO 44; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEB21888 standard; protein; 112 AA.
                                                                          Disclosure; Fig 2; 15pp; Japanese
                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-2003; 2003US-0529517P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-2004; 2004WO-US041788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bowdish KS, Kretz-Rommel A;
                                                                                                                                                                                                                                                                                                                                                           1 KASQSVDYDGDSYMN 15
                                                                                                                                                                                                                                                                                                                                                                                              38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ALEX-) ALEXION PHARM INC
                                                                                                                                                                                                                                                                                                                    15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  24 KASQSVDYDGDSYMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2005-506067/51.
                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                     Sequence 112 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 light chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AEB21888;
                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 35
                                                                                                                 The
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Antibody; ST40; molecular mimetic; CD4; human immunodeficiency virus;

HIV; infection.

WO200109191-A1 Unidentified.

08-FEB-2001

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C cell to another cell, where the bacteria is chosen from Hailtochacter pylori, Klebsiella pneumoniae, Mycobacterium tuberculosis and M. bovis, and the parasite is chosen from Leishmania pignol and Schistosoma mansoni. Also described are: a vaccine comprising Al, a composition comprising Al and a carrier; a diagnostic agent (II) for a tumor characterized by increased DC-SIGN expression, comprising Al, treating a cancer characterized by increased DC-SIGN expression, comprising Al, treating a cancer characterized by increased DC-SIGN expression, comprising Al, treating a cancer characterized by increased DC-SIGN expression, comprising Al, treating C cancer, involves administering to a subject, a demdritic cell xilling amount of a composition comprising Al, and treating (M2) an inflammatory disease, which involves administering to a subject, a demdritic cell xilling amount of a composition comprising Al. Al further comprises a period extended to it. The peptid accomprises an antigen, where the peptid extended to it. The peptid accomprises an antigen, where the peptid extended to it. The peptid accomprises an antigen, where the period extended to it. The peptid accomprises an antigen, where the antibody or an scrope cransmitting virus, also binds to L-SIGN (I) is useful in interaction of DC-SIGN expressing cells and ICMA-expressing cells, which involves administering immune-modulating amount of (I), to a subject. (I) is useful for generating an immune response, which involves administering immune-modulating amount of (I), to a subject suspected of having cancer, which antigen to (I). (I) is useful for delivering an antigen to (I). (I) is useful for delivering an antigen to (I). (I) is useful for the presence of cancer. The determining a tissue sample from a subject suspected of having concer, which harvigen to (I). (I) is useful for blocking infection of the cell virus, bacteria or parasite to the cell blocking infection of the coll virus, bacteria or parasite from the cell coll to the cell virus, bacteria or paras
                            to another cell, where the virus is chosen from HIV, hepatitis C virus (HCV), Ebbla, severe acute respiratory syndrome (SARS), cytomegalovirus (CMV), Sindbis and Dengue, or effectively blocks binding of a bacteria or parasite to the cell, blocks infection of the cell by a bacteria or parasite, and/or blocks transmission of a bacteria or parasite, and/or blocks transmission of a bacteria controlled to another cell, where the bacteria is chosen from Helicobacter
the cell by a virus, and/or blocks transmission of a virus from the cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dendritic cells and/or their function and interaction, studying immune system and for detecting dendritic cells and/or C-type lectins in biological samples. The present sequence represents a human DC-SIGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tolerance, immunotherapy, and in diagnostic and research for studying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibody, light chain, SEQ ID NO:44.
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The present sequence was used in a method for designing a mimetic which exhibits an activity associated with a parent molecule. Such mimetics may be smaller than the parent molecule and correspondingly easier and cheaper to make, since the active region of the parent molecule is normally relatively small. The method is useful where the parent molecule is a binding domain or the hypervariable region of an antibody or other member of the immunoglobulin superfamily. It is useful when the parent molecule is an antibody and the mimetic a peptide, especially an antibody which binds CD4. The mimetics designed and produced are useful diagnostically to detect cells bearing CD4 on their surfaces or may be included in pharmaceuticals e.g. to treat conditions in which CD4 is implicated (e.g. HIV)

Designing molecular mimetics to mimic a parent molecule activity, useful e.g. therapeutically and diagnostically, uses computational screening to identify active chemical groups by accessibility within the parent

Example 1; Fig 1; 85pp; English.

molecule.

Roux F;

**Rees A**,

Lahana R,

Kaczorek M,

Granier C,

Casset F,

SYNT-) SYNT: EM SA

WPI; 2001-168699/17.

02-AUG-2000; 2000WO-GB002972.

99EP-00401968

02-AUG-1999;

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ADI26494;
       ö
                           Gaps
                           ö
            Score 79; DB 9; Length 112;
Pred. No. 4e-05;
Mismatches 0; Indels
                                                                                     AAB71895 standard; protein; 113 AA.
         100.0%; Sco
100.0%; Pre
     Query Match
Best Local Similarity 100.00
Best Local 15; Conservative
                                       1 KASOSVDYDGDSYMN 15
                                                  24 KASQSVDYDGDSYMN
Sequence 112 AA;
                                                                                                  AAB71895;
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Monoclonal antibody ST40 light chain.

(first entry)

09-MAY-2001

RESULT 36 AAB71895

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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody; enzyme; virucide; anti-HIV; cytostatic; antibacterial; helicobacter pylori urease inhibitor; cancer; infectious disease; chemokine receptor CCR-5 antagonist; cancer; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 79; DB 4; Length 113; 100.0%; Pred. No. 4e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADI26494 standard; protein; 113 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori; HIV; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human ECL2B-3-L SEQ ID NO:30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JUL-2003; 2003WO-JP009147.
                                                                                                                                                                                                                                                                                                                                                                                                                              1 KASQSVDYDGDSYMN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                         24 KASQSVDYDGDSYMN 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-APR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       Sequence 113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004009805-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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This invention relates to a novel humanised antibody or antibody fragment which binds to an epitope on an envelope glycoprotein of the Venezuelan equine encephalitis virus, and comprises at least one complementary determining region (CDR) from a non-human antibody and at least one framework region from a human antibody. The invention may be useful for the production of compounds with a virucide activity or vaccines. The humanised antibody is useful for preventing or neutralising viral infection. The present sequence is that of a HY4 26 light chain protein which was used in the exemplification of the invention.
                                                                                                                                                 New humanized antibody or antibody fragment comprising at least one complementary determining region from a non-human antibody and at least one framework region from a human antibody, useful for preventing viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          humanised antibody; epitope; envelope glycoprotein; Venezuelan equine encephalitis virus; complementary determining region; CDR; non-human antibody; framework region; virucide; vaccine; viral infection; human; 384C4 HY4; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New humanized antibody or antibody fragment comprising at least one complementary determining region from a non-human antibody and at least one framework region from a human antibody, useful for preventing viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virucidal antibody-related human 3B4C4 HY4 light chain protein SeqID40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 79; DB 8; Length 113; 100.0%; Pred. No. 4e-05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example; SEQ ID NO 40; 70pp; English.
                                                                                                                                                                                                                                                            Example; SEQ ID NO 91; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADO06796 standard; protein; 113 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAY-2002; 2002US-0379994P
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                                           Hinkel C;
(ALEX-) ALEXION PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
Les 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KASQSVDYDGDSYMN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-376022/35.
                                                                                    WPI; 2004-376022/35.
                                                                                                             N-PSDB; ADO06846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 113 AA;
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                                           Frederickson S,
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                                                                                                                                                                                                                      infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel method for producing antibody enzymes comprising a structural analysis step which confirms the existence in the predicted stereostructure of the antibody based on its amino acid sequence of a catalytic triplet residue structure in which a serine residue, an aspartic acid residue, and a histidine or glutamic acid by the method of the invention has virucide, anti-HIV, cytostatic, and antibacterial activity. The enzyme acts as a helicobacter pylori urease inhibitor, or chemokine receptor CCR-5 (HIV target) antagonist. The method of the invention is useful for the treatment, prevention and diagnosis of cancer and infectious diseases, especially infection by Helicobacter pylori or HIV. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                        Screening potential antibody enzymes by identification of a catalytic triplet residue in the stereostructure for production of antibody enzymes as diagnostic and therapeutic agents for cancer and infectious diseases including HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Virucidal antibody-related HY4 26a light chain protein sequence SeqID91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  humanised antibody; epitope; envelope glycoprotein; venezuelan equine encephalitis virus; complementary determining region; Venezuelan antibody; framework region; virucide; vaccine; viral infection; HY4; light chain.
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Pred. No. 4e-05;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 40; SEQ ID NO 30; 232pp; Japanese.
                                                                                                                                                      (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AD006847 standard; protein; 113 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Sco
100.0%; Pre
                                        2003JP-00051943.
2003JP-00198270.
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                                                                                      17-JUL-2003; 2003JP-00198281,
17-JUL-2003; 2003JP-00198292.
  2002JP-00211756
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                          WPI; 2004-132963/13.
                                                                                                                                                                                               Uda T, Hifumi E;
                                                                                                                                                                                                                                                                   N-PSDB; ADI26495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2004039234-A2
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                         19-JUL-2002;
27-FEB-2003;
                                                                  17-JUL-2003;
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Synthetic.
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AD006847;

RESULT 38 AD006847

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us-10-723-872-16.rag

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This invention relates to a novel humanised antibody or antibody fragment
                    which binds to an epitope on an envelope glycoprotein of the Venezuelan equine encephalitis virus, and comprises at least one complementary determining region (CDR) from a non-human antibody and at least one framework region from a human antibody. The invention may be useful for humanised antibody is useful for preventing or neutralisating viral infection. The present sequence is that of a human 38404 HV4 light chain protein which was used in the exemplification of the invention.
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Sequence 113 AA;

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Gaps
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  Score 79; DB 8; Length 113; Pred. No. 4e-05; Mismatches 0; Indels
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0
  100.0%;
Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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1 KASQSVDYDGDSYMN 15

KASQSVDYDGDSYMN 40

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RESULT 40 AD006849 

ADO06849 standard; protein; 113 AA. (first entry) AD006849;

29-JUL-2004

Virucidal antibody-related HY4 26b light chain protein sequence SeqID93.

humanised antibody; epitope; envelope glycoprotein; Venezuelan equine encephalitis virus; complementary determining region; Venezuelan equine notibody; framework region; virucide; vaccine; viral infection; HY4; light chain.

Homo sapiens

Synthetic.

13-MAY-2004

WO2004039234-A2

13-MAY-2003; 2003WO-US015083

13-MAY-2002; 2002US-0379994P

(ALEX-) ALEXION PHARM INC.

Frederickson S, Hinkel C;

WPI; 2004-376022/35.

N-PSDB; ADO06848

humanized antibody or antibody fragment comprising at least one slementary determining region from a non-human antibody and at least framework region from a human antibody, useful for preventing viral New humanized antibody complementary Infection.

Example; SEQ ID NO 93; 70pp; English.

This invention relates to a novel humanised antibody or antibody fragmen which binds to an epitope on an envelope glycoprotein of the Venezuelan equine encephalitis virus, and comprises at least one complementary determining region (CDR) from a non-human antibody and at least one framework region from a human antibody. The invention may be useful for the production of compounds with a virucide activity or vaccines. The humanised antibody is useful for preventing or neutralising viral infection. The present sequence is that of a HY4 26 light chain protein which was used in the exemplification of the invention.

26 KASOSVDÝDGDSÝMN 40

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RESULT 42

Sequence 113 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to a novel humanised antibody or antibody fragment which binds to an epitope on an envelope glycoprotein of the Venezuelan dequine encephalitis virus, and comprises at least one complementary determining region (CDR) from a non-human antibody and at least one framework region from a human antibody. The invention may be useful for the production of compounds with a virucide activity or vaccines. The humanised antibody is useful for preventing or neutralising viral infection. The present sequence is that of a HY4 26 light chain protein which was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New humanized antibody or antibody fragment comprising at least one complementary determining region from a non-human antibody and at least one framework region from a human antibody, useful for preventing viral
                                                                                                                                                                                                                                                                   Virucidal antibody-related HY4 26c light chain protein sequence SeqID95
                                                                                                                                                                                                                                                                                                               determining region;
                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                humanised antibody; epitope; envelope glycoprotein; Venezuelan equine encephalitis virus; complementary determini CDR; non-human antibody; framework region; virucide; vaccine; viral infection; HY4; light chain.
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Pred. No. 4e-05;
; Mismatches 0; Indels
100.0%; Score 79; DB 8; Length 113; 100.0%; Pred. No. 4e-05; ive 0; Mismatches 0; Indels
                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example; SEQ ID NO 95; 70pp; English.
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                                                                                                                                                                                                                                    (first entry)
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                                Conservative
                                                                                   26 KASOSVDYDGDSYMN
                                                             1 KASQSVDYDGDSYMN
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Matches 15; Conservative
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N-PSDB; ADO06850.
              Local Similarity
les 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004039234-A2
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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Synthetic.
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   Query Match
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Matches
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                                                                                                                                          RESULT 41
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AAR04134

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CPGR is a portion of HIV-1 gpl20 or gpl60 protein. Monoclonal antibodies (MAbs) that react with this and which have the capacity to neutralise the infection of H9 cells in culture by live HIV-1 strains MN and IIIB are claimed. Specifically illustrating the invention are the murine MAD (designated NN-01) produced by hubridoma cell line HB 10726 which is deposited under APCC No. HB 10726. The DNA sequences of the variable regions of the heavy and light chains of MAD NN-01 were cloned by PCR using cDNA generated from hybridoma HB 10726 cytoplasmic RNA as template. The DNA was then sequenced. The DNA and deduced AA sequences are given in AAD56688/R48615. Resequencing the variable regions of MAD NN-01 resulted in the sequences set out in AAD5668/R48616. The heavy chain variable region of NN-01 differs from AAO5688/R48616. The heavy chain variable regions of these CDC and of 120 The 11ght chain variable regions of these two Abs differ by contain variable regions of these chose in the sequences of the three CDRs in the heavy chain (V-H) of the NAC BAT123, while the sequences of the three CDRs in the light chain (V-L) cvary by about 29-4% compared to NM-01. (Updated on 25-MAR-2003 to
                                                                                                                     New humanised antibody specific for epitope on HIV-1 gp 120 - able to neutralise infection of HG cells, also nucleic acid encoding it, useful for passive immunisation to treat or prevent HIV-1 infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matsushita S, Hattori T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 79; DB 2; Length 120;
Pred. No. 4.3e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP90543 standard; protein; 131 AA.
                  (NISP ) NISSIN SHOKUHIN KAISHA LTD
                                                                                                                                                                                             Example; Page 47; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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88JP-00171385
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nes 15; Conservative
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                                                                                    WPI; 1994-083117/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 120 AA;
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20-OCT-1989
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27-AUG-2003
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                                                   Ohno T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be used to form chimeric mouse-variable, human-constant region Abs suggested as being useful as a vaccine to HIV. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence of the monoclonal antibody BAT123 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New chimeric variants of murine antibody anti-leucine - contg. human antibody regions, and DNA encoding sequences.
                                                                                                                                       Anti-Leu 3a light chain variable region gene product, KOL/206 Vl.
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                AAR04134 standard; protein; 115 AA.
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                                                                                                                                                                          HIV; AIDS; anti-Leu3A; vaccine; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                                                                                                    89EP-00310415.
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                                                                                    (revised)
(first entry)
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(first entry)
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Best Local Similarity 100.
Matches 15; Conservative
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N-PSDB; AAQ04041.
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                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                11-OCT-1989;
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22-APR-1993;
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03-SEP-1994
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                                                                                  25-MAR-2003
06-SEP-1990
                                                                                                                                                                                                                                                                                 25-APR-1990
                                                                                                                                                                                                                                                EP365209-A.
                                                                                                                                                                                                                                                                                                                                                                                                                           Hinton R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR48618;
                                                   AAR04134;
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AAR48618
110 AAR4
120 AAR4
120

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Gaps

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A humanized antibody light chain variable region and signal sequence is given in AAR75355. The signal sequence is also provided in AAR70194. The sequences of the 3 CDRs are identical to mouse anti-human II-4 MAD 3B9 light chain CDRs (given in AAR70195-97). (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                           Humanized antibody; antibody engineering; monoclonal antibody; MAb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanized antibody; antibody engineering; monoclonal antibody; MAb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived high affinity mAbs - useful in treatment of IL-4-mediated and IgE-mediated allergic conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 79; DB 2; I
100.0%; Pred. No. 4.7e-05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 71-72; 97pp; English.
                                                                                                              AAR70202 standard; protein; 131 AA.
                                                                                                                                                                                                                            Humanized antibody 3B9 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sylvester DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Humanized antibody 3B9 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR75355 standard; protein; 131 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                     94WO-US010308
                                                                                                                                                                                                                                                                                                                                                                                                                                 93US-00117366.
                                                                                                                                                                                                                                                                            interleukin-4; IL-4; allergy
    1 KASQSVDYDGDSYMN 15
                                  58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                       44 KASQSVDYDGDSYMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                              (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gross MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-123387/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
ses 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     correct PN field.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AA083520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 131 AA;
                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                     07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                 07-SEP-1993;
14-OCT-1993;
                                                                                                                                                                                                                                                                                                                                       WO9507301-A1
                                                                                                                                                                            25-MAR-2003
20-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                      16-MAR-1995.
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20-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Holmes S,
                                                                                                                                               AAR70202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR75355;
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                                                                                                                                                                         The sequence is encoded by a V chi region gene (see AAN90495). The sequence from ABP 21 encodes the L chain variable region. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to correct OS field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be used to form chimeric mouse-variable, human-constant region Abs suggested as being useful as a vaccine to HIV. (Updated on 25-MAR-2003 to correct PF
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human
                                                                             Chimeric anti-human immune virus antibodies - contg. mouse variable regions and human constant regions for diagnosis, treatment and prevention of AIDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-Leu 3a light chain variable region gene product, 206 Vx.
                                                                                                                                                                                                                                                                                     Score 79; DB 1; Length 131;
Pred. No. 4.7e-05;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New chimeric variants of murine antibody anti-leucine antibody regions, and DNA encoding sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 79; DB 2; L
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR04132 standard; protein; 131 AA.
                                                                                                                                           Disclosure, Fig 8; 33pp; English.
                                                                                                                                                                                                                                                                                     100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIV; AIDS; anti-Leu3A; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89EP-00310415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88US-00260558
                                                                                                                                                                                                                                                                                                                                                    1 KASQSVDYDGDSYMN 15
                                                                                                                                                                                                                                                                                                                                                                                  58
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(first entry)
                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                    44 KASQSVDYDGDSYMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1, Fig 2; 12pp;
                               WPI; 1989-229050/32.
N-PSDB; AAN90495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1990-126329/17.
N-PSDB; AAQ04039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oi vT;
                                                                                                                                                                                                                                                         Sequence 131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus.
Takatsuki K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-OCT-1988;
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06-SEP-1990
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RESULT 45 AAR04132

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N-PSDB; AAX85888
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                                                                                    07-JUN-1995;
                                                                                                        07-SEP-1993;
                     Mus sp.
Homo sapiens
                                                                                                                           07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US5928904-A.
                                                                                                                  .-1993;
                                               US5928904-A.
                                                                                                                                                                        Holmes SD,
                                                                  27-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY23779;
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb.
                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                    A humanized antibody light chain variable region and signal sequence is given in AAR75355. The signal sequence is also provided in AAR70194. The sequences of the first 2 CDRs are identical to mouse anti-human IL-4 MAb 3B9 light chain CDRs (given in AAR70195-96), but the third (AAR70201) differs by a single amino acid from the native mouse CDR (AAR70197). (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Light chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin E-mediated allergic reaction; allergic rinintis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.
                                                                                                                                                                                                                                                                                                                              Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated and IgE-mediated allergic conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Light chain variable region of humanised murine IL-4 antibody 3B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                        112. .120
/label= CDR
/note= "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 79; DB 2; Length 131;
Pred. No. 4.7e-05;
                                                                                    "complementarity determining region"
                                                                                                                'note= "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Scor.
100.0%; Pred. No.
                                                1. .20
/label= Sig_peptide
                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                 Gross MS, Sylvester DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY23771 standard; protein; 131 AA.
                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 5, 97pp, English.
                                                                                                                                                                                                                                                   (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                       93US-00117366.
93US-00136783.
                                                                                                                                                                                                    94WO-US010308
interleukin-4; IL-4; allergy
                                                                 43. .57
/label= CDR
                                                                                               73. .79
/label= CDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KASQSVDYDGDSYMN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 KASQSVDYDGDSYMN
                                                                                              .79
                                                                                     'note=
                                                                                                                                                                                                                                                                                                  WPI; 1995-123387/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ73986
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 131 AA;
                                                                                                                                                                                                    07-SEP-1994;
                                                                                                                                                                                                                        07-SEP-1993;
14-OCT-1993;
                   Homo sapiens
                                                                                                                                                               WO9507301-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-SEP-1999
                                                                                                                                                                                 16-MAR-1995,
                                                                                                                                                                                                                                                                                 Holmes S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY23771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                             Peptide
                                                                  Region
                                                                                              Region
                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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The present sequence represents the light chain variable region of a humanised murine interleukin-4 (IL-4) antibody 3B9. The specification describes chimeric and humanised IL-4 monoclonal antibodies. The compositions of the invention are used in therapeutic and pharmaceutical antibodies of the invention are used in therapeutic and pharmaceutical altergic reactions e.g. allergic rehinitis, conjunctivitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New DNA molecules encoding recombinant antibodies useful for treating IL4-mediated conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Light chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; mamunoglobulin B-mediated allergic reaction; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic aesthma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Light chain variable region of humanised murine IL-4 antibody 3B9.
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                                                                                                                                                                                                                                                                                                                              Gross MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY23779 standard; protein; 131 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Fig 5; 50pp; English.
                                                                                                                                                                                                                     (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                   93US-00117366.
93US-00136783.
94WO-US010308.
95US-00483632,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KASQSVDYDGDSYMN 15
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                                                                                                                                                                                                                                                                                                                              Sylvester DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 KASQSVDYDGDSYMN
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This sequence represents the light chain of the humanised 189 antibody of the invention. The antibody is a chimeric or humanised interleukin-4 (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft versus host disease
                                                                                                                                                              Recombinant IL4 antibodies useful for tratment of allergic rhinitis, atopic ashthma and anaphylactic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 79; DB 2; Length 131; 100.0%; Pred. No. 4.7e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: February 23, 2006, 09:39:30 Job time : 155.231 Becs
                               Gross MS
                                                                                                                                                                                                                                             Claim 16; Fig 5; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KASQSVDYDGDSYMN 15
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                               Holmes SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 KASQSVDYDGDSYMN
                                                                                  WPI; 1999-370482/31.
                                                                                                              N-PSDB; AAX79517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 131 AA;
                            Sylvester DR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            humanised murine interior. (IL-4) antibody 3B9. The specification describes chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                New DNA molecules encoding recombinant antibodies useful for treating IL4 -mediated conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibody, interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allaregic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present sequence represents the light chain variable region of
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A;Cross-references: UNIPROT:P01667; UNIPARC:UP1000002A102
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light of hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
E;16-94/Domain: immunoglobulin homology < IMM>
F;23-92/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: protein
A;Residues: 1-111 <MEL>
A;Cross-references: UNIPROT:P01665; UNIPARC:UPI000002A100
R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
B;Mo, J.A.; Bona, C.A.; Holmdahl, R.
A;Mo, J.A.; Bona, C.A.; Holmdahl, R.
A;Title: Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with spectable rece number: $42176; MUID:94009207; PMID:7691608
A;Accession: $42187
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A;Residues: 10-99 <MOJ>
A;Cross-references: UNIPARC:UPI000011655C; EMBL:225444; NID:g407832; PIDN:CAA80931.1; PI
A;NOCE: V-kappa-21E; anti-collagen
A;Accession: S42194
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A;NOte: V-kappa-21E; anti-collagen
A;Accession: S42189
                                                                                                                                                                                                                                                                                                              A,Title: Rearrangement of genetic information may produce immunoglobulin diversity. A,Reference number: A93204; MUID:79073152; PMID:103003
A,Accession: C01937
A,MOLecule type: protein
A,Residues: 1-111 < WEI>
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A;Accession: A01937
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C;Species: Mus musculus (house mouse)
C;Date: 01-Sep-1981 #sequence revision 01-Sep-1981 #text change 09-Jul-2004
C;Accession. A01937; S42187; S42194; S42190; S42189; S42188; S42191; S42192
Accession. M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
                                                                                                                                                                                                        Ig kappa chain V region (PC6308) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accesion: C01937; A01937
C;Accesion: C01937; A01937
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
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; Mismatches 0;
   Score 79; DB 2; 1
Pred. No. 3.9e-06;
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Ig kappa chain V region - mouse (fragment)

C; Species: Mus musculus (house mouse)

C; Species: Mus musculus (house mouse)

C; Accession: $42193

R; Mo, J.A.; Bona, C.A.; Holmdahl, R.

Bur. J. Immunol. 23, 2563-2510, 1993

A; Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec A; Reference number: $42176; MUID:94009207; PMID:7691608

A; Reference number: $42193

A; Accession: $42193

A; Accession: $42193

A; Residues: 1-81 - MOJ>
C; Residues: 1-81 - MOJ>
C; Superfamily: immunoglobulin V region; immunoglobulin homology

C; Keywords: heterotetramer; immunoglobulin homology
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A28601

19 Assolution (163) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C;Accession: A38601
B;Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2144-2142, 1991
A;Title: Common structural features among monoclonal antibodies binding the same antigen A;Reference number: A38601, MUID:91115823, PMID:1703527
A;Accession: A38601
A;Status: preliminary
A;Noblecule type: mRNA
A;Residues: 1-93 <GOS>
A;Residues: 1-93 <GOS>
A;Crosse-references: UNIPARC:UPI0000115175; GB:M57978; NID:g196402; PIDN:AAA63359.1; PID:C;Superfamily: immunoglobulin Nomology
C;Reywords: heterotetramer; immunoglobulin
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S37178
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C90109
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A; Title: Rearrangement of genetic information may produce immunoglobulin diversity.

A; Reference number: A93204; MUID: 79073152; PMID: 103003

A; Accession: B01337

A; Accession: B01337

A; Residues: 1-111 < WEI>
A; Residues: 1-111 < WEI>
A; Cross-references: UNIPROT: P01666; UNIPARC: UPI000002A101

C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin V region: immunoglobulin homology

C; Superfamily: immunoglobulin homology < IMM>
F; 16-94 Domain: immunoglobulin homology < IMM>
F; 23-92/Disulfide bonds: #status predicted
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C,Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kag c,Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kag c,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Superfamily: immunoglobulin V region; immunoglobulin homology
F,16-94/Domain: immunoglobulin homology xIMM>
F,13-92/Disulfide bonds: #status predicted
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A;Experimental source: clone M-T310
A;Accession: S19973
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A;Cross-references: UNIPARC:UPI000116030; EMBL:X65092; NID:g52292; PIDN:CAA46220.1; PII
A;Experimental source: M-T404
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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C'Bate: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C'Bate: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C'Accession: D01937, A01937
R'Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID: 79073152; PMID: 103003
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Best Local Similarity 93.3%; Pred. No. 1.5e-05;
Matches 14; Conservative 1; Mismatches 0;
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A;Molecule type: mRNA
A;Residues: 1-112 <WEI>
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A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Cross = references: UNIPROT: P01669; UNIPARC: UPI000002A104
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin homology < iMM>
F; 16-94/Domain: immunoglobulin homology < iMM>
F; 16-94/Domain: immunoglobulin predicted
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A; Residues: 10-99 <MOY>
A; Residues: 10-99 <MOY>
A; Residues: 10-99 <MOY>
A; Residues: 10-99 <MOY>
A; Notes: V-kappa-21E; anti-collagen
A; Accession: S42192
A; Accession: S42192
A; Accession: S42192
A; Wole: V-kappa-21E; anti-collagen
A; Residues: 10-99 <MOO>
A; Coss-references: UNIPARC: UPI000011655C; EMBL: Z25454; NID: g407842; PIDN: CAA80941.1; PI
A; Residues: 10-99 <MOO>
A; Coss-references: UNIPARC: UPI000011655C; EMBL: Z25454; NID: g407842; PIDN: CAA80941.1; PI
A; Complex: An immunoglobulin herrorteramer subunit consists of two identical light (kappa-11 in some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin V region; immunoglobulin homology
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A;Molecule type: DNA
A;Residues: 12-99 <MOZ>
Czoss-references: UNIPARC:UPI000011655E; EMBL:Z25446; NID:g407834; PIDN:CAA80933.1;
A;Note: V-Kappa-21E; anti-collagen
A;Accession: $42191
                                                                                    A; Cross-references: UNIPARC: UP10000116560; EMBL: Z25448; NID: 9407836; PIDN: CAA80935.1; A; Note: V-kappa-21E; anti-collagen
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C;Species: Mus musculus (house mouse)
C;Dacte: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: E01937; A01937
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
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C.Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C.Accession: B01937, A01937
C.F. Accession: B01937, A01937
S.F. Weigert, M.; Gatmaiten, L.; Loh, B.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
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100.0%; Score 79; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%;
Matches 15; Conservative 0
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A;Molecule type: protein
A;Residues: 1-111 ACKCOSS-TEFEREDCES: UNIPPARC:UPI000002A0FF
A;Cross-Teferences: UNIPROT:P01664; UNIPPARC:UPI000002A0FF
C;Comment: This chain was isolated from a myeloma protein.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kag hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1c C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-94/Domain: immunoglobulin homology < IMM>
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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: UNIPPARC:UPI0000116031; EMBL:X65093; NID:G52298; PIDN:CAA46221.1; PII
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: hecerotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology < IMM>
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C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S19972
R;Weissenborn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
A;Description: Structural characterization of CD4 mAb.
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C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 09-Jul-2004
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R;Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A;Bescription: Structural characterization of CD4 mAb.
A;Reference number: S19963
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86.7%; Pred. No. 0.00032;
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A. Molecule type: mRNA
A. Residues: 1-112 < WEI>
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les 13; Conserv
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nes 12; Conserv
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
C;Accession: PH1205
R;Weissenborn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; Lenz Gene 12. 21-2796, 1992
A;Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and on A;Reference number: PH1224; MUID:93077041; PMID:1446824
A;Reference number: PH1224; MUID:93077041; PMID:1446824
A;Residues: 1-131 <WEI>
A;Residues: 1-131 <WEI>
A;Residues: 1-131 <WEI>
A;Cerosa references: UNIPARC:UP10001153EE; GB:S50265; NID:g260765; PIDN:AAB24320.1; PID: A;Crose tris mouse sequence was hybridized and fused with a human constant region gene C;Superfamily: immunoglobulin V region; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;2-1-131/Product: Ig light chain V region #status predicted <MAT>
F;36-114/Domain: immunoglobulin homology <IMM>
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(g kappa chain V-J region (1E10) - mouse (fragment)

(g) Species: Mus musculus (house mouse)

(g) Species: Musuculus (house mouse)

(g) Accession: S0996

(g) Accession: S0996

(g) A; Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie

(g) A; Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie

(g) A; Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie

(g) A; Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie

(g) A; Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie

(g) A; Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie

(g) A; Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie

(g) A; Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie

(g) A; Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie

(g) A; Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie

(g) A; Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie

(g) A; Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie

(g) A; Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie

(g) A; Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie

(g) A; Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie

(g) A; Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie

(g) A; Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie

(g) A; Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie

(g) A; Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie

(g) A; Title:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig kappa chain V region (CBPC 101) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 131;
                                                                                                          96.2%; Score 76; DB 2; Length 112; 93.3%; Pred. No. 1.5e-05;
                                                                                                                                                                              0; Indels
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93.3%; Pred. No. 1.8e-05;
                                                                                                                                                                                  1; Mismatches
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C;Keywords: heterotetramer; immunoglobulin F;16-94/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                           1 KASQSVDYDGDSYMN 15
                                                                                                                                                                                                                                                                                                 KASQSLDYDGDSYMN 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KASQSVDYDGDSYMN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 KASQSLDYDGDSYMN 58
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                                                                                                                                                                                  14; Conservative
                                                                                                                                     Best Local Similarity
Matches 14; Conserv
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Matches 14; Conserv
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Gaps

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C;Species: Nicotiana tabacum (common tobacco)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 31-Dec-2004
C;Accession: T03793
R;Daah, S.; Lu, Y.; Harrington, H.M.
submitted to the EMBL Data Library, May 1996
A;Bescription: Molecular cloning and characterization of a tobacco calmodulin-binding pr
A;Reference number: 215090
A;Accession: T03793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-551 <DAS>
A;Residues: 1-551 <DAS>
A;Cross-references: UNIPROT:P93370; UNIPARC:UPI00000A238B; EMBL:U58971; NID:g1698547; P1
A;Experimental source: strain Wisconsin 38
C;Genetics:
                    C; Accession: PH0093

S; Schmitter, D; Poch, O; Zeder, G; Heinrich, G.F.; Kocher, H.P.; Quesniaux, V.F.J.;
Mol. Immunol. Immunoglobulin homology

C; Keywords: heterotetramer; immunoglobulin.
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1079
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Tille: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A;Reference number: PH0971; MUID:92381444; PMID:1512540
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 21-Jan-2000
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A; Molecule type: mRNA
A; Residues: 1-102 <TIL>
A; Cross-rences: UNIPARC:UPI00001767CE
A; Experimental source: B cell, strain [NZB x NZW] F1
C; Superfamily: immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Pred. No. 25;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45; DB 2;
Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                     Fi6-94/Domain: immunoglobulin homology CIMM>
Fi24-38/Region: complementarity-determining 1
Fi54-60/Region: complementarity-determining 2
Fi93-101/Region: complementarity-determining 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.0%;
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292 NQVVEYDGKSFLN 304
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Best Local Similarity 53.0-
The Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                 hypothetical protein STY3863 [imported] - Salmonella enterica subsp. enterica subsp. enterica subsp. enterica subsp. enterica serovar Typhi C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AI0948 B;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R; Pickard, D; Wain, J; Churcher, th, T; Connerton, P; Confir, A; Davis, P; Davies, R.M; Dowd, L; Wain, J; Churcher, S; Woule, S; O'Gaora, P. Nature 413, 848-852, 2001 A;Atleite: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21534947; PMID:11677608 A;Retain: AI0948 A;Retains preliminary A;Wolecule type: DNA A;Residues: 1-282 <PAR> A;Catus: preliminary A;Wolecule type: DNA A;Residues: 1-282 <PAR> A;Catus: preferences: UNIPARC:UPI000005A655; GB:AL513382; PIDN:CAD09611.1; PID:g16504722; C;Genetics: A;Gene: STY3863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: B4942
R; Stura, E.A.; Stanfield, R.L.; Fieser, G.G.; Silver, S.; Roguska, M.; Hincapie, L.M.; S Procession: B49492-508, 1992
A; Title: Crystallization, Sequence, and preliminary crystallographic data for an antipep A; Reference number: A49442; MUID:93066166; PMID:1438187
A; Accession: B49442
C; MUID:93060166; PMID:1438187
C; Status: preliminary; not compared with conceptual translation
A; Molecule type: DNA
A; Residues: 1-96 <STUA
A; Residues: 1-96 <STUA
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                          Length 112;
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                                                                                Indels
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                       Score 51; DB 2;
Pred. No. 0.22;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.8%; Score 48; DB 260.0%; Pred. No. 1.8; ive 2; Mismatches
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C;Species: Mus musculus (house mouse)
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263 EALEPDDYDGDIYMN 277
                    Query Match
Best Local Similarity 66.7%;
Matches 10; Conservative
                                                                                                                                      1 KASOSVDYDGDSYMN 15
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24 RASQSVDYNAISYMH 38
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RASESVDDDGNSFLH 30
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Best Local Similarity 60.0
Matches 9; Conservative
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Best Local Similarity
Matches 8; Conserv
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Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: 865596
R;Verdaguer, N.; Mateu, M.G.; Bravo, J.; Domingo, E.; Fita, I.
Mol. Biol. 256, 364-376, 1996
A;Title: Induced pocket to accommodate the cell attachment Arg-Gly-Asp motif in a neutra A;Reference number: 863596, MUID:96174482; PMID:8594203
A;Accession: 865596
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-115 <VER.
A;Cross-references: UNIPARC:UP100001154DD; GB:S81196; NID:g1336821; PIDN:AAB36171.1; PID|
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-94/Domain: immunoglobulin homology <IMM>
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C;Species: Bacillus halodurans
C;Date: 0.1-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: A83958
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;37-115/Domain: immunoglobulin homology <IMM>
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        Length 111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53.2%; Score 42; DB 2; ilarity 53.3%; Pred. No. 7.3; Conservative 4; Mismatches
        DB 2;
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Pred. No. 7.6;
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                                       Pred. No. 7;
3; Mismatches
        Score 42;
    53.2%;
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45 RASESVDNYGISFMN 59
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24 RASESVDNYGISFMN 38
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Best Local Similarity 60.0
Matches 9; Conservative
                                                                                   9; Conservative
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Best Local Similarity
    Query Match
Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-120 <ALA>
                                                                                        Matches
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Cispecies: Mus musculus (house mouse)
Cispecies: Musculus (house mouse)
Cispecies: Musculus (house mouse)
Rimeigert, Musculus (house)
Rimeigert, Musculus (house)
A.Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A.Fitle: Rearrangement of genetic information may produce immunoglobulin diversity.
A.Fitle: Rearrangement of genetic information may produce immunoglobulin diversity.
A.Fitle: Rearrangement of genetic information may produce immunoglobulin diversity.
A.Fitle: McDass references unders. Po1322
A.Fitle: McDass references unders. Po1322
A.Fitle: McDass references unders. Po1323
A.Fitle: McDass references unders. Po1324
A.Fitle: McDass references unders. Po1324
A.Fitle: McDass references unders. Po2434
A.Fitle: McDass references unders. A94239; MuID: 67056897; PMID: 4162931
A.Fitle: McDass references unders. A94239; MuID: 67056897; PMID: 4162931
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C;Species: Mus musculus (house mouse)
C;Species: Musculus (house mouse)
C;Accession: 809969
R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie
A;Reference number: 809955; MUID:90269328; PMID:2347362
A;Residues: 1-11 cREI>
A;Residues: 1-11 cREI>
A;Residues: UniPaRC:UPIO000115E68; EMBL:X51857; NID:955404; PIDN:CAA36150.1; PII
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin homology <IMM>
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                                                                          Similarity 60.0%; Pred. No. 6.4; 9; Conservative 3; Mismatches 3; Indels
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F;16-94/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                      1 KASQSVDYDGDSYMN 15
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24 RASESVDNYGISFMN 38
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24 RASESVDNYGISFMN 38
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Matches 9; Conserv
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A;Cross-references: UNIPARC:UP10000115F8C; EMBL:X59209; NID:g52336; PIDN:CAA41919.1; PI:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-93/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-108 < WEL>
A; Residues: 1-108 < WEL>
A; Cross-references: UNIPROT: P01674; UNIPARC: UP1000002A10F
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kar hain disulfide bonds: In some cases, such as IGA and IGM, the subunits associate into l C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer
                                                                                                                                                                                                                               C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S2634
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein A;Reference number: S26309; MUID:91341421; PMID:1908510
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R; Weigert, W.; Garmattan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A; Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A; Reference number: A93204; WUID: 79073152; PMID: 103003
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C;Species: Mus musculus (house mouse)
C;Species: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004
C;Accession: A93204, A93822, A01934
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Itle: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
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C;Species: Mus musculus (house mouse)
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C;Accession: A01940
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Pred. No. 9.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
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Pred. No. 10;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 53.3%; 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.08;
   :||:||| |:|:
23 RASESVDSYGNSFMH 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KASQSVDYDGDSYMN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :||:||| |:|:|
23 RASESVDSYGNSFMH 37
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                                                                                                                                                                                                   Ig kappa chain V region - mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <STA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A01940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S26344
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KVMS37
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R; Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A; Title: Antibodies that are specific for a single amino acid interchange in a protein e A; Reference number: S26309; MUD:91341421; PMID:1908510
A; Accession: S26343
A; Residues: preliminary
A; Molecule type: mRNA
A; Residues: 1-107 - SSTA-
A; Residues: 1-107 - SSTA-
A; Cross-references: UNIPARC; UPI0000115F8A; EMBL:X59207; NID:952334; PIDN:CAA41917.1; PID
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heteroterramer; immunoglobulin
F; 15-93/Domain: immunoglobulin homology < IMM>
                        A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Reference number: A83650; MUD:20512582; PMID:11058132
A; Accession: A83958
A; Status: Preliminary
A; Molecule type: DNA
A; Residues: 1-303 <570>
A; Experimental source: strain C-125
G; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Conserved type: DNA
C; Co
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Species: Mus musculus (house mouse)
Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 303;
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20;
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Pred. No. 8.3;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.9%; Score 41; DB
53.3%; Pred. No. 9.9;
ive 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 53.2%; Score 42; Local Similarity 53.3%; Pred. No. 188 8; Conservative 3; Mismatc
Nucleic Acids Res. 28, 4317-4331, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.3%;
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24 RASESVDSYGNSFMH 38
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Best Local Similarity 53.3
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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A;Title: Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains v
A;Reference number: A90374; WUID:73140225; PMID:4691517
A;Contents: M63
                                                                                                                                                           A; Molecule type: protein
A; Residues: 21-46, 'Q', 48-53, 'B', 55-57, 'Z', 59-86,'F', 88-131 < MCK>
A; Cross-references: UNIPARC:UP1000017371B
A; Note: this sequence has since ben revised in reference A93822
B; McKean, D.J.; Bell, M.; Potter, M.
Broc., Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A; Title: Mechanisms of antibody diversity: multiple genes encode structurally related mc
A; Reference number: A93822; MUID:79012520; PMID:99744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Molecule type: meNA

A, Residues: 21-122 <TIL>
A, Fersidues: 21-122 <TIL>
C, Comment: The MG3 precursor sequence is shown.
C, Comment: The MG3 precursor sequence is shown.
C, Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into land; Superfamily: immunoglobulin V region; immunoglobulin homology
C, Keywords: heterotetramer; immunoglobulin sexperimental <SIG>
F, 120/Domain: Ig Kappa chain precursor V region #status experimental <MAT>
F, 21-131/Domain: immunoglobulin homology <IMM>
F, 31-112/Disulfide bonds: #status predicted
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 05-Oct-2004
C;Accession: E81146
R;Stover. C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bx adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Molecule type: protein
A;Residues: 21-119, Lv., 125-129, Lv., 131 <WE2>
A;Cross-references: UNIPARC;UPI000002A0FD
B;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B A;Reference number: PH0971; MUID:92381444; PMID:1512540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Rearrangement of genetic information may produce immunoglobulin diversity. A;Reference number: A93204; MUID:79073152; PMID:103003
A;Contents: PC9245; PC4050
A;Accession: C93204
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A;Residues: 21-119,'Y',121-131 <MC3>
A;Cross-references: UNIPARC:UPI000017371C; UNIPARC:UPI000017371D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 1-53;69-107 <MC2>
A;Cross-references: UNIPARC:UP1000017371C; UNIPARC:UP1000017371D
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Pred. No. 12;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L. Nature 276, 785-790, 1978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Wolecule type: protein
A;Residues: 21-119, YY',121-131 <WEI>
A;Gross references: UNIPARC:UPI000002A0FD
A;Accession: D93204
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53.3%; Pred
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44 RASESVDSYGNSFMH 58
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Biochemistry 12, 760-771, 1973
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Best Local Similarity
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                          A; Molecule type: protein
A; Residues: 1-111 < wRE1-
A; Residues: 1-111 < wRE1-
A; Cross-references: UNIPROT: P01660; UNIPARC: UP1000002A0FB
B; McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A; Title: Mechanisms of antibody diversity: multiple genes encode structurally related mc
A; Reference number: A93822; MUID:79012520; PMID:99744
A; Contents: T111
A; Residues: 1-111 < wCK-
A; Residues: 1-111 < wCK-
A; Residues: 1-111 < wCK-
A; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer
F;16-94/Domain: immunoglobulin homology < IWM>
F;23-92/Disulfide bonds: #status predicted
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C.Species: J2-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C.Species: 20-Species: S09963
R.Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Bur. J. Immunol. 20, 771-777, 1990
A.Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie
A.Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie
A.Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie
A.Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie
A.Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie
A.Molecule type: mRNA
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Superfamily: immunoglobulin homology < IMM>
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C;Accession: B90412; B90374; B93822; C93822; C93204; D93204; PH1078; A01935
R;Burstein, Y.; Schechter, I.
B30chentary 17, 2392-24900, 1978
A;Title: Primary structures of N-terminal extra peptide segments linked to the variable expression of immunoglobulin genes.
A;Reference number: A90412; MUID:78235887; PMID:98179
A;Contents: M63
A;Accession: B90412
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-35 -8URA-A;Accession: B90412
A;Residues: 1-35 -8URA-A;Accession: B90412
A;Residues: 1-35 -8URA-A;Accession: B90412
A;CKSB-references: UNIPROT:P01661; UNIPARC:UPI000017371A
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Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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60.0%; Pred. No. 10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.9%; Score 41; DB 53.3%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KASQSVDYDGDSYMN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :||:|||
24 RASESVDSYGNSFMH 38
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nes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Conservative
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Best Local Similarity
Matches 8; Conserv
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Best Local S:
Matches 9
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. T. C. TANGET BY SECTION

Gaps

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Indels

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Length 101;

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DB

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A;Molecule type: mRNA
A;Residues: 1-113 <MAT>
A;Residues: 1-113 <MAT>
A;Cross-references: UNIPARC:UP10000114E24; GB:M24273; NID:g197081; PIDN:AAA63370.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <!WM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ig kappa chain V region (TE34) - mouse Cispecies: Mus musculus (house mouse) Cispecies: Mus musculus (house mouse) Cipate: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 21-Jan-2000 Cist. 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 21-Jan-2000 Cist. Scherf, T.; Levitt, M.; Anglister, J. Bischerf, T.; Levitt, M.; Anglister, J. Bischemistry, 29, 10032-10041, 1990 A;Title: NRR-derived model for a peptide-antibody complex. A;Reference number: A36259; MUID:91104915; PMID:2271636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C'Species: Mus musculus (house mouse)
C'Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C;Accession: F3056,
E.A.
S;Matsuda, T.; Kabat, E.A.
J. Immunol. 142, 863-870, 1989
A;Title: Variable region cDNA sequences and antigen binding specificity of m
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A,Residues: 1-112 <ZIL>
A,Crose-references: UNIPARC:UPI0000176APD, GB:M30459,
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;16-95/Domain: immunoglobulin homology <IMM>
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C32513
Ig kappa chain precursor V region (BXW14) - mouse
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56.2%; Pred. No. 15,
... 4; Mismatches
                                                                                                                                                                                                                                                           4; Mismatches
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                                                                                                                                                                       Score 40.5;
Pred. No. 11;
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                                                                                                                                                                  51.3%;
                                                                                                                                                                                                                                                                                                                                          1 KASQS-VDYDGDSYMN 15
                                                                                                                                                                                                                                                                                                                                                                                               |:||| :| || :| || 24 KSSQSLLDSDGKTYLN 39
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                                                                                                                                                                  Query Match
Best Local Similarity 56.2
Matches 9; Conservative
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Best Local Similarity 56.2
Matches 9; Conservative
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Best Local Similarity 56.2
Matches 9; Conservative
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A;Status: preliminary
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A; Status: preliminary
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F30560
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A36259
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C;Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: $42186; $42195
R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with spect A;Accession: $42176; MUID:94009207; PMID:7691608
A;Accession: $42176; MUID:94009207; PMID:7691608
A;Accession: $42186
A;Accession: $42186
A;Accession: $42186
A;Accession: $42196
A;Accession: $42196
A;Accession: $42195
A;Accession: $42105
A;
                              A; Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathor, A; Reference number: A82950; MUD:20437337; PMID:10984043
A; Reference number: A82950; MUD:20437337; PMID:10984043
A; Reference Parial Residence of 
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R;Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
A;Title: Barly rearrangements of genes encoding murine immunoglobulin kappa-chains, unli
A;Reference number: A33730; MUID:89367325; PMID:2505260
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A;Molecule type: DNA
A;Residues: 1-101 cLAW>
A;Cross-references: UNIPARC:UPI0000114E54; GB:M25996; NID:g197109; PIDN:AAA38911.1; PID:
A;Note: the authors translated the codon CGC for residue 51 as Leu, and TTG for residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 21-Jan-2000
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Pred. No. 33;
4; Mismatches
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Best Local Similarity 54.5%;
Matches 6; Conservative
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Best Local Similarity 56.2
Matches 9; Conservative
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208 AVDFDGDGHIN 218
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Nature 406, 959-964, 2000
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S42186
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GB:M30480; GB:M30481;

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mouse monocle

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Gaps

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Length 113;

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vacuolar sorting protein Vps29 homolog - fission yeast (Schizosaccharomyces pombe) (frag. C;Species: Schizosaccharomyces pombe C;Species: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004 C;Accession: T43335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein At2g20570 [imported] - Arabidopsis thaliana (Cispecies: Arabidopsis thaliana (mouse-ear cress) (Cispecies: Arabidopsis thaliana (mouse-ear cress) (Cispecies: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004 (Cispeciession: H84590 (Cispeciession: H84590 (Cispeciession: H84590 (Cispeciession: H84590 (Cispeciession: H84590 (Cispeciession: Moffat, K.S.; Cronin, L.A.; Shen, M.I.; Town, C.D.; Fujii, C.Y.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.E.; Umayam, L.; Tallon, L. Nature 402, 761-768, 1999 (Cispeciession: Government and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-176 «KAW»
A;Cross-references: UNIPROT:042711; UNIPARC:UPI00006A333; EMBL:AB011824; PIDN:BAA25106.
C;Superfamily: VPS29-like phosphoesterase-related protein
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                                           Length 154;
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                                                                                                                    1; Indels
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A;Reference number: 222436
A;Accesion: r43335
A;Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 24;
4; Mismatches
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Pred. No. 58;
3; Mismatches
                                           Score 40; DB 1
Pred. No. 21;
1; Mismatches
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       Query Match
Best Local Similarity 75.0%,
6; Conservative
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51 AVQAVEYDGRFFLN 64
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Best Local Similarity 63.6
Matches 7; Conservative
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les 7; Conserv
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T43335
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C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C;Accession: C32513
R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.; J. Clin. Invest. 82, 852-860, 1988
A;Title: Immunoglobulin kappa light chain variable region gene complex organization and A;Reference number: A94689; MUID:88331394; PMID:3138286
A;Reference number: A94689; MUID:88331394; PMID:3138286
A;Resation: C32513
A;Molecule type: DNA
A;Residues: 1-132 < KGPF.
A;Residues: 1-132 < KGPF.
A;Residues: 1-132 < KGPF.
A;Residues: 1-132 < KGPF.
A;Coss-references: UNIPARC:UPI0000114D99; GB:M20830; NID:g196939; PIDN:AAA38844.1; PID:C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-115/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig kappa chain V region - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Accession: 537202
R; Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
Submitted to the EMBL Data Library, August 1993
A; Description: Production and cloning of TWV-specific monoclonal antibodies.
A; Reference number: 537202
A; Accession: 537202
A; Status: preliminary
A; Status: preliminary
A; Status: I-111 <FIS.
A; Residues: 1-111 <FIS.
A; Residues: 1-111 <FIS.
C; Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-94/Domain: immunoglobulin homology <INM>
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56.2%; Pred. No. 15;
tive 4; Mismatches 2;
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A;Start codon: GTG
C;Superfamily: Uncharacterized conserved protein
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44 KSSQSLLDSDGKTYLN 59
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24 RASESVDDLGISFMN 38
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Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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RSSQSLVYSDGNTYLN 24
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Best Local Similarity 56.2<sup>3</sup>
Matches 9; Conservative
                                             Query Match 50.6
Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity 50.0
Matches 8; Conservative
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                                                                                                                                              6 VDYDGDSYM 14
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A; Accession: A44259; MUID:93077686; PMID:1447303
A; Accession: A44259
A; Accession: A44259
A; Accession: A44259
A; Accession: A4259
A; Accession: A4259
A; Cross-references: UNIPARC: UPIO000028DDB; EMBL:D12644; NID:9220467; PID
A; Experimental source: brain NCBI backbone (NCBIP:118908)
A; Note: sequence extracted from NCBI backbone (NCBIP:118908)
C; Superfamily: kinesin-related protein KIF2; kinesin motor domain homology
C; Superfamily: kinesin-related protein KIF2; kinesin motor domain homology
C; Superfamily: kinesin motor domain homology ckNOT>
F; 196-531/Domain: kinesin motor domain homology ckNOT>
F; 285-292/Region: nucleotide-binding motif A (P-loop)
F; 291/Binding site: ATP (Lys) #status predicted
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Reference number: A88480; MUD:21074935; PMID:11206551
A; Scaus: Preliminary
A; Molecule type: DNA
A; Residues: 1-698 <STO>
A; Cross-references: UNIPROT:08X542; UNIPARC:UPI0000165752; GB:AE005174; NID:912514249; E
A; Experimental source: strain O157:H7, substrain EDL933
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C;Date: 20-8ep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14513
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, submitted to the Protein Sequence Database, August 1999
A;Reference number: Z18120
A;Accession: T14513
A;Molecule type: DNA
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Tiftle: Kinesin family in murine central nervous system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Mus musculus (house mouse)
.Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
.Accession: A44259, 827871
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A;Experimental source: cultivar Columbia; BAC clone C18G5
C;Genetics:
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Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
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A;Introns: 202/1; 243/3; 333/3; 541/2; 577/3
                                                                                                                                                                                                                                                                                                                  A, Gene: ymcA
C, Superfamily: Vibrio cholerae otnG protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kinesin-related protein KIF2 - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.6%;
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Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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659 TEEVDYDVDSY 669
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222 LEYDGBNYQN 231
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Best Local Similarity
Matches 5; Conserv
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Igrappa chain V region - human

Cispecies: Homo sapiens (man)

Cispecies: Homo sapiens (man)

Cipate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 31-Dec-2004

Cipate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 31-Dec-2004

Cipate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 31-Dec-2004

Riwagner, S.D.; Luzzatto, L.

Riwagner, L
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C;Species: Mus musculus (house mouse)
C;Date: 28-Dec-1987 #sequence_revision 02-Jun-1988 #text_change 16-Aug-1996
C;Accession: B25155
R;Accession: B25155
R;Robbins, P.F.; Rosen, B.M.; Haba, S.; Nisonoff, A.
Proc. Natl. Acad. Sci. U.S.A. 83, 1050-1054, 1986
A;Title: Relationship of V(H) and V(L) genes encoding three idiotypic families of anti-F
A;Reference number: A94083; MUID:86149212; PMID:3081888
A;Accession: B25155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q8TCD0; UNIPROT:Q9UL80; UNIPARC:UP10000176B14; EMBL:X67179
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C;Species: Homo sapiens (man)
C;Date: 06-Mar-1995 #sequence_revision 14-Jul-1995 #text_change 21-Jan-2000
C;Accession: 849572
R;Glachino, C.; Padovan, E.; Lanzavecchia, A.
                                                                                                       Gaps
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A,Residues: 1-89 <ROB>
A,Residues: 1-89 <ROB>
C,Cross-references: UNIPARC;UPI00001769ED
C,Comment: This chain is expressed in an IgM with anti-arsonate activity.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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    Length 808
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                                                                                                       1; Indels
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    Score 40; DB 2;
Pred. No. 1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39.5; DE Pred. No. 14; 3; Mismatches
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                                                                                                  1; Mismatches
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Pred. No. 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-80/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: nucleic acid sequence not shown
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A;Map position: 2p12-2p12
A;Mat position: 2p12-2p12
A;Mitrons: 17/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lain C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
E;1-20/Domain: signal sequence #status predicted <SIG>F;21-133/Product: Ig kappa chain V-II region (RPMI) #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 109) - mouse (Figecies: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: D45722
R;Simpson, U.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu J. Virol. 67, 489-496, 1993
A;Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hy A;Reference number: A45722; MUID:93100833; PMID:7677958
                                                                                                                                                                                                Ig Rappa chain precursor V-II region (RPMI) - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Cpate: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004 C;Cacession: A01890 R;Klobeck, H.G; Meindl, A.; Combriato, G.; Solomon, A.; Zachau, H.G. Nucleic Acids Res. 13, 6499-6513, 1985 A;Title: Human immunoglobulin kappa light chain genes of subgroups II and III. A;Reference number: A93588; MUID:86041852; PMID:2997711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Wolecule type: DNA
A;Residues: 1-133 <KIAO-
A;Cross-references: UNIPROT:P06310; UNIPARC:UPI000012E159
A;Note: the sequence was determined from the differentiated gene
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A;Note: sequence extracted from NCBI backbone (NCBIP:120592)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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49.4%; Score 39; DB 2; Length 111;
Best Local Similarity 53.3%; Pred. No. 22;
Matches 8; Conservative 4; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F.114-122/Region: complementarity-determining 3
F.123-133/Region: framework 4
F.43-113/Disulfide bonds: #status predicted
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Pred. No. 22;
6; Mismatches
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F;36-115/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;75-81/Region: complementarity-determining 2
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F;16-94/Domain: immunoglobulin homology <IMM>
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44 RSSQSLVYSDGNTYLN 59
      ::|||:|:|:|
RSSQSLVYSDGNTYLN
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A;Cross-references: GDB:136265
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Matches 8; Conservative
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Cypecies: Homo sapiens (man)
Cypecies: Homo sapiens (man)
Cypecies: Homo sapiens (man)
Cypecies: O5-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 31-Dec-2004
Cypecession: 842867
Rylautner-Reske, A. Huber, C.; Meindl, A.; Pargent, W.; Schaeble, K.F.; Thiebe, R.; Zchir, Cypecession: 22, 1023-1029, 1992
A;Title: The human immunoglobulin kappa locus. Characterization of the duplicated A regin A;Reference number: A49043; MUID:92201291; PMID:1551402
A;Resconsion: 842867
A;Status: preliminary
A;Residues: DNA
A;Residues: 1-120 cLAU>
A;Cross-references: UNIPROT:Q8TCD0; UNIPARC:UP10000176997; EMBL:X63402
C;Genetics:
A;Introns: 17/3
C;Superfamily: immunoglobulin homology <IMM>
A;Description: k+1+ dual receptor B cells are present in the human peripheral repertoire A;Reference number: 849571
A;Accession: 849572
A;Accession: 849572
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-14 <GIA>A;Access: UNIPARC:UPIO000116709; EMBL:Z46626; NID:g575261; PIDN:CAA86596.1; PICSSuperfamily: immunoglobulin V region; immunoglobulin homology
F;16-95/Domain: immunoglobulin homology <IMM>
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C; Species: Homo sapiens (man)
C; Species: Jo-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 31-Dec-2004
C; Accession: $42568
R; Lautner-Rieske, A.; Huber, C.; Meindl, A.; Pargent, W.; Schaeble, K.F.; Thiebe, R.; Zc
A; Title: The human immunoglobulin kappa locus. Characterization of the duplicated A regin
A; Reference number: A49043; MUID: 92201291; PMID:1551402
A; Recession: S42268
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-120 cLAU>
A; Residues: 1-20 cLAU>
A; Residues: 17/1
C; Genetics:
A; Introns: 17/1
C; Superfamily: immunoglobulin homology cIMM>
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Adf09968
Adf10176
Adf10175
Adf0969
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                                                 ADF10175
ADF09872
ADJ80244
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ADO07312
ADU86533
ADU86534
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ADY75417
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AEB13628
AEB13576
AEB13575
AEB13629
AEB70426
ABB55546
ADY31694
AAW62819
AAW6281
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                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR70196 standard; protein; 7 AA.
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93US-00136783.
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MAb 3B9 light chain CDR.
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14-OCT-1993;
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20-SEP-1995
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 AAR70196;
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Spleen cells from mice immunized with human IL-4 were used to prepare hybridomas, which were screened for anti-IL-4 MAb secretion. Only clone

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                    chain
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3B9 was positive. cDNA clones of the 3B9 light and heavy chains were cloned into pGEM7f+ and transformed into E. coli DH5-alpha. A light chai cDNA clone was sequenced (AAQ83490) that encoded the protein given in AARY0189. 3 CDNS (AARX01895-97) were identified. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antibodies and proteins bind conserved epitope of Fas antigen - usec to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HFETA; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; steroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AlDS; transplant rejection; therapy; complementarity determing region; CDR.
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                                                                                                                                                          100.0%; Score 31; DB 2; Length 7; 100.0%; Pred. No. 2e+06;
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Hiroko Y, Akio S, Shin Y;
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97JP-00169088.
97JP-00276064.
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Best Local Similarity 100.
Matches 7; Conservative
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25-JUN-1997;
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15-MAR-1999
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CONTEMPORAL PROPERTY.

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rheumatoid arthritis, host-versus-graft disease and renal disease. They
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Matches
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          evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimotons disease, graft versus host disease, Sjogren syndrome, pernicious anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocalensis, myocanditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AlDS and transplant rejection (all claimed). (Updated on 25-MAR-2003 to correct DR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New DNA molecules encoding recombinant antibodies useful for treating IL4 -mediated conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Light chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin E-mediated allergic reaction; allergic reintitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a complementarity determining region (CDR) of the light chain variable region of murine interleukin-4 (IL-4) antibody 3B9. The specification describes chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,
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 inhibiting Fas-induced apoptosis in normal cells. They are used to
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Pred. No. 2e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complementarity determining region.
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93US-00136783.
94WO-US010308.
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N-PSDB; AAX85890.
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Best Local Similarity
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14-OCT-1993;
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are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tratment of allergic rhinitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a light chain complementarity determining
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                                                                                                                                                                     100.0%; Score 31; DB 2; Length 7; 100.0%; Pred. No. 2e+06; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Light chain CDR for hIL-4 specific antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant IL4 antibodies useful for atopic ashthma and anaphylactic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gross MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY18115 standard; peptide; 7 AA.
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CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Col 43; 50pp; English.
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93US-00136783.
94WO-US010308.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) SMITHKLINE BEECHAM
) SMITHKLINE BEECHAM
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                                                                                                                                                                                             Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-370482/31.
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                                                                                                               Sequence 7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sylvester DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1995;
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07-SEP-1994;
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AAB14745

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Pas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antivira]; immunomodulatory; cardiant; demaclogatical; immunosuppressive; thyronimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosolerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; hepatotropic; humanized; adoltorid atthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
                                                                                                                 Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, alimination of hymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represents a murine derived complementarity determining region CDR-2 protein fragment which is used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells.
                                                                  Murine CD4/CD34 recognizing antibody light chain CDR-2 region #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 31; DB 3; Length 7; 100.0%; Pred. No. 2e+06; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine anti-Fas antibody peptide fragment #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Miyamura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 77; 111pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW90895 standard; peptide; 7 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Morimoto I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        98JP-00163023
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(ASAH ) ASAHI MEDICAL CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                               98JP-00159957
                                                                                                                                                                                            CDR-2; light chain; murine.
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                        31-MAR-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7 AA;
                                                                                                                                                                                                                                                                                     WO9961629-A1.
                                                                                                                                                                                                                                                                                                                                                                                   24-MAY-1999;
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                                                                                                                                                                                                                                             Mus sp.
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Matches
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ID AAW9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human fas monoclonal antibody HFE7A, or a humanised version of HFE7A containing identical CDRs (complementarity determining regions) to antibody HFE7A. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerilonephitis, articornessis, myocarditis, cardiomyopathy, glomerilonephitis, espection. Sequences AAB14744-B14746 represent CDRs 1-3 of the light chain of the murine anti-human Fas monoclonal antibody HFE7A, which is produced by hybridoma HFE7A (FERM-BP-5828)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody.
                                                                                                                                                                                                                                                                                                                                                   Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                              Mouse anti-Fas antibody HFB7A light chain CDR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 10; Page 65; 139pp; Japanese.
                                                                                                                                                                AAB14745 standard; peptide; 7 AA.
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Matches 7; Conserv
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AASNLES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              light chain.
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Gaps

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AAY51137 standard; protein; 7 AA.

RESULT 6 AAY51137

Query Match

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AAY51137;

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The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. Sequences AAX$9259-61 represent the complementarity determining region (CDR)-1, -2 and CDR-3 fragments in the L chain variable region of the antibody respectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR; complementarity determining region; framework-determining region; FR; heavy chain; light chain; HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 31; DB 3; Length 7; Best Local Similarity 100.0%; Pred. No. 2e+06; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An antibody and the nucleic acid coding the antibody
                         Antibody 4H5 L chain variable region CDR2 fragment.
                                                                    CD4 antigen; anti-human; antibody; 4H5; drug; CDR; complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine Mab 1F7 light chain CDR2 region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 14; 25pp; Japanese.
                                                                                                                                                                                                                                                                                          98JP-00163034
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                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-091351/08.
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N-PSDB; AAL48665.
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                                                                                                                                                                                         JP11332563-A.
                                                                                                                                                                                                                                                                                          26-MAY-1998;
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                                                                                                                                                                                                                                         07-DEC-1999.
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                                                                                                                                              Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel humanized anti-Fas antibody-like

molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas

ligand system, by binding to Fas on the cell surface, and prevents

apoptosis in cells with a normal system, by inhibiting binding between

captionality antidiabetic, anti-allergic, anti-arthritic, antidiamatory, immunomodulatory, dermatological, immunosupressive, thyromimetic, antidiabetic, anti-antimetrility, neuroprotective,

antirheumatic, nephrotropic, antidifertility, neuroprotective,

antiarteriosclerotic, cardiant and hepatropic activity. (I) induce

apoptosis by binding to cell surface Fas or inhibit it by competitive

inhibition of ligand binding (I) are used to treat and/or prevent

clupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft

versus host disease, Sjorgen's syndrome, permicious or hypoplastic

lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft

versus host disease, Sjorgen's syndrome, permicious or hypoplastic

anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's

disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,

multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin

dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,

cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral

(B, C or D) or alcoholic), and transplant rejection. (I) selectively

inhibit apoptosis in normal cells but selectively induce it in abnormal

cells. They bind to both human and murine Fas, so can be evaluated in

murine disease models. (I) act on the active site of Fas, i.e. they mimic

the native ligand, do not induce liver disease, and have reduced risk of

murine disease models. (I) act on the active site of Fas, i.e. they mimic

amurine survivas antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anti-Fas antibody peptide fragment described in the method of
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                      insulin dependent diabetes mellitus, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis, transplant rejection.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Takahashi
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multiple sclerosis; Basedow's disease; thrombopenia
                                                                                                                                                                                                                                                                                                                                                                                                                 Tamaki I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 Haruyama H, Nakahara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 98; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY59260 standard; peptide; 7 AA.
                                                                                                                                                                                                                                         99EP-00307711
                                                                                                                                                                                                                                                                                       98JP-00276881
98JP-00276882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Conservative
                                                                                                                                                                                                                                                                                                                                                                 (SANY ) SANKYO CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-258930/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7 AA;
                                                                                              Mus musculus,
                                                                                                                                                                                                                                         29-SEP-1999;
                                                                                                                                                                                                                                                                                       30-SEP-1998;
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AAY59260;

RESULT 8
AAY59260
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Query Match Matches

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08-NOV-2001
                                                                                                                 AAU70353;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a preventive or treating agent for diseases caused by abnormality in the Fas/Fas ligand system containing, as the active component, an antibody having a light chain subunit and a heavy chain subunit and an activity of combining specifically with mammalian Fas and an activity of inducing apoptosis in a cell expressing Fas. The agent has antiallergic, immunosuppressive and apoptocit activity and is used for preventing and treating autoimmume diseases, allergy, atopy and others. The present sequence is that of a peptide useful to the invention
                                                                                    The present invention relates to coding sequences of the murine 1F7 anti-
idiotypic antibody complementarity-determining region (CDR) or framework-
determining region (FR). The antibody binds to human or primate anti-
human immunodeficiency virus (HIV) antibodies and can be used in the
treatment of HIV infection. The present sequence is a region of the 1F7
light chain
New polynucleotide encoding a complementarity- or framework-determining region of an anti-idiotypic antibody that binds to human or primate antihuman immunodeficiency virus (HIV) antibodies, for use in vaccines
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, mouse, Fas/Fas ligand system, Fas, antibody, light chain,
heavy chain, apoptosis, antiallergic, immunosuppressive, apoptotic,
autoimmune disease, allergy, atopy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drug for preventing or treating e.g. autoimmune disease or allergy, comprises humanized anti-Fas antibody.
                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 31; DB 5; Length 7; Best Local Similarity 100.0%; Pred. No. 2e+06; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                    Similarity 100.0%; Score 31; DB 5; Length 7; Similarity 100.0%; Pred. No. 2e+06; 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Humanised anti-Fas antibody related peptide SEQ ID NO 27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6 (preparatory); Page 26; 154pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                     ABB74910 standard; peptide; 7 AA.
                                                               Claim 4; Page 26; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-MAR-2001; 2001JP-00093243.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAR-2000; 2000JP-00091144.
                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                         AASNLES
                                                                                                                                                                                                                                                            1 AASNLES
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                                                                                                                                                                               Sequence 7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                        30-APR-2002
                                    against HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-DEC-2001
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Gaps

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The invention relates to transforming a population of cells (e.g. plant cells), comprising using a library of two different polynucleotides encoding different immunoglobulin binding protein (IgBP) polypeptides that specifically bind to a ligand or form one or more disulphide bonds with polypeptides in transfected cells, to generate an IgBP that binds to a ligand, and transformed plant cells are selected, and preparing an IgBP argament cells. At least one peptide sequence has at least 75% sequence identity to a framework region (FR) of a native IgM, IgG, IgA, IgC, IgY, kappa or lambda immunoglobulin molecule. The method is useful for preparing an immunoglobulin binding protein array, preferably plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic cells (e.g. insect cells or mammalian cells). The CHBP is useful for the protein array in eukaryotic cells (e.g. insect cells or mammalian cells). The CHBP is useful for the protein array in an array in eukaryotic cells or mannalian cells) and an immunocalian immunoca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          characteristics. The present sequence is a mammalian immunoglobulin derived peptide that may be incorporated into an IgBP of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin; antibody; light chain; heavy chain; CDR; FR; complementarity determining region; framework region; IgBP; transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA; IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
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                                                                                                                                                                                                                                                                                                                               AAU70353 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse Kappa III light chain CDR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAY-2001; 2001WO-US014349.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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Best Local Similarity
1 AASNLES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-FEB-2002
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ABB74864
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Novel antibody that immunospecifically binds to CD30, useful for treating Hodgkin's disease, exerts a cytostatic or cytotoxic effect on Hodgkin's Disease cell line, and is not monoclonal antibody AC10 or HeFi-1.
                                                                                                                                                                                                                                                                                                                                                                                              The invention describes an antibody (I) that immunospecifically binds to CD30, exerts a cytostatic or cytotoxic effect on Hodgkin's Disease cell line, and is not monoclonal antibody Ac10 or HeFi-1 and does not result from cleavage of AC10 or HeFi-1 with papain or pepsin. (I), a protein (II) that competes for CD30 binding with the monoclonal antibodies AC10 or HeFi, or exerts a cytotoxic or cytostatic effect on a Hodgkins' disease cell line and the mucleic acid encoding the protein (III) are useful for the treatment or prevention of Hodgkin's Disease in a subject, by administering (I) to the subject, in the absence of conjugation to acytostatic or cytotoxic agent, respectively and a pharmaceutically acceptable carrier. This is the amino acid sequence of the mouse AC10 antibody light chain complementarity determining region 2 (CDR2), a polypeptide that completes with AC10 for CD30 binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse; chemokine; scFV; CD4 antibody; human immunodeficiency virus; HIV; RANTES; pharmaceutical; infection; acquired immune deficiency syndrome; AIDS; inflammatory; autoimmune disease; gene therapy; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 31; DB 5; Length 7; 100.0%; Pred. No. 2e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                          Wahl AF, Siegall CB;
                                                                                                                                                                                                                                                                                                                                                           Claim 9; Page 99; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE37723 standard; peptide; 7 AA.
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                           28-NOV-2001; 2001WO-US044811.
                                                                     28-NOV-2000; 2000US-00724406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-DEC-2002; 2002WO-EP014683.
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                                                                                                              (SEAT-) SEATTLE GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-NOV-2003 (first entry)
                                                                                                                                                          Francisco JA, Risdon G,
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                   WPI; 2002-557522/59.
N-PSDB; ABK88126.
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1 AASNLES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUL-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mack M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
AAE37723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a preventive or treating agent for diseases caused by abnormality in Fas/Fas ligand system containing as the active component an antibody having as the light chain subunit a polypeptide containing residues 1-218 of one of 3, 239 residue amino acid sequences, or residues 1-451 of one of 3, 470 residue amino acid sequences, all fully defined in the specification and having an activity of combining specifically with mammalian Fas and an activity of inducing apoptosis in a cell expressing Fas. The agent has immunosuppressive and antiallargic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             allergy, atopy and others. The present sequence is that of a peptide, useful to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drug containing humanized anti-Pas antibody, used for preventing and treating autoimmune diseases, allergy, and atopy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapa
                                                                                                                                                                          Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;
light chain subunit; apoptosis; immunosuppressive; antiallergic;
autoimmune disease; allergy; atopic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 31; DB 5; Length 7; 100.0%; Pred. No. 2e+06; ive 0; Mismatches 0; Indels
                                                                                                                                   Humanised anti-Fas antibody related peptide SEQ ID NO 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6 (Preparatory); Page 26; 194pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse AC10 antibody light chain CDR2 (L2)
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ABB74864 standard; peptide; 7 AA
                                                                                                                                                                                                                                                                                                                                                                                                  28-MAR-2001; 2001JP-00093106
                                                                                                                                                                                                                                                                                                                                                                                                                                            29-MAR-2000; 2000JP-00090918
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                                                                                       (first entry)
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7 AA;
                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                       26-APR-2002
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RESULT 13

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AAU99854

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KW Gene

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comprising an antibody that immunospecifically binds CD30 and exerts a cytostatic or cytotoxic effect on an activated lymphocyte and a carrier. The method is useful for treating Th_2-lymphocyte related disorders such as atopic dermatitis, systemic lupus erythematosus, atopic aethma.

C chinoconjunctivitis, allergic rhinitis, Omenn's syndrome, systemic solerosis or chronic graft-versus-host disease. The method is also useful for treating Th 1-lymphocyte-related immunological disorders such as rheumatoid arthritis, multiple sclerosis, psoriasis, Sjogren's syndrome, Hashimoto's thyroiditis, Grave's disease, primary bilary cirrhosis, Wegener's granulomatosis, tuberculosis or acute graft-versus host disease or for treating an immunological disorder due to viral infection that involves Epstein-Barr virus, human immunodeficiency virus (HIV), human T leukaema virus, heaptitis b virus or for treating an activated B lymphocyte-related disorder. The present sequence is mouse anti-CD30 antibody (ACIO) light chain complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antibodies that immunospecifically bind CD30 and exert a cytostatic or cytotoxic effect on a Hodgkin's disease cell line, useful for treating, inhibiting or preventing Hodgkin's Disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD30; cytostatic; cytotoxic; Hodgkin's disease; gene therapy; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 31; DB 7; Length 7; 100.0%; Pred. No. 2e+06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wahl AF, Siegall C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse AC10 CD30 antibody light chain-CDR2, L2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 14; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ87916 standard; protein; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-NOV-2000; 2000US-00724406.
28-NOV-2001; 2001WO-US044811.
31-JUL-2002; 2002US-0400403P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-MAY-2003; 2003US-00447257.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JA, Risdon
S, Toki BE;
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N-PSDB; ADJ87915.
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WAHL A F.
SIEGALL C.
SENTER P D.
DORONINA S.
TOKI B E.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
tes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC10; antibody.
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Doronina S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADJ87916;
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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(RISD/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DORO/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WAHL/)
                                                                                                                                                                                                                                                                                                                                            (CDR)
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                                                                                                                                                                                 The present invention relates to a chemokine construct comprising scFV and a RAWTES chemokine or their fragments. Sequences of the invention are useful for preparing a pharmaceutical composition for treating human immunodeficiency virus (HIV) -infection or acquired immune deficiency syndrome (ALDS) or inflammatory and/or autoimmune diseases. They are used as vaccines and in gene therapy. The present sequence is mouse anti-CD4 VL CDR2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunological disorder; CD30; cytostatic; lymphocyte related disorder; cytocoxic; atopic dermatitis; systemic lupus erythematosus; psoriasis; atopic asthma; rhinoconjunctivitis; allorgic rhinitis; Grave's disease; Omenn's syndrome; tuberculosis; Sjogren's syndrome; multiple sclerosis; graft-versus-host disease; primary biliary dirthosis; viral infection; rheumatoid arthritis; Hashimoco's thyroiditis; Wegener's granulomatosis; human immunodeficiency virus; HIV; therapy; antibody; mouse; CDR;
                                                  New chemokine construct comprising scFV anti-CD4 and a RANTES chemokine, useful for the preparing a composition for treating HIV-infection or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating immunological disorder that is not cancer, in a subject, by administering composition comprising a first antibody that specifically binds CD30 and exerts a cytostatic or cytotoxic effect on activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method of treating an immunological disorder in a subject where the immunological disorder is not cancer. The method involves administering to the subject a pharmaceutical composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 31; DB 6; Length 7; 100.0%; Pred. No. 2e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse anti-CD30 antibody (AC10) light chain CDR2 (L2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                             inflammatory or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complementarity determining region
                                                                                                                                          Claim 11; Page 58; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAO29928 standard; peptide; 7 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klussman K, Wahl AF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-NOV-2002; 2002WO-US037223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-NOV-2001; 2001US-0331750P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SEAT-) SEATTLE GENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
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         N-PSDB; AAD56795.
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                                                                                                                                                                                                                                                                                                                                                              Sequence 7 AA;
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RESULT 15 AA02992 MATTER TOP

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a surface of a proteinaceous material representing a binding surface (epitope) that associates with a predetermined binding surface (epitope) that associates with a predetermined binding surface of a method comprises screening a peptide library with a predetermined binding molecule. The method comprises screening a peptide library with a predetermined binding concerned or a man acids represented by tandem pairs of symbols, and determining clusters of amino acids pairs. Also described are: (i) a condeterminaceous material, which associates with a predetermined binding conteinaceous material, which associates with a predetermined binding conteinaceous material, which associates with a predetermined binding conference). (ii) a method of producing a binding surface on a more of the basic elements of the binding surface of gpl20 that is recognized by a broadly neutralizing antibody, comprising a carrier and one or more of the peptides consisting antibody, comprising a carrier and one or more of the public defined sequence given as SEQ ID NO:1 in the specification, and (iv) a molecule mimetic of the binding surface of gpl20 that is recognized by a broadly neutralizing antibody, obtained by connecting peptides 360-362, 391-396 and 464-468 of SEQ ID NO:1, each in forward or reverse sequence, in such a manner as to form a single molecule that maintains the spatial
                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A method for improved prediction of a region on a surface of proteinaceous material representing a binding surface that associates with a predetermined binding molecule by screening a peptide library with
                CD30 and exert a cytostatic or cytotoxic effect on a Hodgkin's disease. The invention is useful for treating, inhibiting or preventing Hodgkin's disease. The invention is also useful in gene therapy. The present sequence is mouse ACIO CD30 antibody light chain-complementarity determining region (CDR) protein.
  present invention relates to antibodies that immunospecifically bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention relates to a method for improved prediction of a region on
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide library; antibody; mAb CG10; region; CDR.
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                                                                                                                                                                                                                    Indels
                                                                                                                                                      100.0%; Score 31; DB 8; Le
100.0%; Pred. No. 2e+06; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                               ADY93300 standard; peptide; 7 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-SEP-2003; 2003US-0500689P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epitope mapping; screening; complementarity determining
                                                                                                                                                      Query Match
Query Match
Best Local Similarity 100.00
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CG10 light chain, CDR2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the binding molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2005-233509/24.
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                                                                                                                                     Sequence 7 AA;
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CD30
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            362, 391-396 and 464-468 of gpl20. The method is useful for improved prediction of a region on a surface of proteinaceous material representing a binding surface that associates with a predetermined binding molecule. This sequence represents a complementarity determining region (CDR) of a monoclonal antibody (mAb) used in the examples of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR66140-R66146 are peptides complementary to the variable region of the CD-4 antibody, these peptides are fixed onto a claimed nonwoven fabric (average fibre dia. of 1-30 microns) coated with keto-alkyl halide functional groups. This material can be used as a filter for CD-4 positive cells in a medical treatment involving the extra-corporeal circulation of blood
 positioned at 360-
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Material for collecting cells positive for CD-4 antibody - comprises nonwoven fabric having keto-alkyl halide functional gp.
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                                                                                                                                                                                                                                                                                                                                                                                                                         CD-4 antibody variable region; complementary peptide; extra-corporeal blood circulation; cell filter material.
                                                                                                                                             Length
 orientation that the amino acids have when they are
                                                                                                                                                                                                                                                                                                                                                                                              CD-4 antibody variable region complementary peptide.
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0
                                                                                                                                           100.0%; Score 31; DB 9; 100.0%; Pred. No. 2e+06;
                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93JP-00057206
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                                                                                                                                                          Local Similarity 100.
Les 7; Conservative
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hes 7; Conser
                                                                                   present invention.
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                                                                                                                Sequence 7 AA;
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                                                                                                                                                                                                                                                                                                                                                                   12-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-MAR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                           RESULT 18
AAR66144
ID AAR66
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This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used to illustrate the method of the invention
                                                                                                                                                                                                                                                       CD4 or CD34 and their use for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention provides an antibody having affinity to CD4 antigen. Th anti-human CD4 antibody 4H5 is used for the detection of antigen and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 31; DB 3; Length 103; 100.0%; Pred. No. 45; o. Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An antibody and the nucleic acid coding the antibody,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CD4 antigen; anti-human; antibody; 4H5; drug.
                                                                                                                                                                                                                                                       Devices containing antibodies recognising CD4
the separation of CD4 or CD34 positive cells.
                                                                                                                                                          Miyamura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibody 4H5 L chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 15-16; 25pp; Japanese
                                                                                                                                                                                                                                                                                                               Claim 22; Page 79; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY59263 standard; protein; 103 AA
                                                                                                                                                        Soka T, Morimoto I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98JP-00163034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98JP-00163034
    99WO-JP002711
                                        98JP-00159957
98JP-00163023
                                                                                                (ASAH ) ASAHI KASEI KOGYO KK
(ASAH ) ASAHI MEDICAL CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ASAH ) ASAHI KASEI KOGYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                              2000-086720/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-091351/08.
N-PSDB; AAZ58662.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 AASNLES 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AASNLES 7
                                                                                                                                                                                                                  N-PSDB; AAZ44204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 103 AA;
                                      25-MAY-1998;
26-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP11332563-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-1998;
  24-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-DEC-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY59263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus sp.
                                                                                                                                                        Ono M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY59263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes the variable heavy and light chain regions (1) of murine monoclonal antibody (mAB) 1F7. AAY91014 to AAY91016 the represent specifically claimed amino acid sequences of the variable light ending, and AAY91017 to AAY91019 represent specifically claimed amino acid sequence of the variable heavy chain. The antibodies are used for treatment of HIV (human immunodeficiency virus) infection and AIDS (acquired immunodeficiency syndrome). They are also used for detecting HIV in serum and for stimulating HIV antigen related and committed B colls to produce broadly reactive and neutralising antibodies by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cluster differentiation, cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            murine monoclonal antibody 1F7,
                                                                                                            1F7 antibody; murine; monoclonal antibody; diagnosis; HIV; infection; AIDS; anti-HIV; human immunodeficiency virus; detection; acquired immunodeficiency syndrome.
                                                                              variable light chain L2 amino acid sequence SEQ ID NO:6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
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Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Variable heavy and light chain regions of \pi useful for treating HIV infection and AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine derived protein fragment #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY51140 standard; protein; 103 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 8; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                               97US-00984277
                                                                                                                                                                                                                                                                                                                                                     94US-00351193
                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clonotypic stimulation
                                                                                                                                                                                                                                                                                                                                                                                       (IMMP-) IMMPHERON INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Kohler H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-338622/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AASNLES 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 41 AA;
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                                                                            1F7 antibody
                                                                                                                                                                                                                                                                                                               03-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                   30-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000
                                          05-SEP-2000
                                                                                                                                                                                                                                    US6057421-A.
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                                                                                                                                                                                                                                                                         02-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                               Muller S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12
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AAY91015;
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RESULT 20 AAY51140

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Gaps

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RESULT 22 AAE37732

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Antibodies capable of binding FCEL-bound IgE but which are substantially incapable of binding FCEH-bound IgE or inducing histamine release from mast cells or basophils. comprise a human Kabat CDR domain into which has been substituted a positionally analogous residue from a Kabat CDR domain of the murine anti-huigE antibodies MAEI1, MAEI3, MAEI5 or MAEI7. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                        Antibody; high affinity; FCEH; low affinity; FCEL; IgE receptor; histamine; mast cell; basophil; Kabat; CDR; murine; MAE11; MAE13; MAE15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin B; 1gB; anti-human IgE; bispecific antibody; FCEL; FCEH; low affinity binding receptor; high affinity binding receptor; allergy; diagnosis; treatment; histamine release; prevent; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptide(s) binding to specific Fc epsilon receptors - act as IgE antagonists; useful for treating and preventing IgE-mediated disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 31; DB 2; Length 106;
Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Light chain amino acid sequence of mouse antibody MaE15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
 AAR33309 standard; protein; 106 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY85197 standard; protein; 106 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 2; 113pp; English.
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jardieu PM, Presta LG;
                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1993-094004/11
                                                                                                                        MaE15 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 AASNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e.g. allergies.
                                                                                                                                                                                                                                                                WO9304173-A1.
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                                                                                                                                                                                                                                                                                                                                   14-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                    14-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                        07-MAY-1992;
                                                                                                                                                                                                                                                                                                   04-MAR-1993.
                                                                   25-MAR-2003
05-JUL-1993
                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY85197;
                                    AAR33309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus sp.
                                                                                                                                                                                             MAE17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 24
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                                                                                                                                                                                                                                                                                                                                                                                                                  Chemokine; scFV; CD4 antibody; human immunodeficiency virus; HIV; RANTES; pharmaceutical; infection; acquired immune deficiency syndrome; AIDS; inflammatory; autoimmune disease; gene therapy; immunosuppressive; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a chemokine construct comprising scrv anti-CD4 and a RANTES chemokine or their fragments. Sequences of the invention are useful for preparing a pharmaceutical composition for treating human immunodeficiency virus infection or acquired immunodeficiency syndrome (AIDS) or inflammatory and/or autoimmune diseases. They are used as vaccines and in gene therapy. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New chemokine construct comprising scFV anti-CD4 and a RANTES chemokine, useful for the preparing a composition for treating HIV-infection or inflammatory or autoimmune diseases.
                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
application for drugs. It is highly safe in human dose. The present sequence represents the L chain variable region of the antibody 4H5
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                                                                                   Score 31; DB 3; Length 103; Pred. No. 45; 0; Mismatches 0; Indel8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 19; 109pp; English
                                                                                                                                                                                                                                                                             AAE37732 standard; protein; 105 AA.
                                                                                n
Similarity 100.0%;
7; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-DEC-2001; 2001EP-00130746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-DEC-2002; 2002WO-EP014683
                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                     MT413 modified VL protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mack M, Schloendorff
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AASNLES 52
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                                                                                 Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                       1 AASNLES 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-559125/
N-PSDB; AAD56804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 105 AA;
                                                  Sequence 103 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003054017-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified.
                                                                                                                                                                                                                                                                                                                                                  06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUL-2003
                                                                                                                                                                                         46
                                                                                                                                                                                                                                                                                                                 AAE37732;
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Gaps ö

> US6037453-A 14-MAR-2000.

> > RESULT 23 AAR33309

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Matches

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New polynucleotide encoding a complementarity- or framework-determining region of an anti-idiotypic antibody that binds to human or primate antihuman immunodeficiency virus (HIV) antibodies, for use in vaccines
                                                                                                                                                                                                                                             The present invention relates to coding sequences of the murine 1F7 anti-
idiotypic antibody complementarity-determining region (CDR) or framework-
determining region (FR). The antibody binds to human or primate anti-
human immunodeficiency virus (HIV) antibodies and can be used in the
treatment of HIV infection. The present sequence is the 1F7 light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is an L chain variable region from an immunoglobulin with anti-HIV neutralising activity. See AAN90491-3, and AAN90495. (Updated c25-MAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to correct OS field.) (Updated on 24-0CT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric anti-human immune virus antibodies - contg. mouse variable regions and human constant regions for diagnosis, treatment and prevention of AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 31; DB 5; Length 110; 100.0%; Pred. No. 48; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matsushita S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin; L chain variable region; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tokiyoshi S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin L chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KAGA ) CHEMO SERO THERAPEUTIC RES INS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1989-229050/32.
N-PSDB; AAN90491, AAN90492, AAN90493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP90541 standard; protein; 111 AA.
                                                                                                                                                                                                       Claim 9; Page 23-24; 27pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; Page 15; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eda Y, Kimachi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89EP-00101583
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88JP-00171385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
Kohler H;
                                        2002-590668/63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 AASNLES 59
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AASNLES 7
                                                                                                                                                                                                                                                                                                                                                                          Sequence 110 AA;
                                                              N-PSDB; AAL4866]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-1988;
08-JUL-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-AUG-2003
25-MAR-2003
20-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                     against HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-OCT-2003
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  Muller S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takatsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAP90541;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the light chain amino acid sequence of a mouse anti-human immunoglobulin E (1gE) antibody. The invention relates to a bispecific antibody that binds specifically to 1gE when 1gE is bound to its low affinity receptor (FCEI), but does not bind to 1gE, when 1gE is bound to its low affinity receptor (FCEH). The bispecific antibody comparises an IgE-binding arm with human framework residues of a recipient human antibody and donor murine CDR (complementarity determining region) residues, but with at least one human CDR residue replacing the analogous murine residue. The antibody also comprises an FV that is specific for a predetermined antigen other than 1gE. The antibodies work by displacing bound 1gE from 1se receptor, or via competitive inhibition of its binding. The bispecific antibodies are used for diagnosis, treatment and prevention of allergy and other IgE-mediated diseases, also, when the signation of FCE from cells (for research or therapy). The bispecific antibodies of the invention do not cause granulation or release of histamine from mast cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                 New bispecific antibodies, useful for treating immunoglobulin E-mediated disease, binds to IgE, but only when on the low affinity receptor, and to an antigen other than IgE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse, 1F7; antibody; immune modulator; anti-HIV antibody; CDR; complementarity determining region; framework-determining region; FR; heavy chain; light chain; HIV infection.
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                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 2; 48pp; English.
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                   95US-00466151
                                                            92WO-US006860
                                                                               94US-00185899.
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                                                                                                                                                                                    Presta LG, Jardieu PM;
                                                                                                                                         (GETH ) GENENTECH INC.
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54 AASNLES 60
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Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 106 AA;
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                                                                                 26-JAN-1994;
15-MAR-1995;
                   06-JUN-1995;
                                                         14-AUG-1992;
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Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV. The heavy and light chain variable regions from these antibodies were sequenced (AAR55120-R55123). The murine anti-HIV CDRs were introduced into human framework regions to construct chimeric antibodies (AAR55124-R55127). (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse-human chimeric anti-HIV antibody heavy and light chains - and recombinant antibody consisting of the H- and L-chains, useful in AIDS
                                                                                                                                                                                          Mouse-human chimeric anti-HIV mu5.5-derived light chain V region.
                                                                                                                                                                                                                   Immunoglobulin, heavy chain, anti-HIV antibody; neutralisation; human immunodeficiency virus; variable region; VL chain; murine;
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                                                                                            AAR55127 standard; protein; 111 AA.
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/label= FR1
/note= "human"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "murine"
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02. .111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "human"
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/note= "human"
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label= CDR3
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(first entry)
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/label=
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|abel=
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label=
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                     54 AASNLES
 1 AASNLES
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                                                                                                                                                                                                                                                                            Mus musculus.
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                                                                                                                                                                                                                                                                                        Homo sapiens
Chimeric.
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30-JAN-1995
                                                                                                                       AAR55127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse-human chimeric anti-HIV antibody heavy and light chains - and recombinant antibody consisting of the H- and L-chains, useful in AIDS
                                                      Gaps
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                         100.0%; Score 31; DB 1; Length 111; 100.0%; Pred. No. 49;
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100.0%; Score 31; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                    Indels
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                                                                                                                                                                                                                                                            Mouse anti-HIV mu5.5 light chain variable region.
                                                    0, Mismatches
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                                                                                                                                                                         AAR55123 standard; protein; 111 AA.
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/label= CDR1
39. .53
/label= FR2
54. .60
/label= CDR2
61. .92
/label= FR3
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/label= CDR3
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/label= FR1
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/label= FR4
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                                   Local Similarity 100.
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N-PSDB; AAQ65554.
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54 AASNLES 60
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Sequence 111 AA;
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                                                                                                                                                                                                                                                                                                                                Mus musculus.
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                    54 AASNLES
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                                                                                                                                                                   Homo sapiens.
Mus musculus.
Chimeric.
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                                                                                        16-OCT-2003
25-MAR-2003
13-MAR-1995
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                                            RESULT 30
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                                                                                                                                                           Antibody; heavy chain; light chain; human immunodeficiency virus; HIV; acquired immune deficiency syndrome; AIDS: treatment; prophylaxis;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant chimeric anti HIV antibody - useful for the treatment and prevention of HIV.
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                       Gaps
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100.0%; Score 31; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels
       2; Length 111;
                      0; Indels
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                                                                                                                                            Anti HIV antibody light chain variable region.
       DB :
      100.0%; Score 31; DB
100.0%; Pred. No. 49;
ive 0; Mismatches
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/label= Framework region
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/label= Framework region
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/label= Framework region
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                                                                                        AAR60302 standard; protein; 111 AA.
                                                                                                                                                                                                                                                                            51. .92
/label≂ Framework
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                                                                                                                                                                                                                                                      54. .60
/label= CDR2.
61. .92
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/label= CDR3.
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/label= CDR1.
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                                                                                                                                                                           Mus musculus; Homo sapiens.
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Query Match
Best Local Similarity 100.
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54 AASNLES 60
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                                                                                                                                                                                          Mus musculus.
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09-MAR-1995
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The recombinant antibody light chain has neutralising activity against HIV. Chimeric antibodies comprising both mouse and human sequences are useful in the treatment/prevention of AIDS caused by HIV. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-0CT-2003 to standardise OS field)
                                                                                                                                                                                                                              Antibody; heavy chain; light chain; human immunodeficiency virus; HIV; acquired immune deficiency syndrome; AIDS: treatment; prophylaxis; Mus musculus; Homo sapiens.
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/label= CDR3.
/note= "Mouse derived amino acid sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence."
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                                                                                                                                                                                     Chimeric anti HIV antibody light chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4...38
/label= CDR1.
/mre= "Mouse derived amino acid
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label= Framework region 1.
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/label= Framework region 2.
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/label= Framework region 3.
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AAR60306 standard; protein; 111 AA.
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|abel= CDR2
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AAY18123 standard; protein; 111
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N-PSDB; AAX79531.
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                                                                                                                                                                                                                                                                                                                                                                 Sylvester DR,
                                                                                          11-AUG-1999
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                                                                                                                                                                                             Synthetic.
                                                                    AAY18123;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The specification describes chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host-versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New DNA molecules encoding recombinant antibodies useful for treating IL4
                                                                                                                                                                                                                        Light chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin B-mediated allergic reaction; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic aethma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans. The present sequence represents the light chain variable region of Ig REI, and is used in the course of the
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       100.0%; Score 31; DB 2; Length 111; larity 100.0%; Pred. No. 49; Conservative 0; Mismatches 0: Thale
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                                                                                                                                                                                                     Light chain variable region of Ig REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Col 69-70; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gross MS;
                                                                                                                                   AAY23781 standard; protein; 111 AA.
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94WO-US010308.
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                                                                             AASNLES 60
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAX85937
                                                                                                                                                                                                                                                                                                                                                                                                            14-OCT-1993;
07-SEP-1994;
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                                                                                                                                                                               13-SEP-1999
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                                                                                                                                                                                                                                                                                                        Synthetic.
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                                             Antibody, interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cluster differentiation, cell separation, antibody, CD4, CD34, leukemia, hematopoietic, undifferentiated, lymphocyte, bone marrow transplantation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant IL4 antibodies useful for tratment of allergic rhinitis, atopic ashthma and anaphylactic shock.
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Light chain sequence for humanised 3B9 antibody.
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Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gross MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Col 69-70; 50pp; English.
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CORP.
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                             93US-00117366.
93US-00136783.
94WO-US010308.
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differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used to illustrate the method of the invention
                                                                                                                                     Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents a L chain fragment of the antibody 4H5
                                                                                                                                                                                                                                     This invention describes a novel device (I) for separating cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 31; DB 3; Length 111; 100.0%; Pred. No. 49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              An antibody and the nucleic acid coding the antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD4 antigen; anti-human; antibody; 4H5; drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                         Miyamura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 22-23; 25pp; Japanese.
                                                                                                                                                                                                Disclosure; Page 95; 111pp; Japanese.
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                                                         Morimoto I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98JP-00163034
(ASAH ) ASAHI KASEI KOGYO KK.
(ASAH ) ASAHI MEDICAL CO LTD.
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                                                                                                WPI; 2000-086720/07.
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N-PSDB; AAZ58690.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 111 AA;
                                                         Soka T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP11332563-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising of CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cluster differentiation, cell separation, antibody, CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine.
                                                                                                                                                                                                                                                                                                                                                                                                               Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells.
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HIV infection; autoimmune disease; murine.
                                                                                                                                                                                                                                                                                                                   Soka T, Morimoto I, Miyamura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 97-98; 111pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY51144 standard; protein; 111 AA.
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                                                                                                                                                                                              98JP-00159957
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                                                                                                                                                                                                                                                        (ASAH ) ASAHI KASEI KOGYO KK
(ASAH ) ASAHI MEDICAL CO LTD
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54 AASNLES
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                                                                         W09961629-A1
                                                                                                                                                       24-MAY-1999;
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26-MAY-1998;
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The invention relates to a method of treating an immunological disorder in a subject where the immunological disorder is not cancer. The method involves administering to the subject a pharmaceutical composition comprising an antibody that immunospecifically binds CD30 and exerts a cytostatic or cytotoxic effect on an activated lymphocyte and a carrier. The method is useful for treating Th 2-lymphocyte related disorders such as atopic dermatitis, systemic lupus erythematosus, atopic asthma, rhinoconjunctivitis, allergic rhinitis, Omenn's syndrome, systemic sclerosis or chronic graft-versus-host disease. The method is also useful for treating Th 1-lymphocyte-related immunological disorders such as rheumatoid arthritis, multiple sclerosis, psoriasis, Sjogren's syndrome, Hashimoto's thyroiditis, Grave's disease, primary biliary cirrhosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wegener's granulomatosis, tuberculosis or acute graft-versus host disease
                                                                                                                                                          cytotoxic, atopic dermatitis, systemic lupus erythematosus, psoriasis, atopic asthma; rhinoconjunctivitis, allergic rhinitis; Grave's disease; Omenn's syndrome; multiple sclerosis; graft-versus-host disease; primary biliary cirrhosis; viral infection; rheumatoid arthritis; Hashimoto's thyroiditis; Wegener's granulomatosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating immunological disorder that is not cancer, in a subject, by administering composition comprising a first antibody that specifically binds CD30 and exerts a cytostatic or cytotoxic effect on activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or for treating an immunological disorder due to viral infection that involves Epstein-Barr virus, human immunodeficiency virus (HIV), human leukaemia virus (HIV), human activated by involves Epstein-Barr virus or measles virus or for treating an activated Blymphocyte-related disorder. The present sequence is mouse anti-CD30 antibody (AC10) light chain variable region
                                                                                          Mouse anti-CD30 antibody (AC10) light chain variable region.
                                                                                                                                                                                                                                                                            human immunodeficiency virus; HIV; therapy; antibody; mouse.
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                                                                                                                                       CD30; cytostatic; lymphocyte
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                                             (first entry)
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                                                                                                                                       [mmunologica]
                                                                                                                                                                                                                                                                                                                          Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2003.
                                               03-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lymphocyte.
  AA029926;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes an antibody (I) that immunospecifically binds to CD30, exerts a cytostatic or cytotoxic effect on Hodgkin's Disease cell line, and is not monoclonal antibody AC10 or HeFi-1 and does not result from cleavage of AC10 or HeFi-1 with papain or pepsin. (I), a protein (II) that competes for CD30 binding with the monoclonal antibodies AC10 or HeFi, or exerts a cytotoxic or cytostatic effect on a Hodgkins' disease cell line and the nucleic acid encoding the protein (III) are useful for the treatment or prevention of Hodgkin's Disease in a subject, by administering (I) to the subject, in the absence of conjugation to a cytostatic or cytotoxic agent, respectively and a pharmaceutically acceptable carrier. This is the amino acid sequence of the mouse AC10 antibody light, chain variable region, a polypeptide that competes with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel antibody that immunospecifically binds to CD30, useful for treatin Hodgkin's disease, exerts a cytostatic or cytotoxic effect on Hodgkin's Disease cell line, and is not monoclonal antibody AC10 or HePi-1.
                                                                                                                                                                                                                                                                                                                                                                                                        Gene therapy, vaccine, CD10 binding, cytostatic, cytotoxic,
Hodgkin's Disease, mouse, AC10 antibody, light chain variable region.
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                          Indels
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    49;
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  Pred. No.
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                                                                                                                                                                                                                          AAU99852 standard; protein; 111 AA.
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  100.001
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                     7; Conservative
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54 AASNLES 60
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                                                                  1 AASNLES 7
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                     07-OCT-2002
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RESULT 37 AA029926 ID AA02 XX

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New antibodies that immunospecifically bind CD30 and exert a cytostatic or cytotoxic effect on a Hodgkin's disease cell line, useful for treating, inhibiting or preventing Hodgkin's Disease.
                                                                                               28-NOV-2000; 2000US-00724406.
28-NOV-2001; 2001WO-US044811.
31-JUL-2002; 2002US-0400403P.
                                                                         28-MAY-2003; 2003US-00447257
                                                                                                                                                  FRANCISCO J A.
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                                                                                                                                                             RISDON G.
WAHL A F.
SIEGALL C.
SENTER P D.
DORONINA S.
                                                                                                                                                                                                                            TOKI B E.
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                       US2004018194-A1
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Mus musculus.
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Rattus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes an antibody (I) that competitively inhibits binding of TWEFF#19 to TWEFF2. Also described: (1) a pharmaceutical composition comprising the antibody and a carrier; (2) detecting a prostate cancer cell in a biological sample from a patient by contacting the biological sample with the antibody; (3) inhibiting proliferation of a prostate cancer-associated cell by contacting the cell with the antibody; on a prostate cancer with an antibody to TWEFF2. (I) has cytostatic activity and can be used in vaccines. The antibody, composition and method are useful for treating prostate cancer, and method are useful for treating prostate cancer, e.g. primary prostate cancer, metastatic prostate cancer, locally advanced prostate cancer, metastatic prostate cancer, prostate cancer that has been treated with neoadjuvant therapy, or prostate cancer that is refractory to treatment with neoadjuvant therapy. The present that is refractory to treatment with neoadjuvant therapy. The present
                                                          antibody; TMEFF2#19; TMEFF2; binding inhibitor; prostate cancer; cytostatic; vaccine; primary prostate cancer; metastatic prostate cancer; locally advanced prostate cancer; androgen independent prostate cancer.
                                                                                                                                                                                                                                                                                                                                                    New antibody that competitively inhibits binding of TMEFF219 to TMEFF2, useful for treating prostate cancer, e.g. primary, metastatic, locally advanced, or androgen independent prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse AC10 CD30 antibody light chain variable region protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 31; DB 7; Length 111; 100.0%; Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                    TMEFF2#10 light chain variable region SEQ ID NO:8.
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                                                                                                                                                                                                                                                                            Law D,
                                                                                                                                                                                                                                                   (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                         Powers D;
                                                                                                                                                                                                             08-MAR-2002; 2002US-0362837P.
27-DEC-2002; 2002US-0436812P.
                                                                                                                                                                                      07-MAR-2003; 2003WO-US007209.
                                                                                                                                                                                                                                                                            De La Calle A,
             (first entry)
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                                                                                                                                     WO2003075855-A2.
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           18-DEC-2003
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                                                                                                                                                                                                                                                                            Bhaskar V,
                                                                                                              Synthetic.
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AC10;
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The present invention relates to antibodies that immunospecifically bind CD30 and exert a cytostatic or cytotoxic effect on a Hodgkin's disease. The invention is useful for treating, inhibiting or preventing Hodgkin's disease. The invention is also useful in gene therapy. The present sequence is mouse AC10 CD30 antibody light chain variable region protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High mobility group box; HWGB1; monoclonal antibody; antibody therapy; sepsis; antibacterial immunosuppressive; graft rejection; arthritis; antibacterial immunosuppressive; graft rejection; arthritis; antiathratic; asthma; antiasthmatic; lupus erythematosus; antiinflammatory; inflammation; dermatological; psoriasis; respiratory distress syndrome; respiratory-gen.; psoriasis; antipsoriatic; chronic obstructive pulmonary disease; pancreatitis; peritonitis; burns; vulnerary; ischemia; vasotropic; Behcets disease; graft versus host disease; inflammatory bowel disease; gastrointestinal-gen.; multiple sclerosis neuroprotective; cachexia; anabolic; infection; musculoskeletal disease; immune disorder.
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Disclosure; SEQ ID NO 10; 68pp; English.
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Senter PD;

Wahl AF, Siegall C,

Risdon G,

Toki BE;

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Generating variant protein for host, by comparing parent protein sequence with natural protein sequences from host, analyzing and substituting amino acids of parent sequences with corresponding amino acid string of
                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel method for generating a variant protein natural brotein sequence with natural protein sequence with natural protein sequence with corresponding amino acid strings of the parent sequence with corresponding amino acid strings of each of the natural protein sequences, and substituting amino acids of parent protein sequence with corresponding amino acid strings of each of protein sequence on an amino acid string. The method is useful for generating a variant protein, e.g. a variant antibody for a host as compared to a parent protein. The method enables the generation of variant proteins having an increased host string content and reduced immunogenicity. This sequence represents a human variant antibody of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein engineering; immunogenicity; germ cell; light chain variable region; antibody.
                                                                                                                                                                              PW;
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21-UUN-2004; 2004US-0581613P.
113-AUG-2004; 2004US-061965P.
16-OCT-2004; 2004US-0619483P.
                  04-DEC-2003; 2003US-0527167P.
21-JUN-2004; 2004US-0581613P.
13-AUG-2004; 2004US-0601665P.
16-OCT-2004; 2004US-0619483P.
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                                                                                                                                                                           Desjarlais JR,
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Best Local Similarity 100.
                                                                                                                                                                                                                        WPI; 2005-458579/46.
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                                                                                                                                 (XENC-) XENCOR INC
                                                                                                                                                                                                                                                                                                                                    natural sequence.
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54 AASNLES
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                                                                                                                                                                           Lazar GA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention provides antibodies, or their antigen-binding fragments, that bind to a vertebrate high mobility group box (HMGB) polypeptide, to methods of detecting and/or identifying an agent that binds to an HMGB polypeptide, methods of treating a condition in a subject characterized by activation of an inflammatory cytokine cascade, and methods of detecting an HMGB polypeptide in a sample. The antibody (or antigenbinding fragment) binds to a vertebrate HMGB A box but does not specifically bind to non-A box epitopes of HMGB, and inhibits release of a proinflammatory cytokine from a vertebrate cell treated with an HMGB coptein. A method of treating a condition characterized by activation of an inflammatory cytokine cascade comprises administering an antibody of the invention, or its antigen-binding fragment. The condition is selected from sepsis, allograft rejection, arthritis, asthma, lupus, adult respiratory distress syndrome, chronic obstructive pulmonary disease, psoriasis, pancreatitis, peritonitis, burns, ischemia, Behcet's disease, graft versus host disease, inflammatory bowel disease, multiple sclerosis and cachexia, especially sepsis, antimitis, or lupus. The present sequence is that of the A box of human HMGB1. An identical
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                                                                                                                                                                                                                                                                                                                                  New antibody or its antigen-binding fragment specific to a vertebrate high mobllity group box (HWGB) A box that inhibits release of a proinflammatory cytokine from a cell treated with HMGB protein, useful for treating, e.g. sepsis.
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100.0%; Pred. No. 49;
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                                                                                                                                                                                              (CRIT-) CRITICAL THERAPEUTICS INC
                                                                                                                                                                                                                                           Qin S, Okeefe T,
                                                                                                                                                    11-SEP-2003; 2003US-0502568P
                                                                                                       10-SEP-2004; 2004WO-US029527
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Best Local Similarity
Matches 7; Conserv
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                  WO2005026209-A2.
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RESULT 41 AEB13680

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Homo sapiens.
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                                 seguence
                                                                                                                                               for a host. The method involves comparing a parent protein sequence with natural protein sequences from a host, analyzing the amino acid strings of the parent sequences from a host, analyzing the amino acid strings of the parent sequences with corresponding amino acid strings of each of the natural protein sequences, and substituting amino acids of parent protein sequences with corresponding amino acid strings of a natural protein sequence on an amino acid string. The method is useful for generating a variant protein, e.g. a variant antibody for a host as compared to a parent protein. The method enables the generation of variant protein shaving an increased host string content and reduced immunogenicity. This sequence represents the variable light chain of a human antibody protein used in the invention.
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                            Generating variant protein for host, by comparing parent protein sequeith natural protein sequences from host, analyzing and substituting amino acids of parent sequences with corresponding amino acid string
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                                                                                                                                      invention relates to a novel method for generating a variant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein engineering; immunogenicity; germ cell; light chain variable region; antibody.
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                                                                                                       Disclosure; Fig 10a; 137pp; English.
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21-UTW-2004; 2004US-0581613P.
13-AUG-2004; 2004US-060165EP.
16-OCT-2004; 2004US-0619483P.
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Matches 7; Conservative
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WPI; 2005-458579/46
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The invention relates to a novel method for generating a variant protein

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             natural protein sequences from a host, analyzing the amino acid strings of the parent sequence with corresponding amino acid strings of each of the natural protein sequences, and substituting amino acids of parent protein sequences with corresponding amino acid strings of a natural protein sequence on an amino acid string. The method is useful for generating a variant protein, e.g. a variant antibody for a host as compared to a parent protein. The method enables the generation of variant proteins having an increased host string content and reduced immunogenicity. This sequence represents a human germ line variable light chain protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generating variant protein for host, by comparing parent protein sequence with natural protein sequences from host, analyzing and substituting amino acids of parent sequences with corresponding amino acid string of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel method for generating a variant protein atural protein sequence with natural protein sequence stom a host, analyzing the amino acid strings of the parent sequence with corresponding amino acid strings of each of the natural protein sequences, and substituting amino acids of parent protein sequence with corresponding amino acid strings of an atural protein sequence on an acid string. The method is useful for generating a variant protein, e.g. a variant antibody for a host as compared to a parent protein. The method enables the generation of variant proteins having an increased host string content and reduced immunogenicity. This sequence represents the variable light chain of a
host. The method involves comparing a parent protein sequence with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein engineering; immunogenicity; ¿
light chain variable region; antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEB13682 standard; protein; 111 AA.
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21-JUN-2004; 2004US-0581613P.
13-AUG-2004; 2004US-0601665P.
16-OCT-2004; 2004US-0619483P.
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                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                              Sequence 111 AA;
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The framework regions (FR) are derived from the human antibody REI. The CDRs are mouse monoclonal antibody 0.5beta derived sequences. The anti-HIV modified antibody can be used for the prophylaxis and treatment of AIDS. Specific examples of the H chain are given in AAR2456-58 and AAR24560-62. A specific example of the L chain is given in AAR24575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               recombinant modified anti-HIV antibodies - comprise human x mouse
                                                                                                                                                                                Human x mouse modified anti-HIV antibody Light chain RLO.5beta.
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larity 100.0%; Pred. No. 49;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                              CDR; HIV; AIDS; REI; 0.5beta
                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                 AAR24575 standard; protein; 112 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified antibody H and L chains
                                                                                                                                                                                                                                                                                                                                                                                       54. .60
/label= CDR2
61. .92
/label= FR3
                                                                                                                                                                                                                                                                                         1. .23
/label= FR1
24. .38
/label= CDR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      93. .101
/label= CDR3
                                                                                                                                                                                                                                                                                                                                                          39. .53
/label= FR2
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                                                                                                                                               (first entry)
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     54 AASNLES 60
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nes 7; Conserv
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                                                                                                                                                                                                             Heavy; light;
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                                                                                                                                                 08-DEC-1992
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                                                                                                                                                                                                                                            Synthetic
                                                                                                               AAR24575;
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Matches
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                                                   RESULT A
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                                                                                                Gaps
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human antibody protein used in the invention.
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                                                               Score 31; DB; Pred. No. 49; O; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                      protein engineering; immunogenicity; ;
light chain variable region; antibody
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                                                             100.0%;
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13-AUG-2004; 2004US-0601665P.
16-OCT-2004; 2004US-0619483P.
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Best Local Similarity 100.
                                                          Query Match
Best Local Similarity 100.
Matches 7; Conservative
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                                 Sequence 111 AA;
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Gaps

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ABO10750

1 AASNLES 7

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Mouse, murine, antibody, skin disorder, binding agent, PSMA, cytostatic, prostate specific membrane antigen, antipsoriatic, antiathritic, dermatological, antinflammatory, antiallergic, vaccine, dermal disorder, epidermal disorder, inflammatory inflammatory disorder; epidermis, dermis,
                                                                                                                                                                                                                                                                                                                                                                               Ablating/killing aberrant prostate specific membrane antigen-expressing cells for treating skin disorders, by contacting the cell with an antibody that binds to the extracellular domain of prostate specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Page 38, 225pp, English.
                                                                                                                                                                                                                                                                                    (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                         30-MAY-2002; 2002WO-US017204
                                                                                                                                                                                                                                                     08-MAR-2002; 2002US-0362612P.
                                                                                                                                                                                                                                      20-SEP-2001; 2001US-0324100P
                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-313319/30.
                                                                           neoplastic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                membrane antigen.
                                                                                                                                            WO2003024388-A2
                                                                                                            Mus musculus
                                                                                                                                                                         27-MAR-2003
                                                                                                                                                                                                                                                                                                                     Bander N;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to modified (e.g. deimmunised) antibodies are less immunogenic compared to the modified anti-PSWA antibodies are less immunogenic compared to the unmodified anti-PSWA antibodies. The modified antibodies comprise complementarity determining regions (CDRs) from a non-human antibody (e.g. murine antibody J591,J415, J53 or E99), and framework sequences that are less immunogenic in humans (e.g. less antigenic than the murine frameworks in which a murine CDR naturally occurs). The modified antibodies bind with PMSA, preferably human PMSA, with high affinity and specificity. The anti-PMSA antibodies are useful for treating or preventing a prostatic or cancerous disorder, e.g. genitourinary inflammation, prostatitis, benign enlargement, prostatic cancer or testicular cancer, or solid tumours, soft tissue tumours or metastatic lesions, and its associated pain. The present sequence represents a variable region from a murine antibody
                                                        Modified antibody; deimmunised antibody; anti-PMSA antibody; prostate specific membrane antigen; immunogenic; CDR; murine; complementarity determining region; J591; J415; J533; B99; mouse; prostatic disorder; cancerous disorder; genitourinary inflammation; prostatitis; benign enlargement; prostatic cancer; testicular cancer; solif tumour; soft tissue tumour; metastatic lesion; pain; analgesic; antiinflammatory; cytostatic; framework region; variable heavy chain; variable light chain; VH; VL; variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New modified anti-prostate specific membrane antigen (PSMA) immunoglobulins, useful for treating or preventing a prostatic or cancerous disorder, e.g. genitourinary inflammation, prostatits, prostatic or testicular cancer.
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                               Variable region of murine antibody MuVL-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Hamilton A;
                                                                                                                                                                                                                                                                                                                                                                                                 CORR ) CORNELL RES FOUND INC.
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(first entry)
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Best Local Similarity 100
Matches 7; Conservative
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                                                                                                                                                                                                          Mus musculus.
20-AUG-2003
                                                                                                                                                                                                                                                                      12-DEC-2002.
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The present invention describes a method (M1) for ablating or killing an aberrant prostate specific membrane antigen (PSMA)-expressing cell (e.g. an epidermal and a dermal cell). M1 comprises contacting the cell, or a vascular endothelial cell proximate to the cell, with an antibody (or its attigen-binding fragment), which binds specifically to the extracellular domain of PSWA in an amount sufficient to ablate or kill the cell. The antibodies have antiporatelic, antiarthritic, dermatological, cytostatic, antiinflammatory and antiallergic activities, and can be used in vaccines. M1 is useful for treating a skin disorder in a subject, by administering to the subject, an amount of shandled which binds specifically to the extracellular domain of PSWA (the subject is a specifically to the extracellular domain of PSWA (the subject, by ammmal, preferably human and is having, or at risk of, a skin disorder). CC from psoriasis (preferably chronic stationary psoriasis, psoriasis (preferably chronic stationary psoriasis, psoriasis (von Zumbusch), annular pustular speciasis (von Zumbusch), annular pustular contains and prokeratosis, extoliative dermatities, pityriasis rubra planis, pityriasis rosacea, chthyosiform dermatosis, keratodermas, dermatosis, and prokeratosis, confictional dermatosis, keratodermas, dermatosis, and prokeratosis, an inflammatory or neoplastic disorder of the epidermis or dermis, conferently psoriasis. M1 is useful for treating a skin disorder such as an inflammatory or neoplastic disorder of the epidermal activity of PSWA-ceptressing cell, e.g. kidney, liver or brain cell, the exemplification of the exemplification.
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Murine MuVL-3 antibody amino acid sequence SEQ ID NO:81.

(first entry)

25-JUL-2003

ABR44694;

2×4×2×

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ABR44694 standard; protein; 112

ABR44694

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Antibody; ST40; molecular mimetic; CD4; human immunodeficiency virus; HIV; infection.

Monoclonal antibody ST40 light chain.

09-MAY-2001 (first entry)

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The invention relates to the use of an anti-prostate specific membrane antigen (anti-PSNA) antibody or antigen-binding fragment for treating prostate cancer, monitoring a patient receiving an anti-PSNA antibody to treat prostate cancer, or selecting a patient for treatment with an anti-PSNA antibody. Also included are a method of treating prostate cancer in a subject, a method of monitoring a patient receiving an anti-PSNA antibody to treat prostate cancer and a method of selecting a patient for treatment with an anti-PSNA antibody Also disclosed are anti-PSNA antibody or antigen-binding fragment is a human antibody (or antigen-binding fragment), a modified antibody (or an antigen-binding fragment). The modified antibody, delimunized antibody, or antigen binding fragments.

The modified antibody or antigen-binding fragment has one or more CDRs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (complementarity determining region) from a mouse monoclonal antibody selected from 1931, v1813, or EB9. The anti-PSMA antibody or antigen shinding fragment is useful for treating prostate cancer, monitoring a patient receiving an anti-PSMA antibody to treat prostate cancer, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Belecting a patient for treatment with an anti-PSMA antibody. The present sequence is a mouse kabat subgroup consensus sequence for a light or heavy chain variable region used to compare to a sequence from one of the mouse monoclonal antibodies listed above.
                                                                                                                                     antibody; antibody engineering; antibody therapy; prostate tumor; cytostatic; prostate specific membrane antigen; PSMA; heavy chain variable region; light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antigen-binding fragment for treating prostate cancer or monitori
patient receiving an anti-PSMA antibody to treat prostate cancer.
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                                                                                                 Mouse Kabat subgroup VKIII light chain variable region.
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                                                                                                                                                                                                                                                                                                                                               03-MAR-2004; 2004WO-US006586
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30-MAY-2003; 2003US-00449379
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM PHARM INC
                                                         (first entry)
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                                                           10-FEB-2005
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Designing molecular mimetics to mimic a parent molecule activity, useful e.g. therapeutically and diagnostically, uses computational screening to identify active chemical groups by accessibility within the parent

Example 1; Fig 1; 85pp; English.

molecule.

Roux F;

Rees A,

Kaczorek M, Lahana R,

Granier C,

Casset F,

(SYNT-) SYNT:EM SA

WPI; 2001-168699/17

32-AUG-2000; 2000WO-GB002972

WO200109191-A1

08-FEB-2001.

Unidentified.

99EP-00401968

02-AUG-1999;

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The present sequence was used in a method for designing a mimetic which exhibits an activity associated with a parent molecule. Such mimetics may be smaller than the parent molecule and correspondingly easier and cheaper to make, since the active region of the parent molecule is mormally relatively small. The method is useful where the parent molecule is a binding domain or the hypervariable region of an antibody or other member of the immunoglobulin superfamily. It is useful when the parent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              molecule is an antibody and the mimetic a peptide, especially an antibody which binds CD4 and a peptide which binds CD4. The mimetics designed and produced are useful diagnostically to detect cells bearing CD4 on their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           surfaces or may be included in pharmaceuticals e.g. to treat conditions in which CD4 is implicated (e.g. HIV)
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AAB71895 standard; protein; 113 AA.

RESULT 50

AAB71895;

AAB71895 ID AAB7 XX AC AAB7

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Title: Perfect score:

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71.0 224 2 704719 71.0 226 2 C70718 71.0 226 2 C70718 71.0 227 2 S09641 71.0 231 2 T19921 71.0 234 2 T19921 71.0 234 2 T195178 71.0 235 2 A81578 71.0 242 2 A81578 71.0 242 2 A81578 71.0 242 2 A81578 71.0 242 2 D98047 71.0 242 2 D98047 71.0 243 2 A81578 71.0 244 2 T15817 71.0 243 2 A81578 71.0 256 2 C83357 71.0 256 2 C83357 71.0 256 2 C83357 71.0 257 2 T37689 71.0 267 2 A81315 71.0 267 2 A81315 71.0 267 2 A8131 71.0 267 2 T39689 71.0 288 2 A810186 71.0 297 2 T39141 71.0 297 2 T59268 71.0 297 2 T59268 71.0 312 2 A81315 71.0 312 2 A81213 71.0 324 2 D84315 71.0 324 2 D84315 71.0 324 2 D84315	00000000000000000000000000000000000000

us-10-723-872-18.rpr

Best Local Similarity 100.0%; Pred. No. 0.93; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 AASNLES 7        Db 7 AASNLES 13	RESULT 3 A38601 Ig kappa chain V region (1G3) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999 C;Accession: A38601 B;Goshorn, S.C.; Retzel, E.; Jemmerson, R. J. Biol. (Chem. 266, 2134-2142, 1991 A;Title: Common structural features among monoclonal antibodies binding the same antige: A;Reference number: A38601; MUID:91115823; PMID:1703527 A;Accession: A38601 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-93 <gos> A;Cross-references: UNIPARC:UDI0000115175; GB:M57978; NID:g196402; PIDN:AAA63359.1; PID: C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin</gos>	Query Match  Query Match  Best Local Similarity 100.0%; Pred. No. 1.4;  Matches 7; Conservative 0; Mismatches 0, Indels 0; Gaps 0;  Qy 1 AASNLES 7                       Db 35 AASNLES 41  RESULT 4  KWMS10  Ig Rappa chain V region (PC7210) - mouse C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Species: Musculus (house mouse)	C;Accession: D01937, A01937 And A01937 And A01937 And A01937 And A01937, A0193	C;Keywords: heterotetramer; immunoglobulin F;16-94/Domain: immunoglobulin homology <imm> F;23-92/Disulfide bonds: #status predicted Query Match Best Local Similarity 100.0%; Score 31; DB 1; Length 110; Best Local Similarity 100.0%; Pred. No. 1.7; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 AASNLES 7  Db 54 AASNLES 60</imm>	<pre>RESULT 5 KVMS43 Ig kappa chain V region (PC7043) - mouse (fragment) Ig kappa chain V region (PC7043) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004 C;Accession: A01937; S42187; S42184; S42189; S42189; S42189; S42181 C;Accession: A01937; S42187; S42184; S42180; S42189; S42181 R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L. Nature 276, 785-790, 1978</pre>
vacuolar ATPase (E indole-3-glycerol conserved hypothet embryonic protein cysteine-tRNA liga EZ protein - human hypothetical prote	virBlo protein (vi hypothetical prote methylmalonate-sem hypothetical prote hypothetical prote protein disulfide- probable Glu-tRNA dUTP diphosphatase hypothetical prote glutamyl-tRNA amid hypothetical prote probable membrane probable membrane probable membrane probable membrane probable membrane cell death suppres	ne antigen	50.1; PID:	igen	980; NID:g196406; PIDN:AAA63361.1; PID: bbulin homology 2; Length 65;
22 71.0 468 2 22 71.0 468 2 22 71.0 473 2 22 71.0 474 2 22 71.0 480 1 22 71.0 483 2	986 22 71.0 483 2 F71684 987 22 71.0 484 2 T10668 989 22 71.0 485 2 T24677 990 22 71.0 486 2 B66460 991 22 71.0 486 2 B66460 993 22 71.0 488 1 JC2385 993 22 71.0 488 1 JC2385 994 22 71.0 491 2 T43673 995 22 71.0 491 2 T26936 996 22 71.0 493 2 B71725 996 22 71.0 494 2 S57539 999 22 71.0 496 2 AF0165 999 22 71.0 496 2 S61966 1000 22 71.0 499 2 AC2068	RESULT 1 B38601 IG kappa chain V region (7D4) - mouse (fragment) C;Species Mus musculus (house mouse) C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999 C;Accession: B38601 R;Goshorn, S.C.; Retzel, E. Jemmerson, R. J. Biol. Chem. 266, 2134-2142, 1991 A;Title: Common structural features among monoclonal antibodies binding the sar A;Reference number: A38601; MUID:91115823; PMID:1703527 A;Accession: B38601 A;Accession: B38601	A; Residues: 1-65 <gos> A; Residues: 1-65 <gos> A; Cross-references: UNIPARC: UPI0000115176; GB:M57979 C; Superfamily: immunoglobulin V region; immunoglobul C; Keywords: heterotetramer; immunoglobulin Cuery Match Best Local Similarity 100.0%; Score 31; DB 2; Best Local Similarity 100.0%; Pred. No. 0.93; Matches 7; Conservative 0; Mismatches 0 Oy 1 AASNLES 7 Db 7 AASNLES 13</gos></gos>	RESULT 2 C38601 Ig kappa chain V region (2B5) - mouse (fragment) C; Species: Mus musculus (house mouse) C; Date: 30-Aug-1991 #sequence_revision 30-Aug-1995 C; Accession: C38601 R; Goshorn, S.C.; Retzel, E.; Jemmerson, R. J. Biol. Chem. 266, 2134-2142, 1991 A; Title: Common structural features among monoclc A; Reference number: A38601: MIID:91115823; PMID:	A; Accession: C38601 A; Status: preliminary A; Molecule type: mRN C; Molecule type: mRN

Gaps

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Indels

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Length 111;

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A;Cross-references: UNIPROT:P01666; UNIPARC:UP1000002A101
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1 C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>
F;23-92/Disulfide bonds: #status predicted
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C;Comment: This chain was isolated from a myeloma protein.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka.
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into I
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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                                                                  C;Complex: An immunoglobulin heterotetramer subunit consists of two identical lihain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate (S;Superfamily: immunoglobulin V region; immunoglobulin homology (C;Keywords: heterotetramer; immunoglobulin P;16-94/Domain: immunoglobulin homology <IMM>P;18-94/Domain: immunoglobulin homology <IMM>P;23-92/Disulfide bonds: #status predicted
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R;McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A;Title: Mechanisms of antibody diversity: multiple genes encode structurally A;Reference number: A93822; MUID:79012520; PMID:99744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
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C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 09-Jul-2004
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                                           UNIPROT: P01669; UNIPARC: UPI00002A104
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100.0%; Pred. No. 1.7;
ive 0; Mismatches 0;
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F:16-94/Domain: immunoglobulin homology <IN
F:23-92/Disulfide bonds: #status predicted
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Best Local Similarity 100.
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             A;Residues: 1-111 <WEI>
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C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap and in disultide bonds. In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>
F;16-94/Domain: immunoglobulin predicted
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                                                                                             A; Molecule type: protein
A; Residues: 1-111 c/WEI.
A; Residues: 1-111 c/WEI.
A; Residues: 1-111 c/WEI.
A; Cross-references: UNIPROT: P01665; UNIPARC: UP1000002A100
B; Mo. J.A.; Bona, C.A.; Holmdahl, R.
Br. J. Immunol. 23, 2503-2510, 1993
A; Title: Variable region gene selection of immunoglobulin G-expressing B cells with special community of MUD: 94009207; PMID: 7691608
                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: UNIPARC:UPI000011655C; EMBL:225444; NID:g407832; PIDN:CAA80931.1; PI
Note: V-kappa-21E; anti-collagen
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A;Note: V-kappa_21E ; anti-collagen
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A;Molecule type: DNA
A;Molecules: 10-99 A;Molecule type: DNA
A;Molecules: 10-99 
A;Cross-references: UNIPARC:UPI000011655C; EMBL:Z25454; NID:g407842; PIDN:CAA80941.1; PI
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Cross-references: UNIPARC:UPI000011655E; EMBL:225458; NID:g407844; PIDN:CAA80945.1;
Note: V-kappa-21E; anti-collagen
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Cross-references: UNIPARC:UPI000011655E; EMBL:Z25446; NID:g407834; PIDN:CAA80933.1;
Note: V-kappa-21E; anti-collagen
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A;Note: V-kappa-21E; anti-collagen
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A;Accession: A01937
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C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: E01937; A01937
AsWeigert, M.; Gatmaitenn, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin div
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Best Local Similarity
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A, Molecule type: DNA
A, Residues: 15-99 < MOA>
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Residues: 10-99 <MOY>
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Gene 121, 271-278, 1992
A;Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and on
A;Reference number: PH1224; MUID:93077041; PMID:1446824
                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-131 < MEI.
A; Cross-references: UNIPARC:UP100001153EE; GB:S50265; NID:g260765; PIDN:AAB24320.1; PID:
A; Cross-references: UNIPARC:UP100001153EE; GB:S50265; NID:g260765; PIDN:AAB24320.1; PID:
A; Note: this mouse sequence was hybridized and fused with a human constant region gene
C; Superfamily: immunoglobulin V region; immunoglobulin homology
K; Reywords : heteroterramer; immunoglobulin
F; 1-20/Domain: signal sequence #status predicted < SIG>
F; 21-131/Product: Ig light chain V region #status predicted < MAI>
F; 36-114/Domain: immunoglobulin homology < IMM>
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A; Residues: 1-463 <TIGR>
A; Cross-references: UNIPROT: P44903; UNIPARC: UPI000013B3CF; GB:U32766; GB:L42023; NID:g1E
A; Note: best homolog was a hypothetical protein from Escherichia coli
C; Superfamily: multidrug-efflux transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-942 < MOD-
A;Residues: 1-942 < MOD-
A;Residues: 1-942 < MOD-
A;Cross-references: UNIPROT:042938; UNIPARC:UPI00000697AB; EMBL:AL022104; PIDN:CAA17900
A;Experimental source: strain 972h-; cosmid c16H5
R;Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; Lenz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein H10852 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: B64160
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayna, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kirkness, E.F.; Kerlavage, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350610; PMID:7542800
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T3962#
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
Bubmitted to the EMBL Data Library, March 1998
A;Reference number: Z21843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 31; DB 2; Length 131; 100.0%; Pred. No. 2.1; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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74 AASNLES 80
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Best Local Similarity
Matches 7; Conserv
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Matches 7; Conserv
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C;Species: Mus musculus (house mouse)

C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000

C;Accession: $19971; $19973

R;Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.

A;Description: Structural characterization of CD4 mAb.

A;Reference number: $19963

A;Accession: $19971

A;Residues: 1-112 < WEIss

A;Residues: 1-112 < WEIss

A;Residues: 1-112 < WEIss

A;Residues: L-112 < WEIss

A;Residues: L-112 < WEIss

A;Residues: UNIPARC:UPI000116030; EMBL:X65092; NID:g52292; PIDN:CAA46220.1; PIC

A;Experimental source: M-7404

C;Superfamily: Immunoglobulin V region; immunoglobulin homology

C;Superfamily: immunoglobulin homology < IMM>

F;16-94/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                 Ig kappa chain V region (M-T413) - mouse (fragment)
Ig kappa chain V region (M-T413) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Accession: S19976
R; Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
R; Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
A; Description: Structural characterization of CD4 mAb.
A; Reference number: S19963
A; Accession: S19976
A; Cross-references: UNIPARC; UPIO000116031; EMBL; X65093; NID:952298; PIDN: CAA46221.1; PID C; Keywords: heterotetramer; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin homology < IMM>
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S19971
Ig kappa chain V region (CD4 mAb clone M-T310 and others) - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig kappa chain precursor V region (M-T310) - mouse (fragment)
C;Species; Mus musculus (house mouse)
C;Date: 17-Apr.1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
C;Accession: PH1226
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100.0%; Score 31; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels
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Pred. No. 1.7;
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Best Local Similarity 100.
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                                                                                                54 AASNLES 60
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54 AASNLES
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A;Cross-references: GDB:136264
A;Map position: 2pl2-2pl2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kachain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPARC:UP1000116032; EMBL:X65094; NID:952290; PIDN:CAA46222.1; PI:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jul-2000
C;Accession: S06731
R;Alanen, A.; Weiss, S.
Bur. J. Immunol. 19, 1961-1963, 1989
A;Title: Sequence and linkage of the V(kappa)21A and G germ-line gene segments in the A;Reference number: S06731; MUID:90060210; PMID:2583230
Ig kappa chain V-I region (Gal) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A01867
R;Laure, C.J.; Watenabe, S; Hilschmann, N.
R;Laure, C.J.; Watenabe, S; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 354, 1503-1564, 1973
A;Title: The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin)
A;Reference number: A01867; MUID:75059122; PMID:4215718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                 A,Cross-references: UNIPROT:P01599, UNIPARC:UP1000012E142
A,Note: the C region of this chain has the Inv (3) marker
C;Comment: This chain was isolated from a Waldenstrom's macroglobulin.
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    mouse (fragment)

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Pred. No. 10;
1; Mismatches
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Pred. No. 9.7;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;16-94/Domain: immunoglobulin homology <IMM>
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50 AASNLQS 56
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-112 <WEI>
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Best Local Similarity
Matches 6; Conserv
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R; DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, R; DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, R; DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, R; DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, R; DelVecchio, V.G.; Marl. Acad. Sci. U.S.A. 99, 443-448, 2020.
R; Marl. Acad. Sci. U.S.A. 99, 443-448, 2020.
A; Reference number: AD3252; PMID:11756688
A; Reference number: AD3252; PMID:11756688
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-69 - KUR>
A; Cross-references: UNIROT: OBYFLO; UNIPARC: UPI00000580CC; GB: AE008917; PIDN: AAL52691.1;
A; Experimental source: strain 16M
A; Experimental source: strain 16M
A; Cones: BME11510
A; Map position: I
C;Superfamily: ATP-dependent phosphofructokinase, eukaryotic type; 6-phosphofructokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: T00362
R; Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.
DNA Res: 169-176, 1998
A; Title: Frediction of the coding sequences of unidentified human genes. X. The complete
A; Reference number: 214142; MUID:98403880; PMID:9734811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Accession: T00362
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1208 <1SH>
A;Cross-references: UNIPROT:075162; UNIPARC:UPI000006E7D4; EMBL;AB014575; NID:g3327163;
A;Cross-references: brain; clone HK02566
C;Genetics:
A;Note: KIAA0675
F;1144-1193/Domain: RING finger homology <RRN>
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C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                            01-Feb-1999 #text_change 09-Jul-2004
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; Pred. No. 25;
0; Mismatches 0
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Pred. No. 5.9;
1; Mismatches (
                                                Query Match
Best Local Similarity 100.0%; Pred. No. 19; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 01-Feb-1999 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                    hypothetical protein KIAA0675 - human
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Best Local Similarity 100.0
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896 AASNLES 902
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62 AAANLES 68
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Best Local Similarity
Matches 6; Conserv
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hypothetical protein AGR_L_563 [imported] - Agrobacterium tumefaciens (strain C58, Cerec C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2332-2328, 2001
A;Tritle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
Amolecule type: DNA
A;Residues: 1-228 «KUL»
A;Cross-references: UNIPROT:Q8U760; UNIPARC:UPI00000D261B; GB:AE007870; PIDN:AAK88851.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein Atu4594 [imported] - Agrobacterium tumefaciens (strain C58, Dupont; C; Species: Agrobacterium tumefaciens C; Spacession: AF3121 R; Monks, D: Chen, L: Wood, G.E.; Chen, Y: Woo, I R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-232, 2001 A; A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-228 «KUR»
A;Cross-references: UNIPROT:Q8U760; UNIPARC:UP100000D261B; GB:AE008689; PIDN:AAL45388.1
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577, MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nonstructural protein Pns11 - wound tumor virus (strain NJ)
N;Alternate names: segment 11 protein
C;Species: wound tumor virus, WTV
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C;Accession: C41105
R;Hillman, B.I.; Anzola, J.V.; Halpern, B.T.; Cavileer, T.D.; Nuss, D.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 228;
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Pred. No. 22;
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Pred. No. 22;
1; Mismatches
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A;Map position: linear chromosome
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Best Local Similarity 85...
Best Local 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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156 AASNLET 162
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   151 AASNLEA 157
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-120 ALLA
A,Residues: 1-120 ALLA
A,Cross-references: UNIPARC:UPI0000116D68; EMBL:X16955; NID:g55315; PIDN:CAB38573.1; PID
C,Genetics:
A;Introns: 18/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;37-115/Domain: immunoglobulin homology <IMM>
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C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession C87521
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.B.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, Shapiro, L.; Venter, J.C.; Fraser, C.M.
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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A;Cross-referencea: UNIPROT:Q9A698; UNIPARC:UPI0000C763E; GB:AE005673; NID:g13423697;
C;Genetics:
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Pred. No. 11;
1; Mismatches 0; Indels
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1; Mismatches
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90.3%; Score 28; DB
Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches
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Best Local Similarity 85.7%;
Matches 6; Conservative
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Best Local Similarity 85.7%;
Matches 6; Conservative
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64 AASNLQS 70
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75 AASNVES 81
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A; Status: preliminary
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C;Species: Helicobacter pylori
%; Avariety: strain J09
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: D71941
C;Accession: D7
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A,Reference number: A71800; MUID:99120557; PMID:9923682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-632 <ARN>
A;Cross-references: UNIPROT:09ZM66; UNIPARC:UP1000012ACCF; GB:AE001471; GB:AE001439; NI
A;Experimental source: strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: frsH_2
C; Superfamily: cell division protein ftsH; FtsH/SEC18/CDC48-type ATP-binding domain hom-
F;184-395/Domain: FtsH/SEC18/CDC48-type ATP-binding domain homology <VAT>
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CiSpecies: Drosophila melanogaster
CjSpecies: Drosophila melanogaster
CjDate: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
CjAccession: A55236; B41298
R;Pesavento, P.A.; Srewart, R.J.; Goldstein, L.S.B.
A;Cell Biol. 127; 1041-1048, 1994
A;Title: Characterization of the KLP68D kinesin-like protein in Drosophila: possible ro A;Reference number: A55236; MUID:95050960; PMID:7525600
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A, Residues: 1-794 < PES.
A, Cross-references: UNIPROT: P46867; UNIPARC: UPI000012DEC5; GB: U15974; NID: 9595912; PIDN
R, Stewart, R.J.; Pesavento, P.A.; Woerpel, D.N.; Goldstein, L.S.B.
Proc. Nall. Acad. Sci. U.S.A. 88, 8477-8474, 1991
A, Title: Identification and partial characterization of six members of the kinesin supe
A, Reference number: A41298; MUID: 92020874; PMID: 1924306
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A;Residues: 'TC',222-337,'VRGQV' <STE>
A;Cross-references: UNIPARC:UP1000016BC5B; GB:M74431; NID:g157791; PIDN:AAA28658.1; PID
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                                                                                                                                                                                                                                                                                                        ATP-dependent zinc metallopeptidase - Helicobacter pylori (strain J99)
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Pred. No. 71;
1; Mismatches
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A;Cross-references: FlyBase:FBgn0004381
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616 AANNLES 622
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Matches 6; Conser
1 AASNLES
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A;Status: preliminary
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Nucleic Acids Res. 17, 3599, 1988, D.L.
Nucleic Acids Res. 17, 3599, 1988, D.L.
A.Pitile: Complete nucleotide sequence of wound tumor virus genomic segment S11.
A.Reference number: S04139; MUID:89263810; PMID:2726499
A.Recession: S04139; MUID:89263810; PMID:2726499
A.Molecule type: genomic RNA
A.Molecule type: genomic RNA
A.Residues: 1-313 < DAL>
A.Cross-references: UNIPROT:P12326; UNIPARC:UP10000061DB1; GB:X14219; NID:g62264; PIDN:C
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                      Aritle: First field isolation of wound tumor virus from a plant host: minimal sequence A; Reference number: A41705; MUD: 92074261; PMID:1962460
A; Accession: C41705
A; Accession: C41705
A; Residues: 1-313 cHIL>
A; Residues: 1-313 cHIL>
A; Cross-references: UNIPROT: P31611; UNIPARC: UP10000138CA4; GB:M77020; NID:g336172; PIDN: C; Genetics:
A; Map position: segment 11
C; Superfamily: phytoreovirus nonstructural protein Pns9
C; Keywords: nonstructural protein
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A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: a112969
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A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AB2177
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe. A.:
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C;Species: wound tumor virus, WTV
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
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C;Genetics:
C;Genetics:
C;Map position: segment 11
C;Superfamily: phytoreovirus nonstructural protein Pns9
C;Superfamily: phytoreovirus nonstructural protein Pns9
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Best Local Similarity 85.7
Matches 6; Conservative
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Matches 6; Conservative
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294 AASNLDS 300
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294 AASNLDS 300
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A;Molecule type: DNA
A;Residues: 1-579 <KUR>
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A,Molecule type: mRNA
A,Residues: 1-102 «TIL»
A);Cross references: UNIPARC:UP100001767CC
A;Experimentes nource: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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16;
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F;16-94/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 100.
Matches 6, Conservative
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Best Local Similarity 100.
Matches 6; Conservative
   A; Reference number: $25174
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A;Residues: 1-101 <BOS>
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A;Molecule type: mRNA
A;Residues: 1-95 <MO2>
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                                                                                                                                                                                                                                                                                                                      Grappa chain V region - mouse (fragment)
Grappa chain V region - mouse (fragment)
Grappa chain V region - mouse mouse)
Grapte: 07-0ct-1994 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
Gracesaion: 842193
RrWo, J.A.; Bona, C.A.; Holmdahl, R.
Bur. J. Immunol. 23, 2503-2510, 1993
Aritle: variable region gene selection of immunoglobulin G-expressing B cells with spect Argerance number: 842176; MUDD:94009207; PMID:7691608
Argerance number: 842176; MUDD:94009207; PMID:7691608
Argerance preliminary
Argeriule type: DNA
Argesiques: 1-81 <MOJ>
Argeriule type: DNA
Argesiques: 1-81 <MOJ>
Argeriule type: DNA
Argeriule typ
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Musculus (house mouse)
C; Accession: S25462
R; Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
Submitted to the EMBL Data Library, July 1992
A; Beference number: S25174
A; Accession: S25462
A; Status: preliminary
A; Accession: S25462
A; Status: preliminary
A; Status: preliminary
A; Status: Jol kMNA
A; Status: UNIPARC:UPI00001160C5; EMBL:X67623; NID:952188; PIDN:CAA47881.1; PIC
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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C.Species: Mus musculus (house mouse)
C.Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C.Accession: S25177; 8313134
E.Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S. submitted to the EMBL Data Library, July 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                           Gaps
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   DB 1; Length 784;
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100.0%; Pred. No. 13;
ive 0; Mismatches 0; Indels
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14;
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100.0%; Pred. No....
0; Mismatches
                                                           1; Mismatches
   Score 28;
Pred. No.
   90.3%;
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Best Local Similarity 100.0
Matches 6; Conservative
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Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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751 AASNLDS 757
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Best Local Similarity
Matches 6; Conserv
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S42193
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S25462
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Ig light chain V region NIO - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: 559640
R;Bossart-Whitaker, P.; Chang, C.Y.Y.; Novotny, J.; Benjamin, D.C.; Sheriff, S.
A;Mol. Biol. 253, 559-575, 1995
A;Title: The crystal structure of the antibody NIO-staphylococcal nuclease complex at 2.
A;Reference number: $59639; MUID:96068846; PMID:7473734
                                                                           A;Accession: S25177
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Kosidues: 1-95 <MON>
A;Cross-references: UNIPARC:UPI00001160C7; EMBL:X67625; NID:g52146; PIDN:CAA47883.1; PII
A;Accession: S33134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Cross-references: UNIPARC:UP100001160C7; EMBL:X67625; NID:g52146; PIDN:CAA47883.1; PII CS.Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin C; Keywords: heterotetramer; immunoglobulin P:16-93/Domain: immunoglobulin homology <IMM>
A, Description: Structure and binding properties of monoclonal antibodies to core histone
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R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
A; Title: Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1077
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C,Species: Mus musculus (house mouse)
C,Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
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A;Cross-references: UNIPARC:UP1000115F8C; EMBL:X59209; NID:g52336; PIDN:CAA41919.1; PII. C;Superfamally: immunoglobulin V region; immunoglobulin homology C;Superfamar; immunoglobulin munoglobulin homology c;Reywords: heterotetramer; immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C'Species: Homo sapiens (man)
C'Species: Homo sapiens (man)
C'Accession: A91653; A01662; $02573
C'Accession: A91653; A01662; $02573
R'Schiechl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
Hyppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
A'filte: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Sui A;Reference number: A91653; MUID:72189444; PMID:5028201
A;Accession: A91653
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A;Note: the C region of this chain has the Inv (3) marker
R;Fehlhammer, H.; Schiffer, M.; Epp. O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; Ste
Biophys. Struct. Mech. 1, 139-146, 1975
A;Title: The structure decermination of the variable portion of the Bence-Jones protein
A;Reference number: A90729; MUID:77022433; PMID:1234024
A;Contents: annotation; X-ray crystallography
A;Note: the structure of the V region was determined by molecular replacement methods u
R;Steiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Title: Chemical modification of the carboxyl groups of protein substrates enhances th A,Reference number: S02572; MUID:88005152; PMID:3115831
                            A,Title: Antibodies that are specific for a single amino acid interchange in a protein A,Reference number: $26309; MUID:91341421; PMID:1908510
A,Accession: $26344
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-107 <STA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Map position: 2p12-2p12
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light
hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate int
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
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17;
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100.0%; Pred. No. 1...
0; Mismatches
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100.0%; Pred. No. ...
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Best Local Similarity luv...
6; Conservative
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Matches 6; Conservative
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C.Species: Mus musculus (house mouse)
C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C.Accession: 826343
R.Stark, S.E.; Caton, A.J.
A. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein A;Reference number: 826309; MUID:91341421; PMID:1908510
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J. Exp. Med. 176, 761-779, 1992
J. Tap. Med. 176, 761-779, 1992
A;Tille: Both IgM and IgG anti-DNA antibodies are the products of clonally selective A;Reference number: PH0971; MUID:92381444; PMID:1512540
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C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1076
R;Tillman, D.M: Jrn: N m ....
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C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26344
R;Stark, S.E.; Caton, A.J.
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A.Cross-references: UNIPARC:UPI00001767C6
A.Experimental source: B cell, strain [NZB x NZW]Fl
A.Experimental source: B cell, strain [NZB x NZW]Fl
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>
        Length 102;
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No. 16;
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     DB 2;
87.1%; Score 27; DB 100.0%; Pred. No. 16; ive 0; Mismatches
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Matches 6; Conservative
                                                         Conservative
                      Best Local Similarity
Matches 6; Conserv
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <STA>
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A, Status: nucleic aci
A, Molecule type: mRNA
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Best Local &
     Query Match
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A.Molecule type: protein
A.Residues: 1-111 <MCK.
C.Sorosier seferences: UNIPARC: UPI000002A0FB
Ain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C.Superfamally: immunoglobulin V region; immunoglobulin homology
C.Reywords: heterotetramer
F;16-94/Domain: immunoglobulin homology <IMM>
F;23-92/Disulfide bonds: #status predicted
A; Reference number: A93822; MUID: 79012520; PMID: 99744
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Best Local Similarity
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Cipacesion: C01937; A01937
Riweigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
A;Residues: L-111 < WEID.
A;Residues: 1-111 < WEID.
A;Residues: 1-111 < WEID.
A;Cross-references: UNIPROT:P01667; UNIPARC:UPI000002A102
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap thain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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C, Species: Mus musculus (house mouse)
C, Species: Mus musculus (house mouse)
C, Date: O2-Apr-1982 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004
C, Date: O2-Apr-1982 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004
C, Date: O2-Apr-1982 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004
C, Accession: A93204; A93822; A01934
A, Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A, Reference number: A93204; MUID:79073152; PMID:103003
A, Tontents: PG3741
A, Molecule type: protein
A, Residues: 1-111 < WEI>
A, Molecule type: protein
A, Residues: 1-111 < WEI>
A, Molecule type: Potter, M.
B, Residues: 1-111 < WEI>
B, CTOSB-TEEFERNES: WINTROT:P01660; UNIPARC:UP100002A0FB
B, MCCROB-TEEFERNES: WINTROT:P0167, A93913-3917, 1978
B, MCKGBA, D.J.; Bell, M. P. Potter, M.
B, MCCROB-TEEFERNES: WINTROT:P0167, MUID: Multiple genes encode structurally related m
             Fivelgart, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
A;Accession: A01940
A;Residues: 1-108 <WEI>A;Residues: 1-108 <WEI>A;Residues: 1-108 <WEI>A;Cross-references: UNIPROT:PO1674; UNIPARC:UPI000002A10F
A;Cross-references: UNIPROJEDULIN heteroreteramer subunit consists of two identical light (kahain disulfide bonds. In some cases, such as 1gA and 1gM, the subunits associate into ]
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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17;
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Species: Mus musculus (house mouse)
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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55 ASNLES 60
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C; Accession: A01940
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A,Cross-references: UNIPROT:P01672; UNIPARC:UP1000002A109
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into le C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>
F;23-92/Disulfide bonds: #status predicted
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kag c;Complex: An immunoglobulin heterotetramer subunit consists of two identical light of hain disulfide bonds In some cases, such as 1gA and 1gM, the subunits associate into 1 C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>
F;23-92/Disulfide bonds: #status predicted
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Cispecies: Musculus (1938) 401938
Riweigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
Mittle: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
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Nature 276, 785-790, 1978
Affitle: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
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C,Species: Mus musculus (house mouse)
C,Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
                                                                             Gaps
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   Length 111;
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18;
   DB 1;
87.1%; Score 27; DB : 100.0%; Pred. No. 18; ative 0; Mismatches
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100.0%; Pred. No. 18;
tive 0; Mismatches
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Best Local Similarity luv...
6; Conservative
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2.5d 3%

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C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C;Accession: S09966
R;Reininger, L; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-777, 1990
A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodic
A;Accession: S09966
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A; Residues: 1-11 cREI>
A; Residues: 1-11 cREI>
A; Cross-references: UNIPARC:UPI0000115E65; EMBL:X51854; NID:g55397; PIDN:CAA36147.1; PIF
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 16-94/Domain: immunoglobulin homology < IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accesion: 809963
R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Bur. J. Immunol. 20, 771-777, 1990
A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodi.
A;Reference number: 809955; MUID:90269328; PMID:2347362
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                        0. VICL. 07, 4057-407.

1. VILLE: Neutralizing monoclonal antibodies that distinguish three antigenic farities Neutralizing monoclonal antibodies that distinguish three antigenic fareference number: A4572; MUID:93100833; PMID:7677958

A;Reference number: A4572; MUID:93100833; PMID:7677958

A;Recession: D4572

A;Residues: preliminary; not compared with conceptual translation
A;Residues: 1-111 <SIN>
A;Residues: 1-111 <SIN>
A;Residues: 1-111 <SIN>
A;Coss-references: UNIPARC;UPI0000176D43
A;Note: sequence extracted from NCBI backbone (NCBIP:120592)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: glycoprotein
F;16-94/Domain: immunoglobulin homology <IMM>
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C;Superfanily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-94/pomain: immunoglobulin homology <IMM>
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100.0%; Pred. No. 18;
ive 0; Mismatches
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Best Local Similarity 100.0
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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A; Residues: 1-111 <REI>
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                                                                                                                                                                                                                                                                             Ig kappa chain V-J region (106-10E) - mouse (fragment)

Ig kappa chain V-J region (106-10E) - mouse (fragment)

C;Species: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000

C;Accession: 809965

R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.

Bur. J. Immunol. 20, 771-777, 1990

A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie

A;Reference number: 809955; MUID: 90269328; PMID: 2347362

A;Accession: 809965

A;Accession: 809965

A;Accession: 809966

A;Accession: 809966

A;Accession: NUIPARC: UPIO000115E64; EMBL: X51853; NID: 955394; PIDN: CAA36146.1; PIC

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: D45722
R;Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu
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        DB 1; Length 111;
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100.0%; Pred. No. 18;
ive 0; Mismatches 0; Indels
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Query Match 87.1%; Score 27; DB 1
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches
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Best Local Similarity 100.
Matches 6; Conservative
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RESULT 43 S09965

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Gaps

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Length 120; Indels

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A;Cross-references: UNIPARC:UP100001165A7; EMBL:Z27175; NID:g415965; PIDN:CAA81699.1; PI. C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;31-105/Domain: immunoglobulin homology <IMM>
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A,Reference number: A90374; MUID:73140225; PMID:4691517
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R;McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A;Title: Mechanisms of antibody diversity: multiple genes encode structurally related mc
A;Reference number: A93822; MUID:79012520; PMID:99744
A;Contents: M63; AB22
A;Accession: B93822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig kappa chain precursor V regions (M63, AB22, PC9245, PC4050) - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text change 09-Jul-2004 C;Accession: B90412; B90314; B93822; C93822; C93204; D93\(\frac{7}{2}\) PHI078; A01935 R;Burstein, Y; Schechter, I. Biochemistry 17, 2392-2400, 1978 A;Title: Primary structures of N-terminal extra peptide segments linked to the variable
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A; Residues: 21-119, 'I.', 121-123,'A',125-129,'L',131 <WE2>
A; Residues: 21-119, 'I.', 121-123,'A', 125-129,'L', 131 <WE2>
A; Residues: 21-119, 'I.', 121-123,'A', 125-129,'L', 131 <WE2>
A; Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A; Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective A; Reference number: PH0971; MUD:92381444; PMID:1512540
A; Accession: PH1078
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Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
A;Contents: PC9245; PC4050
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A;Reaidues: 1-53;69-107 <MC2>
A;Cross-references: UNIPARC:UPI000017371C; UNIPARC:UPI000017371D
A;Accession: C93822
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A;Residues: 21-119,'Y',121-131 <MC3>
A;Crose-references: UNIPARC:UP1000017371C; UNIPARC:UP1000017371D
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A;Residues: 21-46,'Q',48-53,'B',55-57,'Z',59-86,'F',88-131 <MCK>
A;Cross-references: UNIPARC:UP1000017371B
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A, Residues: 1-35 - BUR>
A, Residues: 1-35 - BUR>
A, Cross-references: UNIPROT: P01661; UNIPARC: UP1000017371A
R, MCKean, D.; Potter, M.; Hood, L.
Biochemistry 12, 760-771, 1973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression of immunoglobulin genes.

A; Reference number: A90412; MUID:78235887; PMID:98179
A; Contents: M63
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100.0%; Pred. No. 2.,
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Pred. No. 20;
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M.Residues: 21-119, YY',121-131 <WEI>
A;Cross-references: UNIPARC:UPI00002A0FD
A;Accession: D93204
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Best Local Similarity 100.0
Servana 6; Conservative
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[Species: Mus musculus (house mouse)

[C;Species: Mus musculus (house mouse)

[C;Accession: $45:15

[R;Kim, H.H.; Kato, K.; Yamato, S.; Igarashi, T.; Matsunaga, C.; Ohtsuka, H.; Higuchi, A. FRES Lett. 346, 246-255, 1994

[R;Kim, H.H.; Kato, K.; Yamato, S.; Igarashi, T.; Matsunaga, C.; Ohtsuka, H.; Higuchi, A. FRES Lett. 345.14; MUID: 94283606; PMID: 8013642

[R;Kim, H.H.; Kato, K.; Yamato, S.; Igarashi, T.; Matsunaga, C.; Ohtsuka, H.; Higuchi, A. F. Reference number: $45712

[R;Kim, H.H.; Kato, K.; Yamato, S.; Igarashi, T.; Mulo: 8013642

[R;Richer and A. A. F. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Usy Kappa Grain V region - mouse (5) Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C; Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C; Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C; Accession: S63596
B; Ward Biol. 256, 364-376, 1996
A; Title: Induced pocket to accommodate the cell attachment Arg-Gly-Asp motif in a neutral A; Reference number: 863596; MUID:96174482; PMID:98594203
A; Reference number: 863596; MUID:96174482; PMID:98594203
A; Residue: S63596
A; Residue: 1-115 cvERA
A; Residue: 1-115 cvERA
A; Residue: 1-115 cvERA
A; Cross-references: UNIPARC:UPI00001154DD; GB:S81196; NID:91336821; PIDN:AAB36171.1; PIL
C; Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-94/Domain: immunoglobulin homology <IMM>
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Cispecies: Homo sapiene (man)
Cispecies: Todan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
Cispace: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
Cispacesion: S46374; S38651
Ribensimon, C.; Chastagner, P.; Zouali, M.
Ribensimon, C.; Chastagner, P.; Zouali, M.
A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rea A;Reference number: S46369; MUID:94313975; PMID:8039491
A;Accession: S46374
A;Molecule type: mRNA
A;Residues: 1-120 <br/>
A;Residues: 1-120 
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19;
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18;
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C;Species: Homo sapiena /man/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.1%; Score 27; DB 100.0%; Pred. No. 19; ive 0; Mismatches
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Best Local Similarity 100.8
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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| SS ASNLES 60
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               ASNLES
               55
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A;Residues: 21-122 <TIL>
A;Cross-references: UNIPARC:UPI000017371E
A;Cross-references: UNIPARC:UPI000017371E
A;Cross-references: UNIPARC:UPI000017371E
C;Comment: The MG3 precursor sequence is shown.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status experimental <SIG>F;21-131/Domain: ig kappa chain precursor V region #status experimental <MAT>F;3-114/Domain: immunoglobulin homology <IMM>F;3-114/Domain: immunoglobulin homology <IMM>F;4-112/Disulfide bonds: #status predicted
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4 77.4 393 2 Q9X5A4_TREDE Q9X5a4 t	77.4 416 2 Q8L5W8 ARXTH 77.4 418 1 G1VA MYCNO 77.4 418 1 G1VA MYCNO 77.4 420 2 Q8L5W8 ARXTH 77.4 420 2 Q8L5W8 THENN 77.4 420 2 Q8L5W8 THENN 77.4 421 2 Q8L5W8 THENN 77.4 422 1 HEAD BPAPS 77.4 422 1 HEAD DPAPS 77.4 422 1 HEAD DPAPS 77.4 422 1 G8SQV ORYSA 77.4 422 1 G8SQV ORYSA 77.4 423 2 Q8SQV ORYSA 77.4 426 2 Q8CX1 ENTWO 77.4 436 2 Q8CXI ENTWO 77.4 440 2 Q8CXI ENTWO 77.4 450 2 Q8CXI ENTWO 77.4 460 1 NP112 HUMAN 77.4 464 1 Q8CXI ENTWO	4 77.4 466 2 QSQR89 MOOSE QSQR89 muserus 4 77.4 468 2 QRRP99_9RHOO Q8rp89 azoarcus 4 77.4 468 2 QRZGPI_YERPE Q8zgpI yersinia 4 77.4 470 1 SRPC_PSEPU O31101 pseudomon 4 77.4 470 1 TYGI_PSEPU Q93pu3 pseudomon 4 77.4 471 2 Q94WW7_PSEAE Q9hwn7 pseudomon 4 77.4 471 2 Q94WA7_PSEAE Q9hwn7 pseudomon

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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE;
Direct protein sequencing;
Immunoglobulin V region.
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Best Local Similarity 100.
Matches 7; Conservative
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              7; Conservative
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Query Match
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                             1 AASNLES 7
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KV3M MOUSE
ID KV3M MOUSE
AC PO1665;
DT 21-UUL-1986 (
                                                                                  KV3L MOUSE
P01664;
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      pongo pygma
mus musculu
                       oryctolagus
                                      orcine lym
                                                                             arabidopsis
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tetraodon n
                                                                                                                   solanum tub
bifidobacte
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vibrio para
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                                                                                                                                                  sphingomona
                                                      leishmania
                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                  MEDLINB=79073152; PubMed=103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
       05rcy8
02860h5
02810h5
0614m5
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Complementarity-determining-2.
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11950 MW; 69F1A5CE886B1249 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.
Immunoglobulin domain;
                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Mus musculus (Mouse)
                                                             QSCAL
QSCG62 CR1...
QSSII9 ARATH
QGCTAB TKLULA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ensembl; ENSMUSG0000053225; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IG-v.
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin
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                             Q6L4MS ORYSA
Q8AYV3 9GAMA
Q6CY22 KLULA
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296DU2 HUMAN
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       OSRCY8 PONPY
K2C6G MOUSE
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05A3G5_C
064391_S
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Q52BZ1_N
                                                      2408X2
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SMR; P01668; 1-110.
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                                                                                                                                                                                                                                                                                                            PROTEIN SEQUENCE.
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KV3P_MOUSE
ID KV3P MOUSE
diversity
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McKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
-I- MISCELLANEOUS: This chain was isolated from a myeloma protein.
                                                             Gaps
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100.0%; Score 31; DB 1; Length 110; 100.0%; Pred. No. 15; ive 0; Mismatches 0; Indels
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Framework-4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                 21-JUJ-1986 (Rel. 01, Created)
21-JUJ-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
RADPA chain V-III region CBPC 101.
Mus musculus (Mouse).
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(Rel. 01, Last sequence update)
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HSSP, P01665; 1QNZ.
SMR; P01664; 1-111.
InterPro; IPMSWNSG00000053225; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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Ig kappa chain V-III region PC 7769.
Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                             Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
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MEDLINE=79073152; PubMed=103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complementarity-determining-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin domain;
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Pred. No. 15;
                                                                                21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
11g kappa chain V-III region PC 7183.
Mus musculus (Mouse).
           111 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ensembl; ENSMUSG0000053225; Mus musculus
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     PRT;
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                                                                                                                                                                                                                                                                                                                                      PROTEIN SEQUENCE.
MEDLINE=79073152; PubMed=103003;
                                                                                                                                                                                                                                                Muridae; Murinae; Mus.
                                                               01, Created)
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InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv.
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Imm
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        STANDARD;
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SMR; P01666; 1-111
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NCBI_TaxID=10090;
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P01669;
        KV3N MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94009207; PubMed=7691608; Mo J.A., Bona C.A., Holmdahl R.; Mo J.A., Bona C.A., Holmdahl R.; "Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen."; Eur. J. Immunol. 23:2503-2510(1993).
                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRUCTURE BY NMR OF 1-111.

MEDLINE=20264305; PubMed=10801487; DOI=10.1016/S0969-2126(00)00119-2;
Tugatinov V., Zvi A., Levy R., Hayek Y., Matsushita S., Anglister J.;
"NMR structure of an anti-gp120 antibody complex with a V3 peptide
reveals a surface important for co-receptor binding.";
Structure 8:385-395(2000).
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                                                                                                                                                                                                                                                                   Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00406; IGv; 1.-
PROSITE; PS50835; IG_LIKE; 1.
3D-structure; Direct protein sequencing; Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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-SEP-2005 (Rel. 48, Last annotation update) kappa chain V-III region PC 7043.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ensembl; ENSMUSG0000053225; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                               PROTEIN SEQUENCE.
MEDLINE=79073152; PubMed=103003;
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                    Nature 276:785-790(1978)
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AASNLES 60
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMID outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Harrison A., Dyer D.W., Gillaspy A., Ray W.C., Mungur R., Carson M.B.,
Zhong H., Gipson J., Gipson M., Johnson L.S., Lewis L., Bakaletz L.O.,
Munson R.S. Jr.;
"Genomic sequence of an otitis media isolate of nontypeable
Haemophilus influenzae: comparative study with H. influenzae serotype
d, strain KW20.";
J. Bacceriol. 187:4627-4636(2005).
EMBL; CP000057; AAX87898.1; -; Genomic_DNA.
InterPro; IPR001134; MFS.
InterPro; IPR001114; MFS.
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                                                                                                                                                                                                                                                                                                            TIGRFAMS; TIGRO0711; efflux EmrB; 1.
PROSITE; PS50850; MFS; 1.
Complete proteome; Hypothetical protein; Inner membrane; Membrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
OrderedLocusNames=NTH11020;
Haemophilus influenzae (strain 86.028NP).
Bacteria; Proteobacteria, Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31; DB 1; Length 463;
Pred. No. 75;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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                                                                                                      EMBL, U32766; AAC22509.1; -; Genomic_DNA.PIR; B64160; B64160.
INGE, H10825.
INGESPO; IPR004638; Efflux_EmrB.
INTERPO; IPR017014; MFS.
INTERPO; IPR017011, MFS.
INTERPO; IPR01101, MFS.
INTERPO; IPR0110158; TCR_TetA.
INTERPO; IPR01411; TCR_TetB.
PRINTS; PR01035; TCRTEIB.
PRINTS; PR01035; TCRTEIB.
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                                                                                                                                                                                                                                                                                                                                                                       Transmembrane; Transport.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95350630; PubMed=7542800; Relacione R.A., Kirkness B.F., Relachmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G.G., Fitzhugh W., Fields C.A., Gocayne J.D., Soct J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom B., Cotton M.D., Witchensor T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Pritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 269:496-512(1995).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: Belongs to the major facilitator superfamily. EmrB
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Pasteurellaceae; Haemophilus.
NCBI_TaxID=727;
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Pred. No. 15;
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Complementarity-determining-1.
Framework-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12011 MW; 6FAA345279356829 CRC64;
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SMR; PO1669; 1-111.
Ensembl; BNSMUSGO000053225; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
DIRCC protein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
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Y852 HAEIN
TYB52 HAEIN
STANDARD; PRT; 463 AA.
AC P44903;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical transport protein H10852.
GN Order-edLocualwanes-H10852;
OS Haemophilus influenzae.
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Best Local Similarity 100.
Matches 7; Conservative
   diversity.";
Nature 276:785-790(1978)
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A Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
Bowyer P., Chen D., Collins M., Coulsen R., Davies R., Dyer P.S.,
Bowyer P., Chen D., Collins M., Coulsen R., Dyer P.S.,
Raman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,
A Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
Kungai T., Lafton A., Latge J.P., Li W., Lord A., Lu C.,
Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
Rabblowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
Sanchez-Ferrero J.C., Saunders D., Saeger K., Squares R., Squares S.,
Takeuchi M., Tekaia F., Turner G., Vazquez de Aldana C.R., Weidman J.,
Mite O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
Machida M., Hall N., Barrell B., Denning D.W.;
Agenomic sequence of the pathogenic and allergenic filamentous fungus
M. Abergillus fumigatus ";
M. Menning C.W., Marken S., Marken
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
NADH-ubiquinone oxidoreductase 49 kDa subunit, putative.
ORFNAmes-Afu2q13710;
Aspergillus funigatus Af293.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI TaxID=330879;
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                              Complete protecome, Hypothetical protein. SEQUENCE 463 AA; 50036 MW; AF67B6A23E621266 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21646F55AF8687A6 CRC64;
                                                                                                    PRINTS; PRO1035; TCRTETA.
PRINTS; PRO1036; TCRTETB.
TIGRPAMS; TIGROOT11; efflux EmrB; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AAHFO100001; EAL93666.1; -; Genomic_DNA.
InterPro; IRR010219; NuoD.
Fins, Pro 1946.01135; Oxidored_49kDa.
Fins, Pro 1946; Complex1 49kDa; 1.
TIGREAMS; TIGR01962; NuoD; 1.
PROSITE; PS000315; COMPLEXI_49k; 1.
NAD; Oxidoreductaes; Ubiquinone.
SEQUENCE 519 AA; 58230 MW; 21646F55AF8687A6
InterPro; IPR006162; Ppantne S
InterPro; IPR001958; TCR_TetA.
InterPro; IPR001411; TCR_TetB.
                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.0%;
Matches 7; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 ASPFU
Q4XOE9 ASPFU PRELIMINARY;
Q4XOE9;
                                                                              Pfam; PF07690; MFS_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 AASNLES 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=A£293;
                                                                                                                                                                                                                                                                                                                         Query Match
S KW D R R R R W S S
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Length 519;

Score 31; DB 2; Pred. No. 86;

100.0%;

Query Match Best Local Similarity

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A Michinear Course of the Course of the Course of the Course of Co
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-1. CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-fructose 1,6-bisphosphate.
-1. PATHWAY: Key control step of glycolysis.
-1. SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-1. SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-89162722; PubMed-9501991;
Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.;
"Identification of open reading frames in Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION IN CELL CYCLE REGULATION.
MEDLINE=22223229; PubMed=12237855; DOI=10.1002/yea.902;
Tallada V.A., Daga R.R., Palomeque C., Garzon A., Jimenez J.;
"Genome-wide search of Schizosaccharomyces pombe genes causing overexpression-mediated cell cycle defects.";
Yeast 19:1139-1151(2002).
                                                                                                                                                                                                                                                                                                      K6PF schro
042978; P78762;
10-0CT-2003 (Rel. 42, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase)
6-phosphofructokinase) (6PF-1-K).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 583-942.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ONA Res. 4:363-369(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces.
                                                                                121 AASNLES 127
1 AASNLES
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HSSP, F.

GenedB_Spomb.

Go, Go:000003472; F.:

Go; Go:000004; Pregulatio...

A InterPro; IPR009161; PFK euk.

JR InterPro; IPR000023; Ppfruckinase; I.

DR PERM; PROMO PFK; IPRCKINASE.

DR PRINTS; PRO0476; PHRCTKINASE.

DR PRODM; PO00707; Ppfruckinase; I.

DR PROSTE; PSO433; ATP FFK euk; I.

DR PROSTE; PSO433; PHOSPHOFBUCTOKINASE; 2.

KW Allosteric enzyme; ATP-binding; Repeat; Transferase.

NP BIND 214 218 ATP (By similarity).

"SIND 372 376 ATP (By similarity).

"BIND 372 376 ATP (By similarity).

"BIND 372 376 ATP (By similarity).

"AS 345 PROTON acceptor (By similarity).

"AS 345 PROTON acceptor (By similarity).

"AS 345 PROTON acceptor (By similarity).

"Substrate (By similarity).
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                                                                                                  This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED outstation the European Bioinformatics in Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DZIP3 MOUSE STANDARD; PRT; 1204 AA.
Q7TPVZ; Q80TU4; QBBYK7;
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2005 (Rel. 45, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Ubiquitin ligase protein DZIP3 (EC 6.3.2.-) (DAZ-interacting protein 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22579291; PubMed=12693553; Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S., Nakajima D., Nagae H.; Ohara O., Koga H.; Prediction of the coding sequences of mouse homologues of KIAA gene: II. The complete nucleotide sequences of 400 mouse KIAA-homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                     CAUTION: Ref.2 sequence differs from that shown due to a frameshift in position 836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                       EMBL; AL022104; CAA17900.1; -; Genomic_DNA.
EMBL; D89110; BAA13773.1; ALT_FRAME; mRNA.
FIR; T39624; T39624.
GREEDB_SPORME; SPBC16H5.02; -.
GO:0003972; P6-Fphosphofructokinase activity; TAS.
GO; GO:00006096; P:04ycolysis; TAS.
GO; GO:0000074; P:regulation of cell cycle; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 31; DB 1; L 100.0%; Pred. No. 1.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity lu...
7; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                  25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Ubiquitin ligase protein DZIP3 (BC 6.3.2.-) (DAZ-interacting protein 3) (RNA-binding ubiquitin ligase of 138 kpa) (hRUL138).
Name=DZIP3; Synonyms=KIAA0675;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
                                          \overline{D}ZIP3 HUMAN STANDARD; PRT; 1208 AA. Q86X1\overline{3}; O75162; Q6P3R9; Q6PH82; Q86X14; Q86X15; Q86X16; Q8IWIO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kreft S.G., Nassal M.;
"hRUI.138, a novel human RNA-binding RING-H2 ubiquitin-protein
                                                                                                                                                                                                                                                                                                                                                NUCLECTIDE SEQUENCE (ISOFORMS 1 AND 2), FUNCTION, SUBCELLULAR LOCATION, RNA-BINDING, TISSUE SPECIFICITY, AND MUTAGENESIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22426342; PubMed=12538761; DOI=10.1242/jcs.00261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98403880; PubMed=9734811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell Sci. 116:605-616(2003).
                                                                                                                                                                                                                                                                                                                                                                                         662-LYS--LYS-666 AND CYS-1187.
TISSUE=Liver, and Uterus;
                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse
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  RESULT 11
                                            HID DEBUT TO THE SET OF SET OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ensembl; ENGNUSGONOGGEOGH; Mus musculus.

MG1; MG1:1917433; 2310047C04Rik.

MG1; MG1:1917433; 2310047C04Rik.

InterPro; IPRO11990; PR-11ke-helical.

InterPro; IPRO11991; Znf_RING.

Pfam; PF00097; zf_C3HC4; 1.

PROSTE; SM00184; RING; 1.

PROSTE; PS50089; ZF_RING_2; 1.

Alternative splicing; Coiled coil; Ligase; Metal-binding; RNA-binding; Ubl conjugation pathway; Zinc; Zinc-finger.

ZN FING

ZN FING

1144 1184 PROFITED

746 861 POCENTIAL:
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/FIId=VSP 010974.
DNEEEEEEEPCVICHENLSP -> VRPNLLTVNTFRSERKRM
                     then directly
                                                                                                                                                                                                                                                                                                        IsoId=Q7TPV2-3; Sequence=VSP_010973, VSP_010974, VSP_010975, VSP_010976;
ubiquitin ligases accept ubiquitin from an E2 ubiquitin-
                 100.0%; Score 31; DB 1; Length 1204; 100.0%; Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9522730708DB570C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Missing (in isoform 3)
                                                                                                                                                                                                                       Name=2;
IsoId=Q7TPV2-2; Sequence=VSP_010977;
Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                              Note=No experimental confirmation available, SIMILARITY: Contains 1 RING-type zinc finger. CAUTION: This is a conceptual translation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D -> G (in Ref. 3).
V -> I (in Ref. 3).
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EMBL; AK039172; BAC30265.1; -; MRNA.
EMBL; BC052893; AAH52893.1; -; MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BI736207; -; NOT ANNOTATED CDS; mRNA. CN535823; -; NOT ANNOTATED CDS; mRNA. BG070132; -; NOT ANNOTATED CDS; mRNA.
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650 650
1204 AA; 138021
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COMPBIAS
VARSPLIC
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TISSUE-Skin, and Teetis?

WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feligoold E.A., Grouse L.H., Derge J.G.,

Riduener R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S. I., Wang J., Heich F.,

D. Hopkins R.F., Jordan H., Moore T., Max S. I., Wang J., Heich F.,

D. Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S.S., Cimwood J., Scherchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rottiguez A.C., Garimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=12511597; DOI=10.1073/pnas.0234478100; Moore F.L., Jaruzelska J., Fox M.S., Urano J., Firpo M.T., Turek P.J., Dorfman D.M., Reijo Pera R.A.; "Human Pumilio-2 is expressed in embryonic stem cells and germ cells and interacts with DAZ (Deleted in AZoospermia) and DAZ-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteins.";
Proc. Natl. Acad. Sci. U.S.A. 100:538-543(2003).
-!- FUNCTION: B3 Ubiquitin ligase proteins mediate ubiquitination and subsequent proteasomal degradation from an E2 ubiquitin. B3 ubiquitin ligases accept ubiquitin from an E2 ubiquitin-conjugating enzyme in the form of a thioester and then directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE OF 641-1208, AND INTERACTION WITH DAZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA sequences."
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Gaps

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Indels

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0; Mismatches

Best Local Similarity 100. Matches 7; Conservative

Query Match

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STRAIN=9-941 / Biovar 1;
PubMed=15805518; DOI=10.1128/JB.187.8.2715-2726.2005;
Halling S.M., Peterson-Burch B.D., Bricker B.J., Zuerner R.L.,
Ging Z., Li L.-L., Kapur V., Alt D.P., Olsen S.C.;
"Completion of the genome sequence of Brucella abortus and comparison to the highly similar genomes of Brucella melitensis and Brucella suis.";
                                                                                                                                            Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                           69 AA; 7301 MW; D6142414631FDEBA CRC64;
                                                                     10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                             J. Bacteriol. 187:2715-2726 (2005).
EMBL; AE017223; AAX73841.1; -; Genomic_DNA.
Complete proteome.
                                                                                                                OrderedLocusNames=BruAb1_0445;
                                                      10-MAY-2005 (TrEMBLrel. 30,
                                                                                                  Cold-shock family protein.
                            O57EU3_BRUAB PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                         Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 AAANLES 68
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AASNLES 7
                                                                                                                               Brucella abortus
                                                                                                                                                                     NCBI_TaxID=235;
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8YFLO;
                                         Q57EU3
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                                                                                                                                                                                                                                                        This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; bubbs.z; -.
InterPro; IPR001841; Znf_RING.
Pfan, PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
PROSITE; PS00618; ZF_RING 2; 1.
PROSITE; PS50089; ZF_RING 2; 1.
Alternative splitcing; Coiled coil; Ligase; Metal-binding; RNA-binding; Ubl conjugation pathway; Zinc; Zinc-finger.
ZN FING 1148 RING-type; atypical.
COILED 14 43 Potential.
                                                                                                          Isold-Q86Y13-1; Sequence=Displayed;
Name=2; Synonyms=Short;
Isold=Q86Y13-2; Sequence=VSP_010971, VSP_010972;
ISOSGENES-2; Sequence=VSP_010971, VSP_010972;
TISSUE SPECIFICITY: Widely expressed at low level. Highly expressed in skeletal muscle, kidney and heart. Expressed at low level in placenta, lung, brain, liver and pancreas.
SIMILARITY: Contains 1 RING-type zinc finger.
CAUTION: Ref. 4 sequence differs from that shown due to a frameshift in position 1127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKKTK->SGSTA: Strongly decreases RNA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ig activity.
Abolishes ubiquitin ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 31; DB 1; Length 1208; 100.0%; Pred. No. 2.2e+02; ive 0; Mismatches 0; Indels (
  transfers the ubiquitin to targeted substrates. Able to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , G (in Ref. 3; AAH56674).
76945A63AF85207E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GE -> EF (in isoform 2)
/FTId=VSP 010971.
Missing (in isoform 2).
/FTId=VSP_010972.
                                                                                    Event=Alternative splicing; Named isoforms=2;
           AB014575; BAA31650.2; ALT_INIT; MRNA. BC039018; AAH39018.1; ALT_TERM; MRNA. BC056674; AAH3674; ALT_TERM; MRNA. BC056382; AAH63882.1; -; MRNA. AP279370; AAK69484.1; ALT_FRAME; MRNA.
                                                                                                                                                                                                                                                                                                                                                                      Other_RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potential.
Potential.
Potential.
Poly-Glu.
Poly-Lys.
Poly-Pro.
Poly-Glu.
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                                                                                                                                                                                                                                                                                                                                          EMBL; AY227651; AAO72967.1; -; mRNA.
EMBL; AY227652; AAO72968.1; -; mRNA.
EMBL; AY227653; AAO7296.1; -; Other.
EMBL; AY227654; AAO72970.1; -; MRNA.
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Best Local Similarity 100.
Matches 7; Conservative
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671
958
1146
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1208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; T00362; T00362.
HSSP; P28990; 1CHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 608672; -
                                                                                                    Name=1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ensembl;
                                                                                                                                                                                                                                                                                                                   removed.
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COTLED
COTLED
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EMBL;
EMBL;
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Gaps

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Length 69; 0; Indels

Score 28; DB 2; Pred. No. 50; 1; Mismatches

90.3%;

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NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=16M / ATCC 23456 / Biotype 1;

MEDLINE=21642680; PubMed=11756688; DOI=10.1073/pnas.221575398;

MEDLINE=21642680; PubMed=11756688; DOI=10.1073/pnas.221575398;

DelVecchio v.G., Kapatral v., Redkar R.J., Patra G., Mujer C., Los T., Ivanova N., Anderson I., Bhattacharrya A., Lykidis A., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N.C., Overbeek R.; The genome sequence of the facultative intracellular pathogen

Brucella melitensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:0006350; P:transcription; IEA.
InterPro; IPR002059; Cold shock.
InterPro; IPR012156; Cold_shock_CspA.
                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobatteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
NCBI_TaxID=29459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
-!- SUBCELLULAR LOCATION: Cyroplasmic (By similarity).
-!- SIMILARITY: Contains 1 CSD (cold-shock) domain.
EMBL, AE005897; AAL52691.1; -; Genomic_DNA.
                                                                                                                                     (TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                    69 AA
                                                    PRT;
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                                                                                                                                                                                                                                                                          COLD SHOCK PROTEIN CSPA.
OrderedLocusNames=BMEI1510;
                                                    Q8YFLO_BRUME PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR012156;
InterPro; IPR011129;
InterPro; IPR012340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; AH3440; AH3440.
HSSP; P15277; IMJC.
                                                                                                                                                                                                                                                                                                                                                                             Brucella melitensis.
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01-MAR-2002
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     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leishmania major.
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Friedlin;
Peacock C.S. Murphy L., Ivens A.C, Berriman M., Blackwell J.,
Smith D., Collins M., Fosker N., Harris D., Oliver K., O'Neil S.,
Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.,
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                    Laure C.J., Watanabe S., Hilschmann N.,
The primary structure of a monoclonal IgM-immunoglobulin
(macroglobulin Gal.), I. The amino acid sequence of the L-chain of
kappa-type, subgroup I.",
Kappa-type, subgroup I.",
Physiol. Chem. 354:1503-1504(1973).
-!- MISCELLANEOUS: The C region of this chain has the INV (3) marke
-!- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Framework-1.
Complementarity-determining-1.
Framework-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complementarity-determining-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 28; DB 1; Length 108;
Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11814 MW; CIAD3CB0F600FF73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                               GO, GO:0005576; C:extracellular region; NAS. GO; 0003823; F:antigen binding; NAS. GO; 0006955; P:immune response; NAS. InterPro; IPR003596; Ig—1ike.
SMART; SMO406; IGV; 1.
PROSTITS; PSS0835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                          PROTEIN SEQUENCE.
MEDLINE=75059122; PubMed=4215718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q4QIM4_LEIMA PRELIMINARY;
Q4QIM4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct protein sequencin Immunoglobulin V region.
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                                                                                                                                                                                                                                                                                                                        PIR; A01867; KIHUGL.
HSSP; P01607; 1BWW.
SMR; P01599; 1-107.
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NUCLEOTIDE SEQUENCE.
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SEQUENCE
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DOI=10.1128/IAI.68.10.5803-5808.2000;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin.";
                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                             Gaps
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Pfam; PF00313; CSD; 1.
PRINF; PIRSF00259; Cold shock_A; 1.
PRINTS; PR00050; COLDSHOGK.
ProDom; PD000621; Cold shock; 1.
SNART; SM00357; CSP; 1.
PROSITE; COLD_SHOCK; 1.
Activator; Complete profeome; DNA-binding; Transcription; Transcription regulation.
SEQUENCE 69 AA; 7301 MW; D6142414631FDEBA CRC64;
                                                                                                                                               Length 69
                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Anti-myosin immunoglobulin light chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11224 MW; EC87D653DB3AAB21 CRC64;
                                                                                                                                              Score 28; DB 2;
Pred. No. 50;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Ilg kappa chain V-I region Gal.
Homo Sapiens (Human).
                                                                                                                                                                                                                                                                                                           103 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ensembl; ENSMUSG0000053225; Mus musculus.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; I.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                         PRT;
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EMBL, AF206026; AF869324.1; -; mRNA.
HSSP, PO1665; LONZ.
SMR; Q9JL80; 1-103.
                                                                                                                                              90.3%;
                                                                                                                                                                                                                                                                                                         Q9JL80 MOUSE PRELIMINARY;
                                                                                                                                           Query Match 90.3
Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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NON_TER 103 1
SEQUENCE 103 AA;
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62 AAANLES 68
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46 AASNVES 52
                                                                                                                                                                                                      1 AASNLES 7
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KV1G_HUMAN
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NCBI_TaxID=29281;
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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STRAIN=ATCC 19089, CB15;
MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
MEDLINE=21173699; PubMed=11259647; DOI=10.1073/pnas.061029298;
Mierman W.C., Felddlyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phacke N.D., Ely B. DeBoy R.T., Dodgon R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J., Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
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Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales; Caulobacteracee; Caulobacteracee; Caulobacteracee; Caulobacteree; Ca
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BRDLINE=29060541; PubMed=2851916;
The C. elegans sequencing consortium;
"Genome sequence of the nematode C. elegans: a platform for
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                                                                                                                                  Query Match 90.3%; Score 28; DB 2; Length 166; Best Local Similarity 85.7%; Pred. No. 1.4e+02; Matches 6; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       investigating biology.";
Science 282:2012-2018(1998).
EMBL, AL132858; CAB60484.1; -; Genomic DNA.
Ensembl; XL13G7A.14; Caenorhabditis elegans.
WormBase; WBGene0001375; Y113G7A.14.
WormBep; Y113G7A.14; CE32883.
Complete proteome; Hypothetical protein.
SEQUENCE 204 AA; 23067 MW; 8968065DF2EA9C7E CRC64;
EMBL; CT005246; CAJ07029.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 166 AA; 17847 MW; 0721B8C4E1F2D8CF CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
1-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein Y113G7A.14.
ORFNames=Y113G7A.14;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein CC2196.
OrderedLocusNames=CC2196;
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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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Q9A698;
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134 SASNLES 140
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Best Local Similarity
Matches 6; Conserv
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0910274
CAE
0901274
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MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Wood L.W., Zabuy Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
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"Characterization of Large-Insert DNA Libraries from Soil for Environmental Genomic Studies of Archaea.";
Environmental Genomic Studies of Archaea.";
Environ. Microbiol. 9:970-980(2004).
Hypothetical protein.
SEQUENCE 228 AA; 26380 MW; DBD6FCE793855BAA CRC64;
Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
11-SEP-2005 (TrEMBLrel. 21, Last sequence update)
Hypothetical profin Atu4594 (AGR L.563p).
OrderedLocusNames=AGR L.563, Atu4594;
Agrobacterium tumefacTens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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Pred. No. 1.8e+02;
1; Mismatches 0; Indels
                                                                                               "Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001). EMBL. ARCOL991, ARK24167.1; -; Genomic_DNA. PIR; C87521; C87521. C9752. C9752.
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Last sequence update)
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NCBI_TaxID=176299;
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QBU760; Q7CVC8;
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nes 6; Conservative
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Best Local Similarity
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STRAIN=IFM 10152;
PubMed=15466710; DOI=10.1073/pnas.0406410101;
PubMed=15466710; DOI=10.1073/pnas.0406410101;
PubMed=15466710; DOI=10.1073/pnas.0406410101;
Shiba J., Hattori M.;
"The complete genomic sequence of Nocardia farcinica IFM 10152.";
Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).
EMBL; AP006618; BAD59571.1; -; Genomic_DNA.
Complete proteome; Hypothetical protein.
SEQUENCE 289 AA; 30105 MW; C03F4CF028534631 CRC64;
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Sabebi G., Loy A., Jung K.H., Partha R., Spudich J.L., Isaacson T.,
Hirschberg J., Wagner M., Beja O.;
"New Insights into Metabolic Properties of Marine Bacteria Encoding
Proteorhodopsins.";
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Corynebacterineae; Nocardiaceae; Nocardia.
NCBI_TaxID=37329;
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85.7%; Pred. No. 2.2e+02;
ive 1; Mismatches 0; Indels
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EMBL; DQ073796; AAY78592.1; -; Genomic_DNA.

InterPro; IPR001425; Bac_rhodopsin.
Pfam; PF01036; Bac_rhodopsin. 1.

PROSITE; PS00950; BACTERIAL OPSIN 1; UNKNOWN 1.

SEQUENCE 250 AA; 27456 MW; 216112D190DE91A3 CRC64;
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                     Q4PKF4 9BACT PRELIMINARY;
Q4PKF4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QSYQHO NOCFA PRELIMINARY;
QSYQHO;
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176 AAANLES 182
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21 AAANLES 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nocardia farcinica.
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42 AASNLDS 48
     1 AASNLES 7
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                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.;
"Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.";
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chunhey F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester E.W.;

"The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=FB24;
US DOB Joint Genome Institute (JGI-PGF);
US DOB Joint Genome Institute (A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Arthrobacter sp. FB24.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Larimer F., Land M.,
"Annotation of the draft genome assembly of Arthrobacter sp. FB24.",
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Micrococcineae; Micrococcaceae; Arthrobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 90.3%; Score 28; DB 2; Length 234; Best Local Similarity 85.7%; Pred. No. 2e+02; Matches 6; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.3%; Score 28; DB 2; Length 228; 85.7%; Pred. No. 1.9e+02; ive 1; Mismatches 0; Indels
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EMBL, AAHG01000026; EAL94496.1; -; Genomic_DNA.

Hypothetical protein.

SEQUENCE 234 AA; 24889 MW; 79E8F0D08F129ACA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome; Hypothetical protein.
SEQUENCE 228 AA; 24816 MW; 4B03E65F8FB8A998 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE009387; AAL45388.1; -; Genomic_DNA.
EMBL; AE008228; AAK88851.1; -; Genomic_DNA.
PIR; A98166; A98166
PIR; AF3121; AF3121.
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US DOE Joint Genome Institute (PGF-ORNL);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 294:2323-2328(2001).
                                                                                                                                   Science 294:2317-2323(2001).
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13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
Hypothetical protein.
ORFNames=ArthDRAFT_0234;
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Q4NAZ3;
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Matches 6; Conservative
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156 AASNLET 162
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313 AA;
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P31611;
SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Dall D.J., Anzola J.V., Xu Z., Nuss D.L.;
"Complete nucleotide sequence of wound tumor virus genomic segment
                                                                                            Gossypium hirsutum (Upland cotton).
Makaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II; Malvales, Malvaceae, Malvoideae, Gossyplum.
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13-SEP-2005 (Rel. 48, Last annotation update)
Structural protein P9 (Capsomere protein P9) (Protein Pns11).
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                                                                                                                                                                                                                                                                                                                                                                                                       / Match 90.3%; Score 28; DB 2; Length 302; Local Similarity 85.7%; Pred. No. 2.7e+02; nes 6; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                     GO; GO:0005634; C:nucleus; IEA.
GO; GO:000567; F:DNA binding; IEA.
GO; GO:000567; F:DNA binding; IEA.
GO; GO:000567; F:DNA binding; IEA.
InterPro; IPRO1280; Homeodomain-rel.
InterPro; IPRO1005; Myb DNA_bG.
FRam; PPO0249; Myb_DNA_bInding; 2.
FROSITE; PSO0334; MYB_2; 1.
FROSITE; PSO0334; MYB_2; 1.
FROSITE; PSO0309; MYB_3; 2.
Nuclear protein; Repeat.
SEQUENCE 302 AA; 33817 MW; 48EESD99921ED2D7 CRC64;
                                                                                                                                                                                          Matz E.C., Burr B.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-1-1. SUBCELLULAR LOCATION: Nuclear (by similarity).
EMBL; AF3352821, AAK19615.1; -; mRNA.
                                              01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
GHMYB10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; dsRNA viruses; Reoviridae; Phytoreovirus.
                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
STRAIN-Acala Maxxa; TISSUE-Day of anthesis ovule;
           302 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             313 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 17:3599-3599(1989).
                                   Created)
           PRT;
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InterPro; IPR008776; Phyto_Pns9_10.
Pfam; PF05878; Phyto_Pns9_10; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last seq
13-SEP-2005 (Rel. 48, Last ann
                                  01-JUN-2001 (TrEMBLrel. 17,
        Q9ATD5_GOSHI PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                            NCBI_TaxID=3635;
                                                                                   Name=ghmyb10;
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Matches
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VP9_WTV
Q9ATD5
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MEDLINE=92074261; PubMed=1962460;
Hillman B.I., Anzola J.V., Halpern B.T., Cavileer T.D., Nuss D.L.;
Hillman B.I., Anzola J.V., Halpern B.T., Cavileer T.D., Nuss D.L.;
First field isolation of wound tunor virus from a plant host: minimal sequence divergence from the type strain isolated from an insect
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PubMed=15703294; DOI=10.1073/pnas.0409900102;
Ruby E.G., Urbanowski M., Campbell J., Dunn A., Faini M., Gunsalus R., Lostroh P., Lupp C., McCann J., Millikan D., Schaefer A., Stabb E., Stevens A., Visick K., Whistler C., Greenberg E.P.;
"Complete genome sequence of Vibrio fischeri: a symbiotic bacterium
                                                                                                                  Gaps
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01-JUL-1993 (Rel. 26, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Structural protein P9 (Gapsomere protein P9) (Protein Pns11).
Wound tumor virus (strain NJ) (WTV).
Viruses; dsRNA viruses; Reoviridae; Phytoreovirus.
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NCBI TaxID=312309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Virology 185:896-900(1991).
-1- SIMILARITY: Belongs to the phytoreoviruses S11 family.
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                                                         Length 313;
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Interpro; IRRO08776; Phyto Pns9 10.
Pfam; PF05878; Phyto Pns9 IO; 1.
SEQUENCE 313 AA; 35552 MW; D9B904785C601C34 CRC64;
35607 MW, 6746F59840AD17F2 CRC64;
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
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Pred. No. 2.8e+02;
1; Mismatches 0
                                                   Score 28; DB 1; 1
Pred. No. 2.8e+02;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical membrane spanning protein.
OrderedLocusNames=VFA1079;
Vibrio fischeri (strain ATCC 700601 / ES114).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362 AA.
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                                                      90.3%;
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ses 6; Conservative
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                                 Query Match
Best Local Similarity
Matches 6: Conso
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Bacteria, Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                  Local Similarity 85.7
hes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                   378 AASNLDS 384
                                     NUCLEOTIDE SEQUENCE
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                NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                       1 AASNLES
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                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=WA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562; DOI=10.1038/mbt820;
Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
Sakaki Y., Hattori M., Omura S.;
"Complete genome sequence and comparative analysis of the industrial
microorganism Streptomyces avermitils.";
Nat. Biotechnol. 21:526-531(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
STRAIN=21477403; PubMed=11572948; DOI=10.1073/pnas.2.11433198;
Omura S., IReda H., IBhikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitilis; deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                 Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                               Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.3%; Score 28; DB 2; Length 368; 85.7%; Pred. No. 3.3e+02; ive 1; Mismatches 0; Indels
                                                                                 90.3%; Score 28; DB 2; Length 352
85.7%; Pred. No. 3.3e+02;
          Proc. Natl. Acad. Sci. U.S.A. 102:3004-3009 (2005).
EMBL; CP000021; AAM88149.1; -; Genomic_DNA.
Interpro; IPR002549; UPF0118.
Pfam; PF01594; UPF0118; 1.
Complete profesome; Hypothetical protein.
SEQUENCE 362 AA; 38664 MW; 59943AB0BED91077 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
EMBL; BA000030; BAC68099.1; -; Genomic DNA.
Complete proteome; Hypothetical protein.
SEQUENCE 368 AA; 39156 MW; B268A4F7DB212E12 CRC64;
                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TYEMBLrel. 20, Created)
01-MAR-2002 (TYEMBLrel. 20, Last sequence update)
01-UUN-2003 (TYEMBLrel. 24, Last annotation update)
All2969 protein.
OrderedLocusNames=all2969;
                                                                                                                                                                                                                                                                                                                                          Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              579 AA.
                                                                                                                                                                                                                                                     01-JUN-2003 (TrEMBLrel. 24, Created) 01-JUN-2003 (TrEMBLrel. 24, Last seq 01-JUN-2003 (TrEMBLrel. 24, Last ann Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anabaena sp. (strain PCC 7120).
with pathogenic congeners.";
                                                                                                                                                                                                              VS_STRAW
QB2QVS_STRAW PRELIMINARY;
Q82QVS;
                                                                                 Query Match
Best Local Similarity 85.7-
                                                                                                                                                                                                                                                                                                     OrderedLocusNames=SAV390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QBYSW1 ANASP PRELIMINARY;
Q8YSW1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                   132 ASSNLES 138
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221 AASNVES 227
                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
                                                                                                                                              1 AASNLES 7
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                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=33903;
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1D 081
AC 081
DT 011
DT 011
DE AI
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495,
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown B.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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--- COPACTOR: Binds 1 zinc ion (Potential).
--- SUBCELLULAR LOCATION: Integral membrane protein.
--- SIMILARITY: In the N-terminal section; belongs to the AAA ATPase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- FUNCTION: Seems to act as an ATP-dependent zinc metallopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori 199 (Campylobacter pylori 199).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genomic sequence comparison of two unrelated isolates of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: In the C-terminal section; belongs to the peptidase
MEDLINE=21995285; PubMed=11759840; Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsumo A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Tabata S.; Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120."; Complete EMBL, BA000019; Bab14668.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.3%; Score 28; DB 2; Length 579; 85.7%; Pred. No. 5.5e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     579 AA; 66557 MW; 5C00EBD8CF31BB97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MXY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Cell division protein fteH homolog (EC 3.4.24.-).
Name=ftsH; OrderedLocusNames=JHP0356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       632 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE001471; AAD05932.1; -; Genomic_DNA.
PIR; D71941; D71941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP, Q9LCZ4; 11Y0.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR003959; AAA_ATPase_centr.
InterPro; IPR003966; AAA sub.
InterPro; IPR005936; Pept_M41_FtsH.
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'The genome sequence of Magnaporthe grisea.";
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InterDro; IPR011546; Pept M41 FtsH ex.

Pfam; PF00004; AAA; I.

Pfam; PF01404; AAA; I.

Pfam; PF0144; Peptidase_M41; 1.

Pfam; PF0144; Peptidase_M41; 1.

Pfam; PF0144; Peptidase_M41; 1.

PROSITE; PS00674; AAA; 1.

PROSITE; PS00674; AAA; 1.

PROSITE; PS01676; Cell cycle; Cell division; Complete proteome; Hydrolase; Metal-binding; Metalloprotease; Nucleotide-binding; Protease; Transmembrane; Zinc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein (Related to nuclear assembly factor NAF1).
Name=NCU04455.1; Synonyms=G21B4.060;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytoplasmic (Potential).
ATP (Potential).
By similarity.
Zinc (catalytic) (By similarity).
Zinc (catalytic) (By similarity).
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.3%; Score 28; DB 1; Length 632; 85.7%; Pred. No. 6.1e+02; ive 1; Mismatches 0; Indels
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Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2FB67B43C51559FB CRC64;
                                                                                                                                                                                                                                                                                                                     Cytoplasmic (Potential).
Potential.
Periplasmic (Potential).
Potential.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69765 MW;
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116
137
632
217
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438
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616 AANNLES 622
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632 AA;
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TRANSMEM
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TRANSMEM
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OTRWEL NEEL

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RC STRAIN-70-15,

RA Artern B., Nubshaun.

RA Arachchi H., Armbruster J., Bachantaang P., Baddwin J., Barry A.,

Bayul T., Blitshistery B., Bloom T., Blye J., Boguslavskiy L.,

RA Borowsky M., Boukhgalter B., Brunache A., Boguslavskiy L.,

RA Borowsky M., Boukhgalter B., Brunache A., Cooke P., Calixce N.,

Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuchoo C.,

RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuchoo C.,

Bayolia M., Folsy S., Dudge S., Dooley K., Dorie P.,

Britsgerald M., Folsy N., Dupes A., Elkins T., Engels R.,

Ritsgerald M., Folsy W., Gage D., Galagan J., Gaarin G., Gnerre S.,

Ritsgerald M., Folsy W., Hudde B., Hulne W., Husby E.,

RA Honan T., Horn A., Hudde N., Huddes I., Hulne W., Husby E.,

Jaffe D., Jones C., Kanal M., Kamat A., Kamysselis M., Karlsson E.,

Ageria C., Marken A., Krisner P., Kodira C., Kulboks B., Leabutti K.,

Ra Lan D., Landers T., Leger J., Lewis D., Lewis T.,

Lindblad-tob K., Liu X., Lokyitsang T., Lokyitsang Y., Maclean C.,

Manning J., Marabella R., Macdonald J., Maclean C., Majora J.,

Manning J., Marabella R., Macdonald J., Maclean C., Mayor J.,

Manning J., Marabella R., Macdonald J., Maclean C., Mayor J.,

RA Manning J., Marabella R., Macdonald J., Maclean C., Mayor J.,

Norbu N., O'donnell P., Okoawo O., Oleary S., Gmotosho B.,

Roberthy M., Mulrain L., Munson G., Naylor C., Nizzari M., Norbu C.,

Ry Norbu N., O'donnell P., Okoawo O., Oleary S., Gmotosho B.,

Ry Norbu N., Sheppen N., Shida R., Smirnov S., Smith C., Sougnez C.,

Spencer B., Stalker J., Stange-thomann N., Sather T.,

Ry Rutman M., Schupbach R., Saman C., Settipalli S., Rachupka T., Rameany U., Rameany C., Ryby Wang S., Tasmla T., Tsomo N., Vallee D., Wang S., Wang S., Yang X., Yang S., Yang X.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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0
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetes incertae sedis, Magnaporthaceae, Magnaporthe.
                                                                                                                                                                                                                                                                                                                                                        Length 701;
                                                                                                                                                                                                                                                                                                                                                    Score 28; DB 2; Length 701
Pred. No. 6.9e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                        11 protein.
701 AA; 75154 MW; 7FF7BE9ABCC2CF45 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-5EP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                 preliminary data.

EMBL; AABXO1000782; EAA26677.1; -; Genomic_DNA.

EMBL; BX080808; CAF05991.1; -; Genomic_DNA.

InterPro; IPR008696; NAF1.

Pfam; PF05492; NAF1.

Hypochetical protein.

SEQUENCE 701 AA; 75154 MW; 7FF7BE9ABCC2CF45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                    Query Match 90.3%;
Best Local Similarity 85.7%;
Matches 6; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OSIPCS MAGGR PRELIMINARY;

AC 051PCS MAGGR PRELIMINARY;

AC 051PCS GTERBELFE1 31,

DT 13-SEP-2005 (TERBELFE1 31,

DE HYPOTHORICAL PICTORIN.

BE HYPOTHORICAL PICTORIN.

CREMANOSTH PROTECTION.

CREMAN
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EMBL; AE003543; AAF50008.1; -; Genomic_DNA.
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Ensembl; CG7293; Drosophila melanogaster.
FlyBase; FBgn0004381; Klp68D.
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                                                                                                                                                                                                                              PERMITMENTALY CARRY BINGS 4 CORDET ions per monomer (By similarity).

REMBL, AACTO101127; EAA48833.1; -; Genomic_DNA.
InterPro; IPR011705; Cu-oxidase 2.
InterPro; IPR011705; Cu-oxidase 2.
InterPro; IPR011707; Cu-oxidase 2.
InterPro; IPR001235; Cu-oxidase 3.
RITHERPRO; IPR001235; Cu-oxidase 3.
RITHERPRO; IPR001235; Pyridoxal_deC.
REMINERPRO; IPR001235; Cu-oxidase 2.
REMINERPRO; IPR001235; Cu-oxidase 2.
REMINERPRO; IPR001235; Cu-oxidase 2.
REMINERPRO; IPR001235; Cu-oxidase 2.
REMINERPRO; IPR001391; Cu-oxidase 2.
REMINERPRO; IPR001392; Cu-oxidase 2.
REMINERPRO; RUITICOPPER OXIDASE1, 1.
REMINERPRO; MULTICOPPER OXIDASE1, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril W.J., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale Q., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
MEDLINE=95050960; PubMed=7525600; DOI=10.1083/jcb.127.4.1041;
Pessavento P.A., Stewart R.J., Goldstein L.S.B.;
"Characterization of the KLP68D kinesin-like protein in Drosophila:
possible roles in axonal transport.";
J. Cell Biol. 127:1041-1048(1994).
                                                                                                                                                                                    CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P46867, Gyvrn8, Created)
01-NOV-1995 (Rel. 32, Created)
13-SEP-2005 (Rel. 32, Last sequence update)
13-SEP-2005 (Rel. 34, Last annotation update)
Kinesin-11ke protein KLP68D.
Name=KLP68D; Synonyms=KLP5; ORFNames=CG7293;
Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Noptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Length 747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.3%; Score 28; DB 2; Length 747
85.7%; Pred. No. 7.4e+02;
ive 1; Mismatches 0; Indels
to the EMBL/GenBank/DDBJ databases.
                                                               Dean R., Mitchell T., Brown D., Pan H., Thon M., Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                  Zhu H., Blackmon B.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEO'TIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
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                                                                                                                                                                                                                     preliminary data.
Submitted (OCT-2003)
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155 ASSNLES 161
                                 NUCLEOTIDE SEQUENCE
                                                                                                                  NUCLEOTIDE SEQUENCE
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Best Local Similarity
Matches 6; Conserv
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RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.W., Cawley S., Dallke C., Davenport L.B., Davies P.,
RA Cherry J.W., Cawley S., Dallke C., Davenport L.B., Davies P.,
RA Cherry J.W., Cawley S., Dellike C., Davenport L.B., Dietz S.W.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Gong F., Garria J.H., Gu Z., Glant W.M., Glasser K.,
R. Glodek A., Gong F., Gorrell J.H., Gu Z., Glant W.M., Classer K.,
RA Hostin D.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D.L., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Rimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
Ra Liako P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K., Nixon K., Nusskern D.R., Pacleb J.M.,
Ra Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E.,
Syirskas R., Tector C., Turner R., Venter B., Wang A.H., Wang X.,
Rang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Hang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Rang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Rang S.-Y., Wassarman D.A., Weinstock G.M., Zhong W., Smith H.O.,
Rang C. P., Myers E.W., Rubin G.M., Venter J.C.,
Raibbs R.A., Wyers E.W., Rubin G.M., Venter J.C.,
Raibbs R.A., Wyers E.W., Rubin G.M., Venter J.C.,
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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
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-I-FUNCTION: Plus-end directed microtubule motor that may be used for anterograde axonal transport and could conceivably move cargoes in fly neurons different than those moved by kinesin heavy chain or other plus-end directed motors.

-I-TISSUE SPECIFICITY: Expressed primarily in the central nervous system and in a subset of the peripheral nervous system during
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-!- SIMILARITY: Belongs to the kinesin-like protein family. Kinesin II
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MEDLINE=22426069; PubMed=12537572;

Mistra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

Hradecky P., Huang Y., Kandinker J.S., Millburn G.H., Prochnik S.E.,

Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.

Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drygdale R.A.,

Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bystematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
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EMBL; M74431; AAA28658.1; -; Genomic_DNA
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PRT; 1097 AA

43, Created)

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MCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;

Palenik B., Brahamsha B., Larimer F.W., Land M.L., Hauser L.,

Pallenik B., Lamerdin J.E., Regala W., Allen B.E., McCarren J.,

Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.;

"The genome of a mortile marine Synechococcus.";

"The genome of a mortile marine Synechococcus.";

Nature 424:1037-1042(2003).

-I. FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as
                                                                                                                             29-WAR-2004 (Rel. 43, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (RNAP beta subunit) (Transcriptase Deta chain) (RNA polymerase beta subunit).
Name=rpoB; OrderedLocusNames=SYNW0613;
                                                                                                                                                                                                                                                 Synechococcus sp. (strain WH8102).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                      STANDARD;
                                                                                                                                                                                                                                                                                      NCBI_TaxID=84588;
                                                                                                               29-MAR-2004
                                                                      SYNPX
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                                               RPOB_SYNPX
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EMBL, AYOS1583; AAK93007.1; -; mRNA.
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Bukaryota, Metazoa; Arthropoda, Hexapoda; Insecta; Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PSO0411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PSS0067; KINESIN_MOTOR_DOMAIN2; 1.
ATP-binding; Microtubule; Motor_protein; Nucleotide-binding.
SEQUENCE 784 AA; 88207 MW; 7A3C6716D22BC05D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28; DB 2; Length 784;
Pred. No. 7.8e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 784;
                                                                                                                                                                                                                                                                                                                                                                                                     Score 28; DB 1; Length (03 Pred. No. 7.88+02;
                                                                                                                                                                                                                                                                                                             SS -> TC (in Ref. 4).
GSRAK -> VRGQV (in Ref. 4).
G -> A (in Ref. 2).
; 94BB9BADF072DFC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PlyBase; PEGG, MAN (1968D. CO); GO: 0003774; F: Procor activity; IDA. GO: 0003774; F: Motor activity; IDA. GO: 00008099; P: Nanterograde axon cargo transport; IBP. InterPro; IFR001752; Kinesin_motor. Pfam; PF00225; Kinesin; 1.
GO; GO:0003774; F:motor activity; IDA.
GO; GO:0008089; P:anterograde axon cargo transport; IEP.
InterPro; IPR001752; kinesin_motor.
Pfam; PF00225; Kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00129; KISC; 1.
                                                                                                                                 PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
ATP-binding; Colled coil; Microtubule; Motor protein;
Nucleotide-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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Potential.
Potential.
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                                                                                                                                                                                                                             Kinesin-motor
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01-DEC-2001 (TrEMBLrel. 19, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last snn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00380; KINESINHEAVY. SMART; SM00129; KISC; 1.
                                                                                                                                                                                                                                                                                                                                                                                 88193 MW;
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Best Local Similarity 85.7%;
Matches 6; Conservative
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Q961H5;
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1es 6; Conservative
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1113
385
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338
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751 AASNLDS 757
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                                                                                                                                                                                                                                                                   351 3
426 5
220 2
338 3
784 AA;
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O961145 DROME
DAC Q961145_DRC-2
DT 01-DEC-2

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NP BIND
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Ruropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                           + RNA(n+1).
SUBUNIT: In cyanobacteria the RNAP catalytic core is composed of 2 alpha, 1 beta, 1 beta, 1 gamma and 1 omega subunit. When a sigma factor is associated with the core the holoenzyme is formed, which can initiate transcription (By similarity).
SIMILARITY: Belongs to the RNA polymerase beta chain family.
CATALYTIC ACTIVITY: Nucleoside triphosphate + RNA(n) = diphosphate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R InterPro; IPR00764; RNA pol B.
R InterPro; IPR00764; RNA pol B.
R InterPro; IPR00764; RNA pol Rpb2 1.
R InterPro; IPR00764; RNA pol Rpb2 2.
R InterPro; IPR007645; RNA pol Rpb2 2.
R InterPro; IPR007645; RNA pol Rpb2 2.
R InterPro; IPR007120; RNA pol Rpb2 3.
R InterPro; IPR007641; RNA pol Rpb2 7.
R InterPro; IPR007641; RNA pol Rpb2 7.
R Pfam; PF04563; RNA pol Rpb2 2; 1.
R Pfam; PF04561; RNA pol Rpb2 2; 1.
R Pfam; PF04565; RNA pol Rpb2 2; 1.
R Pfam; PF04565; RNA pol Rpb2 2; 1.
R Pfam; PF04565; RNA pol Rpb2 2; 1.
R Pfam; PF04560; RNA pol Rpb2 7; 1.
R TIGRRAM; TIGRO13; TpOB; 1.
R ROSITE; PS01166; RNA POL BETA; 1.
R NUCLEOCIGYLTANA POL BETA; 1.
R NUCLEOCIGYLTANA POL BETA; 1.
R NUCLEOCIGYLTANA POL BETA; 1.
R SEQUENCE 1097 A4; 122452 MW; 1FFAIA87DB6079BC CRC64;
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Pred. No. 1.1e+03;
1; Mismatches 0; Indels
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QGC318 YARLI PRELIMINARY;
QGC318 25-0CT-2004 (TEMBLRE1. 28, Created)
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Matches 6; Conservative
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Q6C318 YAR
ID Q6C31
AC Q6C31
DT 25-OC
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Length 73;

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100.0%; Pred. No. 96; ive 0; Mismatches
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MEDLINE=72189444; PubMed=5028201;
                                                         6; Conservative
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Query Match
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Matches 6; Conserv
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                                                                                                            2 ASNLES 7
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A Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
A Lafontaine I., de Montigny J., Marcok C., Neuveglise C., Taila E.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
B Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
B Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
B Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
A Pellenz S., Potier S., Richard G. F., Straub M.-L., Suleau A.,
Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zaniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
Mincker P., Souciet J.-L.;
Mincker P., Souciet J.-L.;
T "Genome evolution in yeasts.";
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Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
Chow Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
Chen Y.-T., Chang C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
Hsiang J.-N., Hsu C.-H., Handy J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
Wu H.-P., Shaw J.-F.;
Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AC135419; AAV25010.1; -; Genomic_DNA.
SEQUENCE 73 AA; 8113 MW; 220127E45BBF6A98 CRC64;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                              OrderedLocusNames=YALIOE34463g;
Yarrowia lipolytica (Candida lipolytica).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
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                    25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similarities with wi|NCU06697.1 Neurospora crassa NCU06697.1
hypothetical protein.
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Pred. No. 1.3e+03;
1; Mismatches 0; Indels
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Pfam; PF00149; Metallophos; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 1260 AA; 131877 MW; 8A4679ABAC53DFCB CRC64;
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Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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GO; GO:0004519; F:endonucleage activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0006281; P:DNA repair; IEA.
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Similarity 85.7%;
6; Conservative
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QGOEB9 ORYSA PRELIMINARY;
QGOEB9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 430:35-44(2004)
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1171 AASNVES 1177
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Name=OSJNBa0044P19.8;
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Best Local Similarity
Matches 6; Conserv
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RESULT 37

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                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jones protein Au.";
Biophys. Struct. Mech. 1:139-146(1975).
-!- MISCELLANBOUS: The structure of the V region was determined by molecular replacement methods using the known structure of the V region of the kappa chain REI.
-!- MISCELLANBOUS: The C region of this chain has the INV (3) marker.
-!- MISCELLANBOUS: This is a Bence-Jones protein.
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        Schiechl H., Hilschmann N.; "Rule of antibody structure of a monoclonal manue of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones protein Au).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=77022433; PubMed=1234024; Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E., Schwager P., Steigemann W., Schramm H.J.; "The structure determination of the variable portion of the Bence-
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SWART; SW00406; IGv. 1.
PROSITE, PS50835; IG_LKE; 1.
3D-ekructure; Bence-Jones protein, Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.
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                                   0; Indels
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DB 2;
96;
                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Homo sapiens (Human).
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Ensemb; ENSG00000137382; Homo sapiens.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:000555; P:immune response; NAS.
InterPro; IPR007110; IG-like.
                                                                                                                                                                                     108 AA
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                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                  MEDLINE=79073152; PubMed=103003; Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
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Complementarity-determining-1.
Framework-2.
Complementarity-determining-2.
Framework-3.
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                                                                                                                               87.1%; Score 27; DB 1; Length 108; 100.0%; Pred. No. 1.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                   11939 MW; E8011187EE6F6FB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin domain;
                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Mus musculus (Mouse).
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HSSP; P01665; 1QNZ.
SMR; P0167; 1-108.
SMR; P0167; 1-108.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM0406; IGv.; 1.
Direct protein sequencing; Immunoglobulin do
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Best Local Similarity luv...
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51 ASNLES 56
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;

Muroidea; Muridae; Mus.

MCBI_TaxID=10090;
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MEDLINE=79012520; PubMed=99744;
MCKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally related mouse kapps variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
-1- MISCELLANBOUS: The PC 3741 and TEPC 111 sequences are identical.
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MEDILLE-3907131-21, Pubmed-10303;
Weigert M., Gatmaiten L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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Complementarity-determining-1.
Framework-2.
Complementarity-determining-2.
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100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0; Indel8
                                                                    87.1%; Score 27; DB 1; Length 108; 100.0%; Pred. No. 1.5e+02; ive 0; Mismatches 0; Indels
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108 AA; 11699 MW; D40921D18DAC4B9E CRC64;
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HSSP; PO1665; 1QNZ.
Ensembl; RNSMVSGO0000060064; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SWART; SMO0406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
REGION
                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Ig kappa chain V-III region PC 3741/TEPC 111.
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Matches 6; Conserv
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55 ASNLES

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                                                                                                                Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Mus Mus
                                                                                                                                                                                                      PROTEIN SEQUENCE (ABPC 22).
MEDLINE-79012520, PubMed=99744;
MECKean D.J., Bell M., Potter M.;
"Meckanisms of antibody diversity: multiple genes encode structurally
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-!- MISCELLANBOUS: The ABPC22 and PC9241 sequences are identical.
                                                                                                                                                                                                                                                                                                                     MEDINE-19071152; Pubmed=103003; MEDINE-19071152; Pubmed=103003; Meigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; Rearrangement of genetic information may produce immunoglobulin
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Complementarity-determining-1.
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Complementarity-determining-2.
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Complementarity-determining-3.
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100.0%; Pred. No. 1.5e+02;
.ive 0; Mismatches 0; Indels
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Ensembl; ENSMUSG000006064; Mus musculus.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003196; Ig-V.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
                                                                                                                                                                                                                                                                 related mouse kappa variable regions."; Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Ig kappa chain V-III region ABPC 22/PC 9245.
                               111 AA
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21-JUL-1986 (Rel. 01, Last sequence update)
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                            STANDARD;
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P01663;
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                            KV3J_MOUSE
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RESULT 41
KV3J_MOUSE
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                           Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
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Complementarity-determining-1.
Framework-2.
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Framework-3.
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                                                                                                                                                                                                                                                                                                                                 Ensembl; ENSMUSSG0000060064; Mus musculus.
InterPro; IPR00710; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
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Pred. No. 1.5e+02;
10-MAY-2005 (Rel. 47, Last annotation update)
Ig kappa chain V-III region PC 4050.
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10-MAY-2005 (Rel. 47, Last annotation update)
Ig kappa chain V-III region PC 6308.
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100.0%; Pred. No. ...
0; Mismatches
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MEDLINE-79073152; PubMed=103003;
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PROTEIN SEQUENCE.
MEDLINE=79073152; PubMed=103003;
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21-JUL-1986 (Rel. 01, Last seq
10-MAY-2005 (Rel. 47, Last ann
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                              Mus musculus (Mouse).
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SMR; P01663; 1-111.
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the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Mammalia; Eutheria; Euarchontoglires, Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0; Indels
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HSSP; P01665; 1QNZ.
SWR; P01670, 1-111.
SWR; P01670, 1-111.
SMR; P01670, 1-111.
SMRAP.
InterPro; IPR007110, Ig-like.
InterPro; IPR003596; Ig_v.
SMRAR; SM00406; IG_v.
SMRAR; SM00406; IG_v.
InterPro; IPS0355; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
                                                                                                                      Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.
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21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
18 kappa chain V-III region PC 6684.
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                                                                     Ensembl; ENSMUSGO000053225; Mus musculus.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; I.
PROSITE; PS50835; IG-LIKE; 1.
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Matches 6; Conservative
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                                          PIR; C01937; KVMS08
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SMR; P01667; 1-111.
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Mus musculus (Mouse)
Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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                     Complementarity-determining-2.
                                    Framework-3.
Complementarity-determining-3.
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Pred. No. 1.5e+02;
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InterPro; IPR03596; Ig-v.
SMART; SM00406; IGv; 1.
PR051TF; PS26315; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
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21-JUL-1986 (Rel. 01, Last sequence update)
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HSSP; P01665; 1QNZ.
SMR; P01671; 2-111.
Ensembl; ENSWUGG00000053225; Mus musculus.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
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PIR, S09963, S09963.
PIR, S59640, S59640.
HSSP, PO1665, 1QNZ.
SMR, Q92089, 1-111.
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                       NUCLEOTIDE SEQUENCE.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
10-MAY-2005 (Mouse).
10-MAY-200
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MEDLINE=79073152; PubMed=103003;
Weigert M., Gatmaltan L., Loh B., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Mus musculus (Mouse).
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InterPro; IPR007110; Ig-like.
InterPro; IPR007595; Ig-v.
SMART; SW00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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QSF217;
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Erlandsson A., Holm P., Ullen A., Stigbrand T., Sundstrom B.B.; "Studies of the interactions between the anticytokeratin 8 monoclonal antibody TS1, its antigen and its anti-idiotypic antibody alphaTS1."; "Mol. Recognit. 16:157-163(2003).
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus
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Reininger L., Shibata T., Ozaki S., Shirai T., Jaton J.C., Izui S.;
"Variable region sequences of pathogenic anti-mouse red blood cell
autoantibodies from autoimmune NZB mice.";
Eur. J. Immunol. 20:771-777(1990).
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Atkin J.D., lape A., Jennings I.G., Horaitis O., Cotton R.G.H.; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Pterin-mimicking anti-idiotope kappa chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 111;
                                                                                                                                                                                                             Erlandsson A.;
Submitted (PEB-2005) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ809031; CAI54295.1; -; mRNA.
INCEPTO; IPR003599; Ig.
InterPro; IPR003110; Ig-like.
InterPro; IPR003110; Ig-like.
InterPro; IPR003596; Ig_v.
Ffam; PF07666; V-set; I.
SWART; SW00409; IG; I.
SWART; SW00409; IG; I.
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100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0;
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J. Mol. Biol. 253:559-575(1995).
EMBL; AF307935; AAL09419.1; -; Genomic_DNA.
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MEDLINE=78235887; PubMed=98179;

Burstein Y., Schechter I.;

Burstein Y., Schechter I.;

"Primary structures of N-terminal extra peptide segments linked to the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled expression of immunoglobulin genes.";

Biochemistry 17:2392-2400(1978).
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McKean D.J., Bell M., Potter M.;
"Mechanisma of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=73140225; PubMed=4691517;
McKean D.J., Potter M., Hood L.E.;
Mouse immunoglobulin chains. Pattern of sequence variation among
kappa chains with limited sequence differences.";
Biochemistry 12:760-771(1973).
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                              111 AA; 12046 MW; 1E46988AA6858526 CRC64;
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PROSTIR: PS50813; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                  DB 2; Le
1.5e+02;
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10-MAY-2005 (Rel. 47, Last annotation update)
1g kappa chain V-III region MOPC 63 precursor.
Mus musculus (Mouse).
                                                                        0; Mismatches
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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Framework-1.
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100.0%; Pred. No.
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PROSITE; PS50835; IG_LIKE; 1.
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SMR; P01661; 21-131
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                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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01-FEB-1995 (Rel. 31, Last sequence update)
01-MAY-2005 (Rel. 47, Last annotation update)
CDP-diacylglycerol-serine O-phosphatidyltransferase (EC 2.7.8.8)
(Phosphatidylserine synthase).
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Okada M., Matsuzaki H., Shibuya I., Matsumoto K.;
Cloning, sequencing, and expression in Bscherichia coli of the Bacillus subtilis gene for phosphatidylserine synthase.";
J. Bacteriol. 176:7456-7461(1994).
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                                                  Complementarity-determining-3
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                                                                                                                                                                                                                      131 AA; 14291 MW; D212EC9F08DC880A CRC64;
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Bacillus subtilis.
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Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zumstein E., Yoshikawa H., Danchin A., "The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                             Nature 390:249-256(1997).
-!- CATALYTIC ACTIVITY: CDP-diacylglycerol + L-serine = CMP + 3-0-sn-phosphatidyl-L-serine.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the CDP-alcohol phosphatidyltransferase
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44.3 80 2 Q8D9R3 VIBVU Q8d9r3 vi 44.3 87 2 Q63F62_BACC2 Q63F62 bz 44.3 88 2 Q50956_NEIGO Q50956 ne	44.3 88 2 Q50958_NEIGO Q50958 n 44.3 95 2 Q5UWU3_HALMA Q5uwu3 h	44.3 96 2 Q50953_NEIGO Q50953_n 44.3 98 2 Q6N714_RHOPA Q6n714_r	44.3 100 2 Q5Y518 STRPN Q5Y518 B 44.3 108 2 Q6G726 STAAS Q6G726 B	44.3 108 2 Q6GEDB_STAAR Q6Ged8 s 44.3 108 2 Q5HDR2_STAAC Q5hdr2 s	44.3 108 2 Q7A424_STAAN Q7a424_sr 44.3 108 2 Q8NV86_STAAW Q8nv86_sr	44.3 108 2 Q99RX7_STAAM Q99rx7 8: 44.3 112 2 Q8T343_PLAFA 08t343 D	44.3 113 2 Q9P1H0_HUMAN Q9p1h0 h 44.3 114 2 Q8T511_PLAFA O8t511 p	44.3 114 2 Q9MFE4_BETVU Q9mFe4_bet 44.3 118 2 OSWDIR BACSX OSWdia had	44.3 127 2 Q6NYP2 BRARE Q6NYP2 D6NYP2 D8 44.3 120 1 HPWRT G10NP	44.3 131 1 FABP2_MANSE P31417	44.3 134 2 Q7PH17_ANOGA Q7ph17 44.3 138 2 Q6W6P1_BRARE Q6w6p1	44.3 141 2 Q81M72_BACAN Q81m72 44.3 142 2 OSBRB DONDY OSTBRB	44.3 144 2 Q682K9_ARATH Q682K9 44.3 144 2 Q01.E71 ADATH Q010.21	44.3 144 2 QSHWR9_CAMUR QShwr9	44.3 150 2 OSEND3 HETTR QSenD3 QSenD3	44.3 151 2 P72503 STRPN P72503	44.3 152 2 Q8GJGO_CAMJE Q98U00	44.3 153 2 Q9AU02_CHLRE Q9au02	44.3 154 2 Q6HEOG_BACHK Q6he06	44.3 154 2 Q731D7 BACCI Q731d7 44.3 155 2 Q8RLY3 NOSPU Q8RLY3	44.3 156 2 P72527 STRPN P72527 44.3 161 2 Q4XHR8_PLACH Q4xhr8	44.3 163 2 Q4KPE6_9VIRU Q4kpe6 44.3 167 2 Q6IAZ6_HUMAN Q6iaz6	44.3 169 2 Q8XW47_RALSO Q8XW47	44.3 173 1 RGS10 HUMAN 043665	44.3 173 2 QBFND4 COREF QBFnd4	44.3 176 2 091BBA3_NPVST 091ba3	44.3 179 2 Q5GZHZ_NEIGO Q5GZhZ 44.3 179 2 Q5GZH9_NEIGO Q5GZh9	44.3 179 2 Q5G2K9 NBIGO Q5G2k9 44.3 179 2 O5G2L4 NBIGO O5G214	44.3 179 2 Q5G2M3_NBIGO Q5G2M8 44.3 179 2 O5G2M8_NBIGO O5G2M8	44.3 179 2 Q5G2NS_NBIGO Q5g2nS 44.3 179 2 Q576Z6_BRUAB Q576Z6	44.3 179 2 QBFX12_BRUSU QBfx12	44.3 181 1 IPYR_UREPA Q8ybd1	44.3 181 2 P79786_CHICK P79786	44.3 186 2 Q75K28_DICDI Q75K28 44.3 186 2 Q552Q1_DICDI 0552Q1	44.3 190 2 Q9HMA3_HALSA Q9hma3 44.3 190 2 Q7VH21_HELHP Q7vh21	44.3 195 2 Q97LB4 CLOAB Q97lB4 44.3 196 2 Q6G4P9_BARHE QGG4P9 44.3 201 2 O54420 STRDN O55420	44.3 202 2 GEMOX4_METMP QEMOX4 DEMOX OF THE TOTAL OF THE TWO TAXABLE THE TAXABLE THE TAXABLE T
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21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
19 kappa chain V-III region PC 7183.
Mus musculus (Mouse).
Bukaryota; Medazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Musinae; Mus.
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MEDLINE=79073152; PubMed=103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                       InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
BROSITE; PS50835; IG_LIKE; 1.
3D-structure; Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 79; DB 1; Length 111; 100.0%; Pred. No. 2.3e-05; ative 0; Mismatches 0; Indels
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Complementarity-determining-1.
Framework-2.
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Complementarity-determining-3.
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SMR; POI666; 1-111.
SMRsembl; ENSMUSGO00053225; Mus musculus.
InterPro; IPR00310; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM0406; IGV, 1.
Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.
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                  PDB; 1QNZ; NMR; L=1-111.
Ensembl; ENSMUSG00000053225; Mus musculus.
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    PIR; A01937; KVMS43.
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MEDLINE=94009207; PubMed=7691608;

Mo J.A., Bona C.A., Holmdahl R.,

"Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen.";

Eur. J. Immunol. 23:2503-2510(1993).
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MEDLINE=20264305; PubMed=10801487; DOI=10.1016/S0969-2126(00)00119-2; Tugarinov V., Zvi A., Levy R., Hayek Y., Matsushita S., Anglister J.; Twgarinov V., Zvi A. an anti-gpl20 antibody complex with a V3 peptide reveals a surface important for co-receptor binding."; Structure 8:385-395(2000).
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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MEDLINE=79073152; PubMed=103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                    mus
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039449
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09b949
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21-JUL-1986 (Rel. 01, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Kappa chain V-III region PC 7043.
OBWGG2_CAEEL
039449_CTCAR
09BRF8_HUWAN
09H9M9_HUWAN
09NUT6_HUWAN
05RT4_PONLY
CALU_MOUSE
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Q61P82_XENLA
Q6NVMS_XENTR
Q4NLG2_9MICC
Q9R2Z6_NEIGO
Q9R2Z9_NEIGO
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O9RF63 NEIGO
O9RF71 NEIGO
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EMBL; Z25446; CAA80933.1; -; mRNA.
EMBL; Z25448; CAA80935.1; -; mRNA.
EMBL; Z25450; CAA80937.1; -; mRNA.
EMBL; Z25452; CAA80939.1; -; mRNA.
EMBL; Z25454; CAA80941.1; -; mRNA.
EMBL; Z25454; CAA80941.1; -; mRNA.
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                                                                                  Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Murinae, Murinae, Mus.
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21-JUL-1986 (Rel. 01, Last sequence update)
10-NAY-2005 (Rel. 47, Last annotation update)
1g kappa chain V-III region PC 7210.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchonicoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                 PROTEIN SEQUENCE.
MEDLINE=79073152; PubMed=103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRÓTEIN SEQUENCE.
MEDLINE=79073152; PubWed=103003;
Medjert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
diversity.";
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Complementarity-determining-1.
Framework-2.
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Pramework-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin domain;
                                 21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
1g kappa chain V-III region PC 7769.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ensembl; ENSMUSSO0000053225; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; II-
PR0STIE; PS50835; IG_LIKE; I.
Direct protein sequencing; Immunoglobulin
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                     Created)
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                 21-JUL-1986 (Rel. 01,
21-JUL-1986 (Rel. 01,
10-MAY-2005 (Rel. 47,
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SMR; P01669; 1-111.
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P01668;
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
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MEDLINE=79073152; PubMed=103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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Pred. No. 2.3e-05;
                                                                  Length 111;
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                                 11952 MW; 2058BB50CE306D31 CRC64;
                                                                 Score 79; DB 1; L. Pred. No. 2.3e-05; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct protein sequencing; Immunoglobulin domain;
                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kappa chain V-III region PC 6308.
Mus musculus (Mouse)
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By similarity.
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 By similarity
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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                                                             Query Match 100.0%; Best Local Similarity 100.0%; Matches 15; Conservative (
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Les 15; Conservative
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KV3Q_MOUSE
ID KV3Q_MOUSE
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MEDLINE=79012520; Pubmed=99744;
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Q57HKO_SALCH PRELIMINARY;
                                                                       13; Conservative
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HSSP, P01665; 1QNZ.
SMR; P01664; 1-111.
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KV3L_MOUSE
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                         This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MRR-2004 (TrEMBLrel. 26, Last annotation update)
Anti-human Fc gamma receptor III 3G8 kappa light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Fragment).
Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
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Bruenke J., Fischer B., Barbin K., Schreiter K., Wachter Y., Mahr K., Titgemeyer F., Niederweis M., Peipp M., Zunino S.J., Repp R., Valerius T., Fey G.H.:

"A recombinant bispecific single-chain Fv antibody against HLA class II and FcgammaRIII (CD16) triggers effective lysis of lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Framework-3.
Complementarity-determining-3.
Framework-4.
By similarity.
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Pramework-2.
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Pred. No. 7.4e-05;
1; Mismatches 0; Indels
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PROSITE; PS50815; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.
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SMR; Q81106; 1-111.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR00110; Ig-like.
InterPro; IPR003596; Ig_v.
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Br. J. Haematol. 125:167-179(2004)
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PROSITE; PS50835; IG LIKE; 1.
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Best Local Similarity 93.33
Matches 14; Conservative
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Q811UG;
Nature 276:785-790(1978)
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110 AA;
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081106 MOUSE
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DT 01-JUN-20
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DE Anti-hum
DE STRAIN=BR
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RX PROSITE;
RX RRECEDIOT
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"Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
-I- MISCELLANEOUS: This chain was isolated from a myeloma protein.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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Complementarity-determining-1.
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                                                   89.9%; Score 71; DB 2; Length 111;
86.7%; Pred. No. 0.00053;
.ive 2; Mismatches 0; Indels
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86.7%; Pred. No. 0.0017;
iive 1; Mismatches 1; Indels
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111 AA; 12101 MW; CEDECEE157F2C94A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ensembl, ENSWINSG0000053225; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003566; Ig-v.
SWART; SW00406; IGV; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                      PO1664,
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
1G kappa chain V-III region CBPC 101.
Mus musculus (Mouse).
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By similarity.
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ACCOUNT THE PROPERTY OF THE PR

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Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.; "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                         Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain C. Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia N. Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Rroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Ouail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Simmonds M., Skelton J., Stevens K., "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
                                                                                                                                                                                                                                                                Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOI=10.1128/JB.185.7.2330-2337.2003;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48; DB 2; Length 282;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
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Complete proteome; Hypothetical protein; Repeat.
SEQUENCE 282 AA; 31930 MW; EBCE0B08DBD6E877 CRC64;
                                                                                                                                     01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
10-WAY-2005 (TrEMBLrel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                     282 AA
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EMBL; AE016846; AA071108.1; -; Genomic_DNA.
InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
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NUCLEOTIDE SEQUENCE.
STRAIN=LT2 / SGSC1412 / ATCC 700720;
                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
                                                                                                                                                                                                                           OrderedLocusNames=STY3863, t3606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Bacteriol. 185:2330-2337(2003)
                                                                                                                                                                                                                                                                  Bacteria, Proteobacteria, Gamma
Enterobacteriaceae, Salmonella.
                                                                                                                                                                                                     Hypothetical protein STY3863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Putative cytoplasmic protein.
263 EALEPDDYDGDIYMN 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OrderedLocusNames=STM4015;
                                                                                                QBZ2S9 SALTI PRELIMINARY;
Q8Z2S9; Q7C6K9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QBZKUO_SALTY PRELIMINARY;
Q8ZKUO;
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Best Local Similarity
                                                                                                                                                                                                                                              Salmonella typhi
                                                                                                                                                                                                                                                                                                           NCBI_TaxID=601;
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                                                          RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-ATCC 9150 (SARB42; PubMed=155318B2; DOI=10.1038/ng1470; PubMed=155318B2; DOI=10.1038/ng1470; PubMed=155318B2; DOI=10.1038/ng1470; PubMed=155318B2; DOI=10.1038/ng1470; Purclilland M., Sanderson K.E., Clifford T., Ozersky P., McLellan M., Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G., Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D., Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P., Delehaunty K., Fronick C., Magrini V., Nhan M., Warren W., Florea L. Spieth J., Wilson R.K.;
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restricted serovars of Salmonella enterica that cause typhoid.";
Nat. Genet. 36:1268-1274(2004).
                                                                                                                                                                                                                                                                               Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y., Wang H.-S., Lee Y.-S.,
"The genome sequence of Salmonella enterica serovar Choleraesuis, highly invasive and resistant zoonotic pathogen.";
Nucleic Acids Res. 33:1690-1698(2005).
BMEL; ABOIT220; AAX67812.1; -; Genomic_DNA.
InterPro; IPR004611; LER.
PRINTS; PR00019; LEURICHRPT.
                                                                                                                                   Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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Pred. No. 12;
2; Mismatches 4; Indels
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SEQUENCE 282 AA; 31862 MW; 975753A4590FEE62 CRC64;
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SEQUENCE 282 AA; 31876 MW; BAE188CF20EABB27 CRC64;
            10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein.
OrderedLocusNames=SPA3856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                          STRAIN=SC-B67;
PubMed=15781495; DOI=10.1093/nar/gki297;
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Pred. No.
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                                                                           Putative cytoplasmic protein.
OrderedLocusNames=SC3906;
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263 EALEPDDYDGDIYMN 277
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PRINTS; PR00019; LEURICHRPT.
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QSPKD6;
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Matches 9; Conservative
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Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                    Salmonella choleraesuis.
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RESULT 13
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Matches
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The content of the conten
                      McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
1140 of Kluyveromyces lactis.
OrderedLocueNames=KLLA0B035869;
Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
                                                                                                                                                                                                                                                                                                                                                                     Complete proteome; Repeat.
SEQUENCE 282 AA; 31896 MW; 192C4AE31679D2C6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 734 AA.
                                                                                                                                                                                                          LT2.";
Nature 413:852-856(2001).
EMBL; AE008887; AALZ2854.1; -; Genomic_DNA.
EMBL; PRO 1 PRR01611; LRR.
PRINTS; PR00019; LEURICHRPT.
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InterPro; IPR000061; Pkinase C.
InterPro; IPR00019; Prot kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PP00168; C2; 1.
Pfam; PP00168; Pkinase; 1.
Pfam; PP00169; Pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
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Best Local Similarity 60.0%,
Local 9; Conservative
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QECWJS;
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SMART; SM00239; C2; 1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582; Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B., Rapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A., Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T., Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D., Overbeek R., Kyrpides N.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of Bacillus cereus and comparative analysis with Bacillus anthracis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                              58.2%; Score 46; DB 2; Length 734; 72.7%; Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Length 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria, Firmicutes, Bacillales, Bacillaceae; Bacillus,
                                                                                                                                                                                                              734 AA; 82341 MW; DB9A39CBA2E2B888 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 423:87-91(2003).

EMBL, AE017007; AAP09904.1; -; Genomic DNA.

Complete protecome; Hypothetical protein.

SEQUENCE 94 AA, 11075 NW; 36130065840543B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-070-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
Ordered.cousNames=BC2956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Ig kappa chain V-III region MOPC 70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
SMART; SM00220; S_TKC; 1.
SMART; SM00133; S_TK_X; 1.
SMART; SM00219; TYRKC; 1.
PROSITE; PS50004; C2_DOMAIN_2; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00118; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN SEQUENCE.
MEDLINE=67056897; PubMed=4162931;
Gray W.R., Dreyer W.J., Hood L.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Muroidea; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
10-MAY-2005 (Rel. 47, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QBIC28_BACCR PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 72.7
                                                                                                                                                                                                                                                                                                                 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                    714 SVDYDGDHHMD 724
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                                                                                                                                                                                                                                                                                                                                                                    5 SVDYDGDSYMN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 SVDYDGQLYIN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus cereus group.
NCBI_TaxID=226900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 SVDYDGDSYMN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                 Complete proteome.
SEQUENCE 734 AA;
                                                                                                                                                                                                                                                                                 Local Similarity
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P01656;
                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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CONTRACTOR CONTRACTOR

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Sabehi G., Loy A., Jung K.H., Partha R., Spudich J.L., Isaacson T., Hirschberg J., Wagner M., Beja O.; "New Insights into Metabolic Properties of Marine Bacteria Encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]

VOLEOTIDE SEQUENCE.

PubMed=15305915; DOI=10.1111/j.1462-2920.2004.00676.x;
Sabehi G., Beja O., Suzuki M.T., Preston C.M., DeLong E.F.;
"Different SAR86 subgroups harbour divergent proteorhodopsins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORFNames=Red20E09_24;
uncultured marine gamma proteobacterium EBAC20E09.
Bacteria; Proteobacteria; Gammaproteobacteria; SAR86 cluster;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLOS Biol. 3:e273-e273(2005).

EMBL; DQ077553; AAY82601.1; -; Genomic_DNA.

InterPro; IPR011757; MltB.

TIGRPAMS; TIGR02282; MltB.

SEQUENCE 294 AA: 333961 NW; CE4E2219AC008176 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              296 AA; 34268 MW; F807CDF4AB869BBD CRC64;
                                                                                                                                                                                                                      13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2006 (TremBLrel. 31, Last annotation update)
10-SEP-2006 (TremBLrel. 31, Last annotation update)
10-SEP-2006 (TremBLrel.)
13-SEP-2005 (TremBlrel.)
13-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Predicted membrane-bound lytic transglycosylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 2;
Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 2;
Pred. No. 57;
                                                                                                                                                       294 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Environ. Microbiol. 6:903-910(2004).
EMBL; AY552545; AAS73027.1; -; Genomic_DNA.
InterPro; IPR011757; MltB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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SEQUENCE 296 AA: 34268 MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S5.7%;
Best Local Similarity 54.5%;
Matches 6; Conservative '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.5%;
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Q9NJD9 ONCVO PRELIMINARY;
Q9NJD9;
01-0CT-2000 (TrEMBLrel. 15,
01-0CT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QGQ940 9GAMM PRELIMINARY;
QGQ940;
                                                                                                                                                    Q4PKA4 9BACT PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ::||||| |::
190 AIDYDGDGYID 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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192 AIDYDGDGYVD 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S SVDYDGDSYMN 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=332273;
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9
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                                                                                                                  9BACT
                                                                                                                                                                                         Q4PKA4;
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29NJD9 ONCY
1D Q9NJD9
AC Q9NJD9
DT 01-0CT
DT 01-0CT
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Matches
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                                                                                                                                                                          This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR007110; Ig-11ke.
InterPro; IPR03596; Ig-v.
SWART; SM0406; IGv; 1.
PR051TE; PS50835; IG LIKE; 1.
Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
Mechanism of antibody synthesis: size differences between mouse kappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales,
Sphingomonadaceae, Erythrobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-HTCC2594;
Glovannoni S.J., Cho J.-C., Ferriera S., Johnson J., Kravitz S.,
Halpern A., Remington K., Beeson K., Tran B., Rogers Y.-H.,
Friedman R., Venter J.C.;
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
-:-CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complementarity-determining-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complementarity-determining-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45; DB 1; Length 111; Pred. No. 13;
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EMBL; AAGG01000001; EAL76791.1; -; Genomic_DNA.
SEQUENCE 652 AA; 70199 MW; BBDB32736EE382C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11904 MW; 4FE7ABC9DF0FC125 CRC64;
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Last annotation update)
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Pred. No. 94;
3; Mismatches
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13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
Putative sulfatase.
ORFNames=ELI0597;
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24 RASESVDNSGISFMN 38
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Q4TRC9;
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221 AAQATDFDGDGY 232
                                                                  Science 155:465-467(1967)
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nes 9; Conservative
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Matches 7; Conservative
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SMR; P01656; 1-111.
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"Complete genome sequence of the genetically tractable hydrogenotrophic methanogen Methanococcus maripaludis.";

"Dadcreriol. 186:6956-6969(2004).

"Dadcreriol. 186:6956-6969(2004).

"EMBL, BX55721; CAF30580.1; -; Genomic_DNA.

GO, GO:0005524; F.ATP binding; IEA.

GO, GO:0008094; F.DNA binding; IEA.

R GO; GO:0008094; F.DNA dependent ATPase activity; IEA.

R GO; GO:0008094; F.DNA replication initiation; IEA.
                                                                                                                                                                                           MEDLINE=20278137; PubMed=10816503;

X DOI=10.1128/IA1.68.6.3491-3501.2000;
Lizotte-Waniewski M., Tawe W., Guiliano D.B., Lu W., Liu J.,
Lizotte-Waniewski M., Tawe W., Guiliano D.B., Lu W., Liu J.,
Lizotte-Waniewski M., Tawe W., Guiliano D.B., Lu W., Liu J.,
Millams S.A., Lustigman S.

"Identification of potential vaccine and drug target candidates by
"I rexpressed sequence teg analysis and immunoscreening of Onchocerca
volvulus larval cDNA libraries ",
Infect. Immun. 68:3491-3501(2000).

IR EMBL; AFISSTO, ARF64251.1; -; mRNA.
GO; GO:0005509; P:calcium ion binding; IBA.
InterPro; IPR001992; EF-Hand_type.
R InterPro; IPR011992; EF-Hand_type.
R PR0071E; PS000036; EFhind Ca_bd.
PRMRT; SM00054; EFh; 10.

R PR057IE; PS00018; EF_HAND; UNKNOWN_7.
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                                                                              Bukaryota, Metazoa, Nematoda, Chromadorea, Spirurida, Filarioidea,
Onchocercidae, Onchocerca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 2; Length 542;
Pred. No. 1.1e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             542 AA; 61270 MW; 94E3D57FB72D805B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Calcium-binding protein CBP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MCM family related protein.
OrderedLocusNames=MMP1024;
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ProDom; PD001041; MCM; 1.
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QELYG7;
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                                                            Onchocerca volvulus.
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                                                                                                                               NCBI_TaxID=6282;
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RA WOOD V., GWilliam R., Rajandream M.A., Lyne M.H., Lyne R., Stewart A., Wood V., GWilliam R., Rajandream M.A., Lyne M.H., Lyne R., Stewart A., Brouk W. G., Peat N., Hayles J., Baker S.G., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Goble A., Hamilin N., Harris D.E., Hiddled T., Fraser A., Mandlin N., Harris D.E., Hiddled J., Jagels K., James K.D., Jones L., Jones M., Chorle S., McDonald S., McLean J., Mooney P., Moule S., Mungall K.L., Murphy L.D., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Seeger K., Sharp S., Riment S., Staunders D., Seeger K., Sharp S., Stevens K., Stamond M.N., Squares R., Squares S., Stevens K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J.R., Volckaert G., Aert R., Robben J., Grymonprez B., Woodward J.R., Volckaert G., Aert R., Robben J., Grymonprez B., Gobel C., Fuchs M., Duesterhoeft A., Fritzc C., Holzer E., Woetl D., Galien E., Dreano S., Gloux S., Lehaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Daga R.R., Cruzado L., Jimmenez J., Sanchez M., Galzon A., Thode G., Barkli D., Moren S., Armstrong J., Forsburg S.L., Namburg R.A. Bonito J., Sanchez M., Borsty D., Barrell B.G., Nurse P., Nambure 415:871-880 (2002)

RA Daga R.R., Cruzado L., Jimmerz J., Sanchez M., Detashkin J., Nambure 415:871-880 (2002)

RA Daga R.R., Cruzado L., Jimmerz J., Sanchez M., Detashkin J., Nambure 415:871-880 (2002)

RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Nather S.M., Nather Bennes sequence of Schizosaccharomyces pombe.";

Ra Raylor M. Ras a role in regulating DNA replication complexes Acts C. -- Funcrithan Loranton M. Paulses of mitosis.
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"mcll+, the Schizosaccharomyces pombe homologue of CTF4, is important for chromosome replication, cohesion, and segregation.";
Bukaryot. Cell 1:758-773(2002).
                                                                                                                                                                                                                     Gaps
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MEDLINE-22343090; PubMed=12455694; DOI=10.1128/EC.1.5.758-773.2002;
                                                                                                                                                                                                                 ö
                                                                                                                      Length 710;
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Complete proteome.
SEQUENCE 710 AA; 80486 MW; 6BA543F5C2DBDF6D CRC64;
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Schizosaccharonyces pombe (Fission yeast).
Bukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaes;
                                                                                                                 55.7%; Score 44; DB 2; L
40.0%; Pred. No. 1.5e+02;
tive 5; Mismatches 4;
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10-OCT-2003 (Rel. 42, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
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-!- SIMILARITY: Contains 6 WD repeats.
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NCBI_TaxID=4896;
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use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lutzelschwab C., Pejler G., Aveskogh M., Hellman L., Resectory granule proteases in rat mast cells. Cloning of 10 different serine proteases and a carboxypeptidase A from various mast cell populations.";
J. Exp. Med. 1851.13-29(1997).

EMBL; U67913; AA448266.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0030195; P:negative regulation of blood coagulation; IEA.
GO; GO:0006508; P:procteolysis and peptidolysis; IEA.
InterPro; IPR001254; Peptidase_S1_S6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                          SMART; SM00320; WD40; 6.
PROSITE; PS00678; WD REPEATS 1; PALSE_NEG.
PROSITE; PS50082; WD_REPEATS 2; 1.
PROSITE; PS50294; WD_REPEATS RECTON; 1.
Complete proteome; DNA replication; Nuclear protein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97149430; PubMed=8996238; DOI=10.1084/jem.185.1.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.7%; Score 44; DB 1; Length 815; 80.0%; Pred. No. 1.8e+02;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                               EMBL, ALS90605; CAC36919.1; -; Genomic_DNA.
GeneDB_Spombe; SPAPBIE7.02c; -
GO; GO:000606; P:0NA replication; TAS.
GO; GO:0007062; P:sister chromatid cohesion;
GO; GO:000723; P:telomere maintenance; IMP.
InterPro; IPR001680; WD40.
Emm; PPF00400; WD40; 6.
SMART; SM00320; WD40; 6.
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Name=Mcpt10; Synonyms=RMCP-10;
Rattus norvegicus (Rat).
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PROSITE; PS50240; TRYPSIN DOM; 1.
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P97596 RAT
ID P97596 RAT PRELIMINARY;
AC P97596;
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Length 137;

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54.4%; Score 43;

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MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;

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Rosler C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,

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Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mobbries D.,

Manner B. McMiller B., McIntosh T.C., McLeod M.P., Mobbries D.,

Manner B. McMiller B., McIntosh T.C., McLeod M.P., Mobbries D.,

Manner B. McMiller B., McMiller B
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"The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carlson J.W., Halpern A.,
   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hoxapoda, Insecta, Pterygota, Neoptera, Endopteryota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
Indels
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Last annotation update)
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Mismatches
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                                                                                                             29 KAKPHENYDGDSHFN 43
                                                                                                                                                                                                                                                         Q9W2LO DROME PRELIMINARY;
Q9W2LO;
                                                      1 KASQSVDYDGDSYMN
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DT 01-NOV-1997 (
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                                                                                   MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
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                                                                                                                                                                                                                                                                         MEDLINE=22426069; PubMed=12537572;
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                                                                                                                                                                                   "The transposable elements of the Drosophila melanogaster euchromating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (Tremble 13, Last annotate)
13-SEP-2005 (Tremble 13, Last annotate)
13-SEP-2005 (Tremble 13, Nepterygii, Teleostei, Suteleostei, Neoteleostei, Acanthomorpha; Acanthomorpha; Acanthomorpha; Percomorpha; Tetraodontiformes;
13-SEP-2005 (TrEMBLrel. 31, Percomorpha; Tetraodontiformes;
14-TaxID=99883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith
Yu C., Rubin G.;
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
                                                                                                                                                                                                            a genomics perspective.";
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melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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56 KATDSVDYPGEAHL 69
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Q4SMD4;
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Best Local Similarity 50.0
Matches 7; Conservative
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Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
Ratuad C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
Rellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M.,
Lindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
T. the early vertebrate proto-karyotype.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genoscope, Whitehead Institute Centre for Genome Research;
Submitted (FBS-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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Pred. No. 1.7e+02;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match
Local Similarity 53.3%; Pred. No. 1.1e+02;
Less 8; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Wisconsin 38;
Dash S., Lu Y., Harrington H.M.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, US6991; AAB37246.1; -; mRNA.
PIR; T03793; T03793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAAE01014553, CAF98198.1; -; Genomic DNA.
NCE 380 AA; 41957 MW; C3E19B5FADB6A673 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                551 AA; 61598 MW; 813879E25125C374 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAY-1997 (TrEMBLrel. 03, Created)
01-WAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 551 AA
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(Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nicotiana tabacum (Common tobacco).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KASQSVDYDGDSYMN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Calmodulin-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :| |:||| |::|
292 NOVVEYDGKSFLN 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P93370 TOBAC PRELIMINARY, P93370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 SOSVDYDGDSYMN 15
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 431:946-957(2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary data.
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CONTRACTOR OF THE PARTY OF THE

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Attaubberg R.L., Feingold E.A., Grouse L.H., Derge d.G.,

Straubberg R.L., Feingold E.A., Grouse L.H., Derge d.G.,

Altachul S.P., Zeeberg B. Buetow K.H., Schemen C.M., Schuler G.D.,

Altachul S.P., Zeeberg B. Buetow K.H., Schemen C.M., Schuler G.D.,

Hopkins R.F., Jordan H., Moore T., Mas J.L., Wang J., Haileh F.,

Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., Morley K.C., Hale S., Garcinci P., Prange C.,

Richards S., Worley K.C., Hale S., Garcinci P., Prange C.,

Richards S., Worley K.C., Hale S., Garcinci P., Prange C.,

Richards S., Worley W., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rachiguez A.C., Grimwood J., Schwichenko Y., Boulfard G.G.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Broneration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                         MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS0041; KINESIN MOTOR DOMAIN1; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SEQUENCE 686 AA; 77854 MW; 20997A76672471D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 686;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Embryo;
Klein S., Strausberg R.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC057698; AAH57698.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO:0005874; Cimicrotubule; IEA.
GO:0005875; Cimicrotubule associated complex; IEA.
GO:0005524; F:ATP binding; IEA.
GO:0005777; Fimicrotubule motor activity; IEA.
GO:0007018; P:microtubule-based movement; IEA.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43; DB 2; I
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1841 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001752; kinesin_motor.
Pfam; PP00225; kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00129; KISC; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          '5 ARATH
Q7XZF5 ARATH PRELIMINARY;
Q7XZF5;
                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   629 TEEVDYDADSY 639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q6PF78; 175-535.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Embryo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RST1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SIMILARITY: Belongs to the kinesin-like protein family. MCAK/KIF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                     Walczak C.E., Mitchison T.J., Desai A.;
"XKGNI: a Xenopus Kinesin-related protein that regulates microtubule
dynamics during mitchic spindle assembly.";
Cell 84:37-47(1996).
                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96140638; PubMed=8548824; DOI=10.1016/S0092-8674(00)80991-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 682;
13-SEP-2005 (Rel. 48, Last annotation update)
Kinesin-like protein KIF2 (Kinesin-related protein XKIF2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43; DB 1; Lengt... pred. No. 2.2e+02;
                                                                                                                                                                                                                                                        Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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InterPro; PR001752; kinesin_motor.
Pfam; PF00225; Kinesin; 1.
BRINTS; PR00139; KISC; 1.
PROSITE; PS00411; KINESINIMOTOR DOMAINI; 1.
PROSITE; PS0067; KINESIN MOTOR DOMAINI; 1.
ATP-binding; Coiled coil; Microtubule; Motor protein; Nucleotide-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (By similarity). Globular (Potential). Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 subfamily.
-!- SIMILARITY: Contains 1 kinesin-motor domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kinesin-motor.
                                                                                                                                                                                          NUCLEOTIDE SEQUENCE, AND SEQUENCE REVISION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U36486; AAC59744.2; ALT_INIT; mRNA.
                                                             Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE OF 124-682.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77414 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KESCL.

QGPF78 XENLA
TD QGPF78 XENLA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          625 TEEVDÝDADŠÝ 635
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Name=kif2-A-prov;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        543 (682 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P33173; 115S
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                                                                                                                                                    NCBI_TaxID=8355;
                                                                                                                                                                                                                 TISSUE=Ovary;
                                                                                                                                                                                                                                        Walczak C.E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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BIND DOMAIN REGION COILED

RESULT 26

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Gaps

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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                    PROTEIN SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20277480; PubMed=10819329;
Sato S., Makamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;
"Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequer
features of the regions of 4,504,864 bp covered by sixty Pl and TAC
                                                                                                                                                                                                                                                                                                                                       01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 16, Last sequence update)
01-0RA-2004 (TrEMBLrel. 26, Last amotation update)
Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone: MGF10.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Subraryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta, Spermatophyta; Magnoliophyta, eudicotyledons; core eudicotyledons; cosids: Il Brassicales; Brassicaceae; Arabidopsis.
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Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AB018114; BAB02691.1; -; Genomic_DNA.
InterPro; IPR001395; Aldo/ket_red.
InterPro; IPR000276; GPCR Rhodgpsn.
PROSITE; PS00037; GPRR RDUGTASE 3; UNKNOWN 1.
PROSITE; PS00237; GPROTEIÑ RECEP FI_1; UNKNOWN_1.
SEQUENCE 1868 AA; 206711 MW; 0799ADC38CCOC5F0 CRC64;
                                                                                                                                                                    54.4%; Score 43; DB 2; Length 1841; 60.0%; Pred. No. 6.5e+02; Live 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.4%; Score 43; DB 2; Length 1868; 60.0%; Pred. No. 6.6e+02; ive 1; Mismatches 5; Indels
                                               Chen X., Goodwin S.M., Liu X., Jenks M.A.;
Submitred (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AX307371; AAP74222.1. mRNA.
InterPro; IPR001395; Aldo/ket red.
InterPro; IPR000276; GPCR Rhodpsn.
PROSITE; PS00063; ALDOKETÖ REDUCTASE 3; UNKNOWN I.
PROSITE; PS00279; G PROTEIN RECEP F1 1; UNKNOWN I.
SEQUENCE 1841 AA; 203599 WW; DAAD558B64BEA1ZF CRC64;
eurosids II; Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Last sequence update) 10-MAY-2005 (Rel. 47, Last annotation update) Ig kappa chain V-III region PC 2880/PC 1229. Mus musculus (Mouse).
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                                                                                                                                                                                                                                                 1047 EASASSDIDSDSYRN 1061
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                                                                                                                                                                                                                                                                                                                 Q\( \overline{\text{Q}}\) LVX3 ARATH PRELIMINARY;
Q\( \overline{\text{Q}}\) CYX3;
                                                                                                                                                                                               9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clones.";
DNA Res. 7:131-135(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 60.0
nes 9; Conservative
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                                      NUCLEOTIDE SEQUENCE
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Best Local Similarity
Matches 9; Conserv
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          NCBI_TaxID=3702;
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P01654;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi;
Muroidea; Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                              Nature 276:785-790(1978).
-!- MISCELLANEOUS: The PC 2880 and PC 1229 sequences are identical.
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Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                   Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
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InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P01655;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
IG kappa chain V-III region PC 7132.
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P01665; 1QNZ.
SMR; P01654; 1-111.
Ensembl; ENSMUSG0000053225; Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Framework-1
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                                                                                                                                         PubMed=103003;
Muroidea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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24 RASESVDNYGISFMN 38
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                                                                                                                                     MEDLINE=79073152;
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RZ TRAIN=NCC 2705;

RX MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.212527599;

RX Schell M.A., Karmitzantzou M., Snel B., Vilanova D., Berger B.,

RA Schell M.A., Karmitzantzou M., Snel B., Vilanova D., Berger B.,

RA Pridmore R.D., Arigoni F.;

RT The genome sequence of Bifidobacterium longum reflects its adaptation

RT The genome sequence of Bifidobacterium longum reflects its adaptation

RT The Genome sequence of Bifidobacterium longum reflects its adaptation

RT The Genome sequence of Bifidobacterium longum reflects its adaptation

RT The Genome sequence of Bifidobacterium longum reflects its adaptation

RD Co. Natl. Acad. Sci. U.S.A. 99:14422-14427 (2002).

CC -!- SUBUNIT: Homodiner (By similarity).

R EMBL; AROH4704; F:magnesium ion binding; IEA.

GO; GO:0001676; F:magnesium ion binding; IEA.

GO; GO:0001676; F:magnesium ion binding; IEA.

GO; GO:0004310; P:purine salvage; IEA.

DR GO; GO:004310; P:purine salvage; IEA.

BR InterPro; IPR000836; PRRransferase.

R InterPro; IPR000836; PRRransferase.

R InterPro; IPR000836; PRRransferase.

R InterPro; IPR000895; PRP Lanns.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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                         Gaps
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Bifidobacteriaceae, Bifidobacterium.
NCBI_TaxID=216816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome; Glycosyltransferase; Magnesium; Transferase SEQUENCE 193 AA; 20769 MW; 1480E1D885AF6B75 CRC64;
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                         Indels
                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Xanthine phosphoribosyltransferase.
Name-xpt; OrderedLocusNames=BL0891;
Bifidobacterium longum.
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Last annotation update)
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Pred. No. 78;
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                                                                                                                                                                                                             193 AA
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                            Mismatches
      Pred. No.
                                                                                                                                                                                                             PRT;
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TIGRFAMS; TIGR01744; XPRTase; 1
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  61.5%;
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PubMed=11819679;
Cui D.X., Zeng G.Y., Wang F
Yan X.J., Hou Y., Su C.Z.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q925S1 MOUSE PRELIMINARY;
Q925S1;
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36 ASQPIQYNFDSYM 48
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Best Local Similarity 53.0
7; Conservative
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81 KKAQSINLDGDQY 93
                                                                2 ASQSVDYDGDSYM 14
                                                                                                                                                                                                             QBGSW1_BIFLO PRELIMINARY;
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                       8; Conservative
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Best Local Similarity
Matches 8; Conserv
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MEDLINE=21179187; PubMed=11094061; DOI=10.1074/jbc.M010244200;
Perez-Martines X., Antaramian A., Vazquez-Acevedo M., Funes S.,
Tolkunova B., d'Alayer J., Claros M.G., Davidson E., King M.P.,
Gonzalez-Halphen D.;
                                                                                                                                                                                                                              Framework-1.
Complementarity-determining-1.
Framework-2.
Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                               Complementarity-determining-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Match 53.2%; Score 42; DB 1; Length 112; Local Similarity 60.0%; Pred. No. 43; les 9; Conservative 3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Subunit II of cytochrome c oxidase in Chlamydomonad algheterodimer encoded by two independent nuclear genes."; J. Biol. Chem. 276:11309(2001).
EMBL; AF30542; AAK32116.1; -; Genomic_DNA.
EMBL; AF305079; AAK30366.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                     5F0DD25EE20BE611 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polytomella sp. Pringsheim 198.80.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
Chlamydomonadales; Chlamydomonadaceae; Polytomella.
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GO; GO:0005507; F:copper ion binding; IEA.
GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:006118; F:electron transport; IEA.
InterPro; IPR001505; Copper_CuA.
InterPro; IPR0012429; Cyt_c_ox_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Cytochrome c oxidase subunit II (EC 1.9.3.1).
                                                                             Ensembl; ENSMUSGG0000053225; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SSA06066; IGv; II-v.
PROSITE; PSS0835; IG LIKE; I.
Direct protein sequencing; Immunoglobulin domain;
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                                                                                                                                                                                                                                                                                                                  Framework-3
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01-JUN-2001 (TrEMBLrel. 17, Last seq
01-FEB-2005 (TrEMBLrel. 29, Last ann
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PRINTS; PR01166; CYCXIDASEII.
ProDom; PD000131; COPPEr_CUA; 1.
PROSITE; PS00078; COX2; 1.
PROSITE; PS0857; COX2_CUA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                        12054 MW;
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24 RASESVDNYGISFMN 38
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                                         HSSP; P01665; 1QNZ.
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SEQUENCE
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Q9AQY5_9CF
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                                                                                          Curborance.

A Cui D., Zeng G., Yan X., Li X., Su C.;

A Cui D., Zeng G., Yan X., Li X., Su C.;

ATRAIN=BALB/C;

RT "Cloning of mouse genes related to repairing of intestinal epithelium of the irradiated mice by treatment with the intestinal RNA of mice of RT the same strain.";

RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).

RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).

BR EMBL, ARZ40168; AAX43733.1; -; mRNA.

BR ENSembl; ENSWUSG0000058040; Mus musculus.

BR InterPro; IPR003596; Ig_V.

BR SMART; SM0406; IGV; I.

BR SMART; SM0406; IGV; I.

BR SMART; SM0406; IG LIKE; I.

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"Mechanism of exogenous nucleic acids and their precursors improving the repair of intestinal epithelium after gamma-irradiation in mice."; World J. Gastroenterol. 6:709-717(2000).
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Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
Hall M., Florens L., Janssen C.S., Pain A., Churcher C.,
James K., Rutherford K., Harris B., Harris D., Churcher C.,
Quail M.A., Ormond D., Doggett J., Truenan H.E., Mendoza J.,
Bidwell S.L., Rajandream M.A., Carucci D.J, Yates J.R., Kafatos F.C.,
Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
A comprehensive survey of the Plasmodium life cycle by genomic,
transcriptomic, and proteomic analyses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5821;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              53.2%; Score 42; DB 2; Length 218; 60.0%; Pred. No. 89;
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SEQUENCE 223 AA; 26408 MW; 6E5A0316FDE1F4E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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159 RASESVDNIGISFMN 173
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Best Local Similarity 60.0v
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Q4z6L2;
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Q728X5 DESVH PRELIMINARY;
Q728X5;
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ORFNames=PB000331.00.0;
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                                                                                   NUCLEOTIDE SEQUENCE
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"Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis.";

Nuclaic Acids Res. 2814317-4331(2000).

-I. FUNCTION: Site-specific tyrosine recombinase, which acts by catalyzing the cutting and rejoining of the recombining DNA molecules. The xerC-xerD complex is essential to convert dimers of the bacterial chromosome into monomers to permit their segregation at cell division. It also contributes to the segregational stability of plasmids (By similarity).

-I. SUBUNIT: Forms a cyclic heterotetrameric complex composed of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Publication of the property of
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                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio.
                                                                                                                                                                                                                                                   Name=pstS; OrderedLocusNames=DVU2477;
Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
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BEDLINES-20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
Takami H., NakaBone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                          05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Phosphate ABC transporter, periplasmic phosphate-binding protein
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Bacillus halodurans.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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Pred. No. 1.1e+02;
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10-OCT-2003 (Rel. 42, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0065215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR011862; PtsS. 2.
InterPro; IPR006659; SBP bac 1.
Pfam; PF01547; SBP bac 1; 1.
TIGRPAMS; TIGR02135; ptsS. 2; 1.
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05-JUL-2004 (TrEMBLrel. 27, Created)
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190 KNSKAISYDGIGYVN 204
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SEQUENCE 270 AA;
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Horikoshi
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STRAIN=ATCC 43049;
PubMed=1552087; DOD=10.1101/gr.2700304;
Baliga N.S., Bonneau R., Facclotti M.T., Pan M., Glusman G.,
Butlech E.W., Shannon P., Chiu Y., Weng R.S., Gan R.R., Hung P.,
Date S.V., Marcotte B., Hood L., Ng W.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                               Olsen G.J., Sogin M.L.;
"Draft sequence of the Giardia lamblia genome.";
submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                        Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
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                                                                                                                                                                                                  GLP 177 18980 17217.
Giardia lamblīa ATCC 50803.
Bukaryota, Diplomonadida, Hexamitidae; Giardiinae; Giardia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 53.2%; Score 42; DB 2; Length 587 Local Similarity 58.3%; Pred. No. 2.7e+02; es 7; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          587 AA; 66458 MW; A3CSFC5DEF358A09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome, Hypothetical protein.
SEQUENCE 653 AA, 74990 MW, 772A3303B13EC236 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haloarcula marismortui (Halobacterium marismortui).
Archaea, Buryarchaeota, Halobacteria, Halobacteriales,
                                                                                                                01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-2005 (TrEMBLrel. 29, Last sequence update) 01-FEB-2005 (TrEMBLrel. 29, Last annotation update) Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary data.

EMBL, AACB0100072; EAA19336.1; -; Genomic_DNA.
GO; GO:0005509; F:calcium ion binding; IEA.
INCENTO; IPR011992; EF-Hand_type.
InterPro; IPR002048; EF_Hand_Ca_bd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 2;
Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  587 AA
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EMB1. AXS96297, AAV47081.1; -; Genomic_DNA.
GQ0; GO:005856; C:Cytoskeleton; IEA.
InterPro; IPR002017; Spectrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00036; efhand; I. - - PROSITE; PS00018; EF_HAND; UNKNOWN_1.
                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OrderedLocusNames=rrnAC2250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Halobacteriaceae; Haloarcula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-2005 (TrEMBLrel. 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KASQSVDYDGDSYMN 15
                                                             QTQWA9 GIALA PRELIMINARY;
Q7QWA9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QSV072 HALMA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 QSVDYDGDSYMN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 QAVDMDGDGYVS 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
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Best Local Similarity
                                                                                                                                                                                                                                                                                     NCBI TaxID=184922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Calcium; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=2238;
                                                                                                                                                                                                                                                                                                                                                                             STRAIN=WB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches
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COSVO72 HALL
DOSVO73
AC GSV07
AC GSV07
DT 01-FE
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NR PIR; AB958; Abs.

NR PIR; AB958; Abs.

NR HSSP, P21891; 1AOP.

NR HAMAP; NF 01808; -; 1.

NR HOFPRO; IPR004107; Phage_integran.

NR InterPro; IPR011931; Recomb XerC.

NR PFam; PF02899; Phage_integrase.

NR Pfam; PF02899; Phage_integrase.

NR Cell cycle; Cell division; Chromosome partition; Complete proteome; XW DMA integration; DNA recombination; DNA binding.

FT ACT_SITE 174 174 By similarity.

FT ACT_SITE 249 249 By similarity.

FT ACT_SITE 249 249 By similarity.

NAT_SITE 252 252 By similarity.

NAT_SITE 275 275 By similarity.

O-(3'-phospho-DNA)-tyrosine intermediate

'o. similarity.

'o. similarity.

'o. similarity.
                                                                                                                                       This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
molecules of xerC and two molecules of xerD (By similarity). SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: Belongs to the "phage" integrase family. XerC type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J., Smith D., Collins M., Fosker N., Harris D., Oliver K., O'Neil S., Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G., Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.

EMBL, CT005270; CAJ06862.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 53.2%; Score 42; DB 2; Length 465; Best Local Similarity 50.0%; Pred. No. 2.1e+02; Matches 6; Conservative 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 465 AA; 51898 MW; F5429A02B0F03301 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 KKSKSVDLPGDLFLN 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
Hypochetical protein.
ORFNames=LmjF33.3100,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KASQSVDYDGDSYMN 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 53.2
Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :|:||||| :::|
415 KSMDYDGTAFLN 426
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                                                                                     subfamily
                                                                                                                                                                                                                                                          removed
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Gaps

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KV3V_MOUSE
AC POIG 74,
DT CA13V MOUSE
AC 21-JUL-1986
DT 21-JUL-1986
DT 21-JUL-1986
DT 10-MAY-2005
DE IG KADPA cha
OS Mammalia; Eu
OC Marmalia; Eu
OC Marmalia; Eu
OC Marmalia; Eu
OC Margier M.,
RP PROTIEN SEQUE
RR MEDLINE-7907
RA Weigert M.,
RI (1) TextDell
RR MEDLINE-7907
RA Weigert M.,
RR MEDLINE-7907
RA Weigert M.,
RR MEDLINE-7907
RA Weigert M.,
RR CO C This Saise P
CC This Saise P
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CC This Saise P
CC The Buropean
CC Use as long
CC The Buropean
CC Use as long
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sucgang R., Berriman M., Song J., Olsen R., Száranski K., Xu Q., Sucgang R., Berriman M., Song J., Olsen R., Száranski K., Xu Q., Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F., Bankier A.T., Lehmann R., Hamiln N., Davies R., Gaudet P., Fey P., R. Pilcher K., Chen G., Saunders D., Sodergren E., Davis P., Rerbornou A., Nie R., Hall N., Anjard C., Hemphill L., Bason N., Rerborner B., Desany B., Just E., Morio T., Rost R., Churcher C., Ra Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C., Ra Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C., Ra Muzny D., Mourier T., Pain A., Lindesy R., Hauser H., Mangall R., Oliver K., Price C., Quail M.A., A., Chursheged H., Mungall R., Oliver K., Price C., Quail M.A., Churshinara H., Hernandez J., Rabbinowitsch E., Steffen D., Sanders M., Sharp S., Simmonds M., Spiegler S., Tivey A., Sharp S., Simmonds M., Spiegler S., Tivey A., Sharp S., Simmonds M., Spiegler S., Tivey A., Shalsholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R., Hilams C., Dear P.H., Noegel A.A., Barrell B., Kuspa A.; Hre genome of the social amoeba Dictyostelium discoideum."; Nature 0:00-0(2005)
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Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Diplomonadida, Hexamitidae, Giardiinae, Giardia.
NCBI_TaxID=184922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.2%; Score 42; DB 2; Length 724; 40.0%; Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olsen G.J., Sogin M.L.;
"Draft sequence of the Giardia lamblia genome.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 724 AA; 83687 MW; 60DA7BA74CA92273 CRC64;
                                                                                                                                                                                                                                                                                                            Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                        13-5EP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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., AAF101000082; EAL66086.1; -; Genomic_DNA.
                                                                                                                                                  724 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Mismatches
                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:: :||: |||::
215 KSNTEIDYNSDSYVS 229
: | : | : | : | : | | | | : | 85 RAGDAVQFDGDGYLD 99
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Giardia lamblia ATCC 50803.
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Q7RSJS GIALA PRELIMINARY;
Q7RSJS;
                                                                                                                                             Q54SI1 DICDI PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                   Hypothetical protein.
ORFNames=DDB0204766;
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Best Local Similarity
6, Conserve
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=AX4;
                                                                                                                                                                         054SI1
                                                                                          CONTESTS.

ACT ON THE CONTESTS.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinse, Mus.
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                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-79073152; PubMed=103003; Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
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-i- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which preliminary data.

EMBL, AACBO1000004; EAA42647.1; -; Genomic_DNA.

GO; GO:0005198; Fatructural molecule activity; IEA.

InterPro; IPR000535; MSP.
                                                                                                                                                                                                                              Length 4034;
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Complementarity-determining-2.
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Complementarity-determining-3.
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                                                                                                                                                                                                                                                                               4; Indels
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                                                                                                                                                                             4034 AA; 447855 MW; B62BC7FB8EAD4F0F CRC64;
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InterPro; IPR03596; Ig_v.
SMART; SM00406; Ig_v.
IGv. 1.
PROSITE; S08035; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
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                                                                                                                                                                                                                      53.2%; Score 42; DB 2; I
53.3%; Pred. No. 2.3e+03;
ive 3; Mismatches 4;
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21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Ig kappa chain VIII region PC 2154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 AA.
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By similarity
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                                                                                                                                                                                                                                                                                                                                1 KASQSVDYDGDSYMN 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diversity.";
Nature 276:785-790(1978).
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                                                                                                                                                                                                                                                                               8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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53
60
101
108
108
                                                                                                                                                PROSITE; PS50202; MSP;
SEQUENCE 4034 AA; 44
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                                                                                                                                                                                                                                                  Best Local Similarity
Matches 8; Conserv
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SMR; P01674; 1-108
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CONTRACTOR CONTRACTOR

RESULT 43

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                                                                                                                                                                          PROTEIN SEQUENCE (ABPC 22).

MEDLINE=79012520; PubMed=99744;

McKean D.U., Bell M., Potter M.;

"Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";

Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                       PROTEIN SEQUENCE (PC 9245).
MEDIJURE-79073152, PubMed=103003;
Weigert M., Garmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 276:785-790(1978).
-!- MISCELLANEOUS: The ABPC22 and PC9241 sequences are identical
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Complementarity-determining-1.
Framework-2.
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Pred. No. 62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ensembl; ENSMUSGO000060064; Mus musculus.
InterPro; IPR00710; 19-like.
InterPro; IPR003596; 1g-v.
SWART; SW00406; IGv, 1.
PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.
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  kappa chain V-III region ABPC 22/PC 9245
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PROTEIN SEQUENCE.
MEDLINE=79073152; PubMed=103003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
10-MAY-2005 (Rel. 47, Last ann
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24 RASESVDSYGNSFMH 38
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                          Mus musculus (Mouse).
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                                                                                                                             NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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"Rearrangement of genetic information may produce immunoglobulin
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Pramework-4.
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(Rel. 01, Last sequence update)
(Rel. 47, Last annotation update)
                                                                                                                                                                       21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
1g kappa chain V-III region PC 3741/TEPC 111.
                                                                                                     111 AA.
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53.3%; Pred. No. 62;
ive 5; Mismatches
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Ensembl; ENSMUSG0000060064; Mus musculus.
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MEDLINE=79073152; PubMed=103003;
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InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ilarity 53.3%;
Conservative
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24 RASESVDSYGNSFMH 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 276:785-790(1978).
                                                                                               STANDARD;
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                                                                                                                                                                                                                                                    Mus musculus (Mouse)
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les 8; Conserv
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10-MAY-2005 (
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P01660;
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'Mechanisms of antibody diversity: multiple genes encode structurally
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                                                                                              This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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MEDLINE=78215887; PubMed=98179;
Burstein Y., Schechter I.;
"Primary structures of N-terminal extra peptide segments linked to the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McKean D.J., Potter M., Hood L.E.;
Mouse immunoglobulin chains. Pattern of sequence variation among
kappa chains with limited sequence differences.";
Biochemistry 12:760-771(1973).
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 111;
62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12005 MW; 39D87619313453CB CRC64;
                                                                                                                                                                                                                                                                                                                                         1.
Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-VMX-2005 (Rel. 47, Last annotation update)
1G kappa chain V-III region MOPC 63 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 1
Pred. No. 62;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     By similarity.
                                                                                                                                                                                                            HSSP; P01665; 1QNZ.
SMR; P01663; 1-11.
Ensembl; ENSWUSG00000000064; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Framework-2.
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MEDLINE=73140225; PubMed=4691517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       precursors: implications on the of immunoglobulin genes.";
Biochemistry 17:2392-2400(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=79012520; PubMed=99744;
MCKean D.J., Bell M., Potter M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                          SWART; SW00406; IGV; I.P. PROSITE; PS50835; IG_LIKE; Inmunoglobulin V region. REGION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :||:|||
24 RASESVDSYGNSFMH 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                        diversity.";
Nature 276:785-790(1978)
                                                                                                                                                                                                                                                                                                                                                                                                                38
53
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the SMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736 (03)12659-1;

MAKINO K., OSHIMA K., KUrokawa K., Yokoyama K., Uda T., Tagomori K.,

Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae.";

Lancet 361:743-749(2003).

EMBL: BA000003; BACGEI13:1; -; Genomic_DNA.

Complete proteome; Hypothetical protein.

SEQUENCE 156 AA; 17946 MW; D57A8B5CAEFD99IF CRC64;
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Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBI_TaxID=670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complementarity-determining-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 1; Length 131;
Pred. No. 75;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 156;
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                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00406; IGV; 1.—
PROSITE; PSS0835; IG LIKE; 1..
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region; Signal.
related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.9%; Score 41; DB 2; 50.0%; Pred. No. 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                          HSSP; P01665; 1QNZ.
SMR; P01661; 21-131.
Smsembl; RNSWUSG0000060064; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
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01-JUN-2003 (TrEMBLrel. 24, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
Hypothetical protein VPA0770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.9%;
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44 RASESVDSYGNSFMH 58
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Q9J166; Q6PG02; Q8BV71;
11.-SEP-2005 (Rel. 48, Created)
13-SEP-2005 (Rel. 48, Last annotation update)
Diphosphoinositol polyphosphate phosphohydrolase 1 (EC 3.6.1.52)
Diphosphoinositol polyphosphate phosphohydrolase 1 (EC 3.6.1.52)
(DIPP-1) (muDIPP1) (Diadenosine 5',5''-P1,P6-hexaphosphate hydrolase 1) (EC 3.6.1.-) (Nucleoside diphosphate-linked moiety X motif 3)
                                                                                                                                                                                                                     NUCLECTIDE SEQUENCE.
PubMed=14960714; DOI=10.1093/nar/gkh258;
Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
Rasko D.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
Shores K.A., Fouts D.E., Fraser C.M., Read T.D.;
"The genome sequence of Bacillus cercus ATCC 10987 reveals metabolic
adaptations and a large plasmid related to Bacillus anthracis pXO1.";
Nucleic Acids Ree. 32:977-988(2004).
EMBL. ABOINTST; AAS41918.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                     Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sclurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diphosphoinositol polyphosphate signaling through the ERK1/2 pathway.";
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NUCLEOTIDE SEQUENCE [MRNA], TISSUE SPECIFICITY, AND MUTAGENESIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
STRAIN-C57BL/6, and FVB/N; TISSUE-Brain, and Mammary tumor;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=15212765; DOI=10.1016/j.cellsig.2004.02.009;
Chu C., Alapat D., Wen X., Timo K., Burstein D., Lisanti M.,
Shars S., Kohtz D.S.;
"Ectopic expression of murine diphosphoinositol polyphosphate
                                                                                                                                                                                                                                                                                                                                                                              51.9%; Score 41; DB 2; Length 160; 70.0%; Pred. No. 93;
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                          Bacillus cereus (strain ATCC 10987).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
Bacillus cereus group.
                                                                                                                                                                                                                                                                                                                                        Complete proteome; Hypothetical protein.
SEQUENCE 160 AA; 18815 MW; 547CADOCC78F8E93 CRC64;
                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
                                                                               160 AA.
                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 93;
1; Mismatches
                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Nudt3; Synonyms=Dipp, Dippl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphohydrolase 1 attenuates sig
Cell. Signal. 16:1045-1059(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Muridae; Murinae; Mus
                    ASESTQYIGDOFLN 105
12
                                                                                                                                                 OrderedLocusNames=BCE3007;
                                                                             Q73524_BACC1 PRELIMINARY;
Q73524;
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 70.0
Matches 7; Conservative
2 ASQSVDYDGDSYMN
                                                                                                                                                                                                                                                                                                                                                                                                                          6 VDYDGDSYMN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 VDYDĞQLYIN 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                 NCBI TaxID=222523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                               TIGR: BCE3007;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muroidea;
                    92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOUSE
                                                     RESULT 48
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Altending F. F. Czelberg B. Bustrow K.H.; Schaefer C.F. Bint N. K.,
Altending S.F.; Czelberg B. Bustrow K.H.; Schaefer C.F. Bint N. K.
B. Bischen M.; Godzae M. B. Duatdow K.H.; Schaefer C.F. Bint N. K.
B. Bischen M.; Godzae M. B. Bonaido M. F.; Casawant T.L.; Scheer T.E.;
B. Banak S. M. Godzae M. B. Bonaido M. F.; Casawant T.L.; Scheer T.E.;
B. Brownen M. J. Bischir T.B. Tolkyani S. Carrinto J. B. M. Millany B. J.
B. Milland D.K. Warny D.W.; Scherger B. J. M. Cay L.J.; Blubk S. M.
B. Milland D.K. Warny D.W. Soderger B. J. Mack Gibbs R. S., Sanchez A.,
B. Milland D.K. Warny D.W. Soderger B. J. Mack Gibbs R. S.,
Blakesley R.W. Tolkohan J. W. Schern E.D., Dickson M.C.,
Blakesley R.W. Tolkohan J. W. Schern E.D., Dickson M.C.
Blakesley R.W. Tolkohan J. W. Schern E.D., Dickson M.C.
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                      This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are to restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-SEP-2005 (Rel. 48, Created)
13-SEP-2005 (Rel. 48, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Diphosphoinositol polyphosphate phosphohydrolase 1 (EC 3.6.1.52)
Diphosphoinosine 5,','-Pl,P6-hexaphosphate hydrolase 1)
(BC 3.6.1.-) (Nucleoside diphosphate-linked moiety X motif 3) (Nudix
                                                                                                                                                                                                                                                                                                                                                                                                  Important for substrate recognition (By similarity).
Important for substrate recognition (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      E->Q: Loss of enzyme activity, but retains ability to regulate the ERKI/2
                                                                                                   EMBL; AF264064; AAF74761.1; -; mRNA.

R EMBL; BC016534; AAH16534.1; -; mRNA.

EMBL; BC046805; AAH46805.1; -; mRNA.

R EMBL; BC046805; AAH46805.1.; -; mRNA.

R EMBL; BC057331; AAH5731.1; ALT SEQ; mRNA.

R EMBL; AK079658; BAC37717.1; -; mRNA.

EMBL; AK079658; BAC37717.1; -; mRNA.

R MG1; MG1:1928444; Nud42:

R G0; G0:0005622; C:intracellular; ISS.

G0; G0:0019722; P:calcium-mediated signaling; ISS.

G0; G0:001935; P:calcium-mediated signaling; ISS.

G0; G0:0016242; P:intracellular signaling cascade; ISS.

G0; G0:0046907; P:intracellular riansport; ISS.

G0; G0:0046907; P:intracellular riansport; ISS.

R G0; G0:004681; P:regulation of RNA-nucleus export; ISS.

R InterPro; IPR000086; NUDIX_hydrolase.
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PROTEIN SEQUENCE OF 3-17; 20-115 AND 117-121, FUNCTION, ENZYME
ACTIVITY, COFACTOR, ENZYME REGULATION, AND SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

S1.9%; Score 41; DB 1; Length 168;
Best Local Similarity 53.8%; Pred. No. 99;
Matches 7; Conservative 3; Mismatches 3: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH - Mammalian Gene Collection (MGC) project;
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                         Magnesium (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E543BE5CBE520910 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 AA.
                                                                                                                                                                                                                                                                                                                               PROSITE; PS00893; NUDLA; 1.
Hydrolase; Magnesium; Metal-binding.
72 NUDIX box.
                                                                                                                                                                                                                                                                                                                                                                                      Magnesium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1] -
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
it is chimeric at the C-terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           motif 3).
Name=Nudt3; Synonyms=Dipp, Dippl;
                                                                                                                                                                                                                                                                                                        Pfam; PF00293; NUDIX; 1.
PRINTS; PR00502; NUDIXFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 AA; 19030 MW;
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KSNQTRTYDGDGY 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                             removed.
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
               Safrany S.T., Caffrey J.J., Yang X., Bembenek M.E., Moyer M.B., Rabart W.A., Shears S.B.;

Burkhart W.A., Shears S.B.;

A novel context for the 'MutT' module, a guardian of cell integrity,

T a novel context for the 'MutT' module, a guardian of cell integrity,

In a diphosphoinositol polyphosphate phosphohydrolase.";

ENBO J. 17:6599-6607(1998).

-!- FUNCTION: Cleaves a beta-phosphate from the diphosphate groups in

PP-INSPS (diphosphoinositol pentaxisphosphate) and [PP]2-InsP4

(Disdiphosphoinositol tertakisphosphate) and [PP]2-InsP4

(Disdiphosphoinositol tertakisphosphate); suggesting that it may

play a role in signal transduction. InsP6 (inositol

hexakisphophate) is not a substrate. Acts as a negating the

confine ERK1/2 pathway. Also able to catalyzes the hydrolysis of

dinucleoside oligophosphates, with Ap6A and Ap5A being the

preferred substrates. The major reaction products are ADP and D4a

from Ap6A and ADP and APP from Ap5A. Also able to hydrolyze PRPP

C. Catalytic ACTIVITY: Diphosphate + phosphate.

Myo-inositol polyphosphate + phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SUBUNIT: Monomer.
-i- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-i- SIMILARITY: Belongs to the Nudix hydrolase family. DIPP subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct protein sequencing; Hydrolase; Magnesium, Metal-binding.

MOTIF 51 72 NUDIX box.
METAL 66 66 Magnesium (By similarity).

SITE 84 84 Important for substrate recognition (By similarity).

SITE 91 91 Important for substrate recognition (By similarity).
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MEDLINE=99043866; PubMed=9822604; DOI=10.1093/emboj/17.22.6599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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Pred. No. 99;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CÓFACTOR: Magnesíúm.
-!- ENZYME REGULATION: Inhibited by fluoride and InsP6.
-!- BIOPHYSICOCHEMICAL PROPERTIES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6743B325524B634E CRC64;
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InterPro; IPR000086; NUDIX_hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; BC093618; AAH93618.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KM=340 nM for PP-InsP5;
KM=34 nM for [PP]2-InsP4;
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                                                                                                         February 23, 2006, 09:29:34; Search time 77.5385 Seconds (without alignments) 50.999 Million cell updates/sec
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Aay18116 I
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Adr15140 V
Adr28675 M
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Aaw30278 I
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Aay23779 II
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Aay18120 I
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Adr70201 II
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Biocceleration Ltd.
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Copyright (c) 1993 - 2006
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                                                                                  sw model
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ABU5699
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AAX30202
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Gapop 10.0 , Gapext 0.5
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## ALIGNMENTS

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Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived high affinity mAbs - useful in treatment of IL-4-mediated and IgE-mediated allergic conditions.
                                                                                                         Chimeric antibody; humanized antibody; antibody engineering; monoclonal antibody; MAb; interleukin-4; IL-4; allergy; CDR; complementarity determining region.
                                                                                                                                                                                                                                                                                             Sylvester DR;
                   AAR70197 standard; protein; 9 AA
                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                 93US-00117366.
93US-00136783.
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                                                                    (first entry)
                                                                                      MAb 3B9 light chain CDR
                                                           (revised)
                                                                                                                                                                                                                                                                                             Gross MS,
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                                                                                                                                                                       WO9507301-A1
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20-SEP-1995
                                                                                                                                                                                           16-MAR-1995.
                                                                                                                                                                                                                                                                                             Holmes S,
                                      AAR70197;
                                                                                                                                                   Mus sp.
RESULT 1
          AAR70197
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Sequence 9 AA;

from

Spleen cells from mice immunized with human IL-4 were used to prepare hybridomas, which were screened for anti-IL-4 MAb secretion. Only clone

Disclosure, Page 56; 97pp; English.

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3B9 was positive. cDNA clones of the 3B9 light and heavy chains were cloned into pGEM7f+ and transformed into E. coli DH5-alpha. A light chain cDNA clone was sequenced (AAQ83490) that encoded the protein given in AAR70189. 3 CDR8 (AAR70195-97) were identified. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New DNA molecules encoding recombinant antibodies useful for treating IL4-mediated conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a complementarity determining region (CDR) of the light chain variable region of murine interleukin-4 (ILL-4) antibodis 3B9. The specification describes chimeric and humanised ILL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating ILL-4 mediated and Immunoglobulin E-mediated allergic reactions e.g. allergic refinitis, conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host-versus-graff disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess ILL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Light chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin B-mediated allergic reaction; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic astehma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy;
                                                                                                                                                                                 Gaps
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                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             CDR of the light chain variable region of antibody 3B9.
                                                                                                                                           100.0%; Score 50; DB 2;
100.0%; Pred. No. 2e+06;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complementarity determining region
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                                                                                                                                                                                                                                                                                                                                       AAY23774 standard; peptide; 9 AA.
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Best Local Similarity 100.
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an epitope specifically bound by an antibody expressed by a clone such as clone $25, C25, C39, IC6 and clone 1F3, where the antibody binds to and neutralises botulinum neurotoxin type A (BONT)A). Also included are a polypeptide comprising BoNTA neutralising epitope comprising an epitope which is specifically bound by the antibody, where the polypeptide is not a full-length botulinum neurotoxin H of fragment and making an anti-BONTA antibody that neutralises BONTAA by contacting several antibody expressed by any of the nepitope specifically bound by an antibody expressed by any of the novel clones and isolating an antibody that specifically binds to the pitope and isolating an antibody that specifically binds to the copitope). The antibody is useful for neutralising a BONTAA, by contacting botulinum neurotoxin type A with the antibody comprising VH CDR (heavy chain variable region complementarity determining region) and with a second anti-BONTA antibody which comprises a VH CDR, where the second antibody. The antibody that the treatment of pathologies associated with botulinum neurotoxin poisoning, for rapid detection diagnosis of botulism and in the detection and/or rapid cute in indicative of a Clostridium botulinum infection of the organism which is indicative of a Clostridium botulinum infection of the organism chain antibody. The present sequence is a light chain variable region (VL) of a single
                                                                                                                                                                                                   Botulinum neurotoxin type A; BoNT/A; mouse; light chain variable region; scFv; antibody; botulism; antibacterial; single chain antibody; VL; :immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated antibody that specifically binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel antibody that specifically binds and neutralizes botulinum neurotoxin type A useful for neutralizing botulinum neurotoxin and treating botulism.
                                                                                                                                                          BONT/A Hc binding antibody scTv VL region from 1B6 #2
                           ABU56909 standard; protein; 52 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; Page 23; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              98US-00144886
                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marks JD, Amersdorfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MARK/) MARKS J D.
(AMER/) AMERSDORFER P.
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                                                                                                                                                                                                                                                                                                                                     US2002155114-A1.
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                                                                                                                04-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                            31-AUG-1998;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a light chain complementarity determining region (CDR) from an antibody of the invention. The antibody is a chimeric or humanised interleukin-4 (II4) monoclonal antibody for the treatment of immunoglobulin B (IgB) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft versus host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease; complementarity determining region; CDR.
                                                                       Gaps
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                    100.0%; Score 50; DB 2; Length 9; llarity 100.0%; Pred. No. 2e+06; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                Light chain CDR for hIL-4 specific antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atopic ashthma and anaphylactic shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gross MS;
                                                                                                                                                                                                                                                                  AAY18116 standard; peptide; 9 AA
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94WO-US010308.
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Query Match
Best Local Similarity
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N-PSDB; AAX79515.
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995;
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07-SEP-1994;
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                                    100.0%; Score 50; DB 6; Length 52; 100.0%; Pred. No. 0.27;
                                                       0; Indels
                                                       Mismatches
chain antibody (scFv) of the invention
                                                                                                                                           ADR38683 standard; peptide; 107 AA.
                                      100.0%;
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                                                                                     OOSNEDPPT
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ADR38683
ID ADR3
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OOSNEDPPT

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RESULT 4 ABUS6909

ADR38683;

Mus sp.

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DNA molecules encoding recombinant antibodies useful for treating IL4
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                                                                                                                                                                      Light chain variable region of 1g REI.
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                    AAY23781 standard; protein; 111 AA
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94WO-US010308.
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                                                                                                                      (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-OCT-1993;
07-SEP-1994;
                                                                                                                      13-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                      US5928904-A.
                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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                                                                      AAY23781;
                                                                                                                                                                                                                                                                                                                                       Ig REI
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AAY23781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes an isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a specific clone where (I) binds to and neutralises botulinum neurocoxin type A (BONT/A). An isolated antibody expressed by a clone chosen from clone specifically binds to an epitope specifically binds to an epitope (25, 225, 239, 106, 302, 84, 187, huc25, Ari, Ari, Mri(Y), 3-1, 28, 3-10 and ING1, where (I) binds to and neutralises botulinum clone comprising BONT/A neutralising epitope having an epitope that is comprising BONT/A neutralising epitope having an epitope that is comprising BONT/A neutralising epitope having an epitope that is comprising BONT/A neutralising epitope having an epitope that is comprising I); and a composition (III) comprising several anti-confilmum neutrotoxin antibodies, where each antibody is specific for a different epitope of a botulinum neutralisation than the single antibodies shows greater toxin neutralisation than the single antibodies shows greater toxin neutralisation than the single antibodies shows greater toxin neutralisation than the comprising (I); and a kit comprising (I) is useful for neutralising BONT/A antibody and for neutralising a botulinum neutotoxin which is precific for a different epitope of the botulinum neutotoxin which is precific for a different epitope of the botulinum neutotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplue. (I) is useful for diagnosing the botulism correcting pathologies specificity and affinity towards BONT/A. (I) enables rapid detection or diagnosing the botulism. This is the amino acid condensition or antibodies specificity and affinity towards BONT/A. (I) enables rapid detection or diagnosic, it is expecificated with botulism. This is the amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated antibody that neutralizes botulinum neurotoxin type A, useful for diagnosing botulism or for treating pathologies associated with botulinum neurotoxin poisoning.
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                                                                                                                                     antibacterial; antibody; botulinum neurotoxin type A; BONT/A; BONT/A neutralising epitope; anti-botulinum neurotoxin antibody; toxin neutralisation; botulinum neurotoxin poisoning; mouse; light chain variable region; single chain antibody; scFv.
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                                                                                          Mouse light chain variable region scFv segid 85.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID NO 85; 110pp; English.
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01-AUG-2002; 2002US-0400721P.
                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-2003; 2003US-00632706
                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amersdorfer P;
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                              US2004175385-A1.
                                             02-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                09-SEP-2004.
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Marks JD,

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The specification describes chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic asthma, anaphylactic shock, rheumatoid arthxitis, host-versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans. The present sequence represents the light chain variable region of Ig REI, and is used in the course of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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100.0%; Pred. No. 0.57;
ive 0; Mismatches 0; Indels
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ID AAY1
XX AC AAY3
XX II-P
XX DT II-P
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Query Match

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Synthetic.

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The invention comprises anti-protein C inhibitor (PCI) antibody. The anti-PCI antibody of the invention is useful for treating or preventing a disease which develops and/or progresses due to reduced activated protein C (aPC) activity. Such diseases include: sepsis, disseminated intravascular coagulation, and arterial thrombosis. The present amino acid sequence represents a mouse anti-protein C inhibitor antibody.
                                                                                                                                                 New anti-protein C inhibitor (PCI) antibody, inhibiting PCI with respect to activation protein C (apc) activity, and apc production by thrombin/thrombomodulin composite, useful for treating sepsis, arterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes an isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated antibody that neutralizes botulinum neurotoxin type A, useful for diagnosing botulism or for treating pathologies associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibacterial; antibody; botulinum neurotoxin type A; BONT/A; BONT/A neutralising epitope; anti-botulinum neurotoxin antibody; toxin neutralisation; botulinum neurotoxin poisoning; mouse; light chain variable region; single chain antibody; scFv.
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                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 21; 105pp; Japanese
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20-JAN-2003; 2003JP-00011529
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01-AUG-2002; 2002US-0400721P.
                                                                           Yoshino
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                                    (CHUS ) CHUGAI SEIYAKU KK
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                                                                                                                WPI; 2004-593430/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                           Kimura N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QOSNEDPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2004175385-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADR38675;
                                                                         Koga T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the light chain of the humanised 3B9 antibody of the invention. The antibody is a chimeric or humanised interleukin-4 (IL4) monoclonal antibody for the treatment of immunoglobulin B (IgB) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic achima and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft versus host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anti-protein C inhibitor antibody, anti-PCI antibody, activated protein C; aPC; sepsis; disseminated intravascular coagulation; arterial thrombosis; protein C inhibitor; mouse; murine.
              Antibody, interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease.
            mediated disease; s: atopic dermatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant IL4 antibodies useful for tratment of allergic rhinitis, atopic ashthma and anaphylactic shock.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 50; DB 2; Length 111; 100.0%; Pred. No. 0.57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse anti-protein C inhibitor antibody #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               Gross MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Col 69-70; 50pp; English.
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                                                                                                                                                                                                                                                                                                                                                (SMIK ) SMITHKLINE BEECHAM PLC. (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                  93US-00117366.
93US-00136783.
94WO-US010308.
                                                                                                                                                                                                                               95US-00483636.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 111 AA;
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                                                                                                                                                                                                                               07-JUN-1995;
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                                                                                                                                                                                                                                                                                        14-OCT-1993;
07-SEP-1994;
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93

Query Match

Best Loc Matches

ò g ADR15140;

ADR15140 RESULT

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Gaps

N-PSDB; AA030757

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clone where (I) binds to and neutralises botulinum neurotoxin type A (BoNT/A). An isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a clone chosen from clone 525, C25, C39, IC6, 3D12, B4, IP3, huC25, Ari, Ar2, WRI(V), WRI(T), 3-1, 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum neurotoxin type A (BoNT/A). Also described are: a polypeptide (II) comprising BoNT/A neutralising pitope having an epitope that is specifically bound by an antibody expressed by clones as mentioned in (I) producing (I); and a composition (III) comprising several antibodies shows greater toxin neutralisation than the single antibodies in surplus. The following are disclosed: a pharmaceutical composition comprising several models in surplus. The following are disclosed: a pharmaceutical composition comprising (I); and a kit comprising (I). (I) is useful for neutralising specific for a different epitope of the botulinum neurotoxin which involves contacting neurotoxin with (I) is useful for diagnosing the botulism combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. (I) is useful for diagnosing the botulism or for treating pathologies associated with botulinum neurotoxin and the single antibodies in surplus. (I) is useful for diagnosing the botulism or for treating pathologies associated with botulinum neurotoxin condiction or diagnosis of botulism. This is the amino acid sequence of a mouse light chain variable fragment anti-botulinum toxin
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heavy chain; variable region; mouse; monoclonal; hybridoma; AUK64-7;
plasmid; p64-k4; p64-k2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 50; DB 8; Length 112; Best Local Similarity 100.0%; Pred. No. 0.58; Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21. .131
/note= "Mature peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92WO-JP000544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92JP-00032084
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QQSNEDPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 112 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-FEB-1992;
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30-MAR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
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                                                                                                           The sequences given in AAR29008-09 were encoded by plasmids which were used in example to illustrate the production of a human antibody which recognises human interleukin-6 receptor (IL-6R). The antibody comprises light (L) chain and heavy (H) chain variable regions which were derived from a mouse monoclonal antibody produced from the hybridoma AUK64-7 which contained the plasmids p64-K4 and p64-h2. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from
             Reconstituted human antibody to human interleukin-6 receptor - has leanigenicity and contains mouse V-region complementarily determining regions.
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      engineering; monoclonal antibody; MAb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived high affinity mAbs - useful in treatment of IL-4-mediated and IgE-
                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                          100.0%; Score 50; DB 2; Length 131; 100.0%; Pred. No. 0.67; tive 0; Mismatches 0; Indels
                                                                                 Disclosure; Page 124-125; 207pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 71-72; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     AAR70202 standard; protein; 131 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanized antibody 3B9 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sylvester DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
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93US-00136783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       high affinity mAbs - useful i
mediated allergic conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody; antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94WO-US010308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interleukin-4; IL-4; allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
(first entry)
                                                                                                                                                                                                                                                                                        9; Conservative
                                                                                                                                                                                                                                                                                                                                              113 QOSNEDPPT 121
                                                                                                                                                                                                                                                                                                                     1 QOSNEDPPT 9
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N-PSDB; AAQ83520.
                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      correct PN field.)
                                                                                                                                                                                                                                Sequence 131 AA;
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20-SEP-1995
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                                                                                                                                                                                                                                                             Query Match
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Matches
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us-10-723-872-20.rag

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HuM4TS.11; antibody; platelet; beta receptor; PDGF-R beta; inhibition; intimal hyperplasia; vasculature; restenosis; angioplasty; light chain.
                                                                                                                                                                                                                                                                                                                                                                     "Mature protein"
                                                                                                                                                                                                                           Location/Qualifiers
                                                                              AAW30274 standard; protein; 131 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PROT-) PROTEIN DESIGN LABS INC. (BOEF ) BOEHRINGER MANNHEIM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Martin U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 13; Fig 8B; 87pp; English.
                                                                                                                                                                                                                                                                                                                             mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-US004198
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                                                                                                                                                                                                                                                         protein"
24
                                                                                                                                                                                                                                                                                         protein"
25
                                                                                                                                                                                                                                                                                                                                                                                                                          protein"
112. 120
                                                                                                                                               Light chain of HuM4TS.11
                                                                                                                                                                                                                                                                                                                                                            61. .393
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/note= "(
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                 113 QOSNEDPPT 121
   1 QOSNEDPPT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-503114/46.
N-PSDB; AAT90981.
                                                                                                                                                                                                                                     Misc-difference 23
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                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                         07-JUL-1998
                                                                                                                                                                                                     Homo sapiens.
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                                                                                                   AAW30274;
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                                                                                                                                                                                                                                                                                                                                                            Protein
                                                        RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibodies to platelet derived growth factor beta receptor - inhibit PDGF BB-induced proliferation of cells expressing the receptor, used particularly for inhibiting intimal hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the amino acid sequence for the light chain of muM4TS.11, a novel antibody which specifically binds to the platelet derived growth beta receptor (PDGF*R beta). but not within the fifth extracellular 19-like domain, where the antibody inhibits PDGF BB-induced proliferation of a cell expressing the PDGF beta receptor. The antibody can be used in a method of inhibiting intimal hyperplasia in the vasculature of a mammal. The antibodies can be used for the treatment of disorders related to PDGF activity such as disorders involving proliferation of smooth muscle cells, and including restenosis following angioplasty
                                                                                                                                                                                                                       MuM4TS.11; antibody; platelet; beta receptor; PDGF-R beta; inhibition; intimal hyperplasia; vasculature; restenosis; angioplasty; light chain.
                                  Gaps
                                  ;
0
                                                                                                                                                                                                                                                                                                                                              /note= "Complementarity determining region z" 112. .120
/note= "Complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                         "Complementarity determining region 1"
            DB 2; Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

100.0%; Score 50; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 9; Conservative 0; Mismatches 0; Indels
                                 0; Indels
                                                                                                                                                                                                                                                                                                                                 .80
.e= "Complementarity determining
                     0.67;
           ; Score 50; DB
; Pred. No. 0.67
0; Mismatches
                                                                                                                                                                                                                                                                                                   "Mature protein"
                                                                                                                                                                                                                                                                                ocation/Qualifiers
                                                                                                                                AAW30278 standard; protein; 131 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Landolfi NF, Martin U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PROT-) PROTEIN DESIGN LABS INC. (BOEF ) BOEHRINGER MANNHEIM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Fig 7B; 87pp; English.
           100.0%;
ilarity 100.0%;
Conservative 0
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                                                                                                                                                                             (first entry)
                                                                                                                                                                                                  Light chain of MuM4TS.11
                                                                                                                                                                                                                                                                                                               .58
                                                                  112 QQSNEDPPT 120
                                                                                                                                                                                                                                                                                                                          /note=
Query Match
Best Local Similarity
'-hem 9; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-503114/46.
                                                      1 QQSNEDPPT
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                                                                                                                                                                                                                                                                                                              Binding-site
                                                                                                                                                                                                                                                                                                                                                          Binding-site
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                                                                                                                                                                              07-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                09-OCT-1997.
                                                                                                                                                        AAW30278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chang C,
                                                                                                                                                                                                                                                                                         Protein
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Antibodies to platelet derived growth factor beta receptor - inhibit PDGF BB-induced proliferation of cells expressing the receptor, used particularly for inhibiting intimal hyperplassa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Optionally Val at position 62 of the mature
                                                                                                                                                                                                                                                                                       position 25 of the
note= "Optionally Val at position 3 of the mature
                                                                                                                                             'note= "Optionally Leu at position 4 of the mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73. .80
/note= "Complementarity determining region 2"
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/note= "Complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                           "Complementarity determining region 1"
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1 QOSNEDPPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAX79543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 131 AA;
                                                                                                                                                                                                                                                                                                                                                                                               Sylvester DR,
                                                                                                                                                                                                                                                                                           07-JUN-1995;
                                                                                                                                                                                                                                                                                                                  07-SEP-1993;
                                                                                                                                                                                                                                                                                                                              14-OCT-1993;
                                                                                                                                                                                                                                                                                                                                       07-SEP-1994;
                                                                                                                                                                                                                                                 US5914110-A.
                                                                                                                                                                                                                                                                      22-JUN-1999
                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR70189;
                                                                                                  AAY18126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR70189
                                                                  AAY18126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin E-mediated allergic refinities, conjunctivities, atopic dermatities, atopic aethma, anaphylactic shock, rheumatoid arthritis, versus-graft disease and renal disease. They are also useful in the production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New DNA molecules encoding recombinant antibodies useful for treating IL4
                                                                                                                                                                                                                                             Light chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; IImmunoglobulin E-mediated allergic reaction; allergic rhinitis; conjunctivitis; actopic dermatitis; atopic aethma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents the light chain variable region of a humanised murine interleukin-4 (IL-4) antibody 3B9. The specification describes chimeric and humanised IL-4 monoclonal antibodies. The
                                                       Gaps
                                                                                                                                                                                                                          variable region of humanised murine IL-4 antibody 3B9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 50; DB 2; Length 131; llarity 100.0%; Pred. No. 0.67; Conservative 0; Mismatches 0; Indels
                               Length 131;
                              100.0%; Score 50; DB 2; Length 13
100.0%; Pred. No. 0.67;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Col 61-62; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gross MS;
                                                                                                                                                         AAY23779 standard; protein; 131 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                              93US-00117366.
93US-00136783.
94WO-US010308.
                                                                                                                                                                                                                                                                                                                                                                                                           95US-00483632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Holmes SD, Sylvester DR,
                                                                                                                                                                                                    (first entry)
                                                     9; Conservative
                                                                                          113 QQSNEDPPT 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -mediated conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-429500/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 9; Conserv
                               Query Match
Best Local Similarity
Matches 9; Conserv
                                                                             1 QOSNEDPPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 131 AA;
            Sequence 131 AA;
                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                07-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                        14-OCT-1993;
07-SEP-1994;
                                                                                                                                                                                                                         Light chain
                                                                                                                                                                                                    13-SEP-1999
                                                                                                                                                                                                                                                                                                                                                             US5928904-A.
                                                                                                                                                                                                                                                                                                                                                                                    27-JUL-1999,
                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                              AAY23779;
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                                                                                                                                                                                                                                                                                                                                                                                                Antibody, interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the light chain of the humanised 3B9 antibody of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant IL4 antibodies useful for tratment of allergic rhinitis, atopic ashthma and anaphylactic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                            Light chain sequence for humanised 3B9 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Col 59-62; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gross MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR70189 standard, protein, 132 AA.
                                                                                                                                                              AAY18126 standard; protein; 131 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SMIK ) SMITHKLINB BEECHAM PLC. (SMIK ) SMITHKLINB BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-00483636.
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94WO-US010308.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SD,
                                                                                                                                                                                                                                                                                  11-AUG-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 QQSNEDPPT 120
112 QQSNEDPPT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Holmes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QQSNEDPPT 9
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20-SEP-1995
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The present sequence represents the light chain variable region of murine interleukin-4 (IL-4) antibody 3B9. The sequences are used in the production chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin B-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autojummune disease; graft versus host disease.
                                                                                                                                                                                                                                                                                                                                                               New DNA molecules encoding recombinant antibodies useful for treating IL4
chimeric antibody, humanised antibody, IL-4 mediated allergic reaction, Immunoglobulin E-mediated allergic reaction, allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma; anaphylactic shock; rheumatoid arthritis, host-versus-graft disease; renal disease; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 50; DB 2; Length 132;
larity 100.0%; Pred. No. 0.68;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Light chain sequence for murine 3B9 antibody.
                                                                                                                                                                                                                                                                                         Gross MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY18120 standard; protein; 132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Fig 1; 50pp; English.
                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM CORP (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                   93US-00136783.
94WO-US010308.
                                                                                                                                                            95US-00483632
                                                                                                                                                                                       93US-00117366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                         Sylvester DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                              -mediated conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  σ
                                                                                                                                                                                                                                                                                                                     WPI; 1999-429500/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
tes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 QOSNEDPPT
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                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAX85884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 132 AA
                                                                                                                                                                                                   14-OCT-1993;
07-SEP-1994;
                                                                                                                                                          07-JUN-1995;
                                                                                                                                                                                       07-SEP-1993;
                                                                                                   US5928904-A
                                                                                                                               27-JUL-1999
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                                                                                                                                                                                                                                                                                       Holmes SD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                        Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spleen cells from mice immunized with human IL-4 were used to prepare hybridomas, which were screened for anti-IL-4 MAb secretion. Only clone 3189 was positive. cDNA clones of the 3189 light and heavy chains were cloned into pGBN7f+ and transformed into B. coll DH5-alpha. The clones were sequenced (AAQ83490-91), and used for antibody engineering. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated and IgE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Light chain variable region; interleukin-4; IL-4; antibody 3B9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                        Chimeric antibody; humanized antibody; antibody engineering; monoclonal antibody; MAb; interleukin-4; IL-4; allergy.
                                                                                                                                                   /44...5
/label= CDR
/note= "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 50; DB 2; Length 132; 100.0%; Pred. No. 0.68; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                          /note= "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Light chain variable region of murine IL-4 antibody 3B9
                                                                                                                                                                                              74. .80
/label= CDR
/note= "complementarity determining
                                                                                                                              1. .20
/label= Sig_peptide
                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gross MS, Sylvester DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY23767 standard; protein; 132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 1; 97pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                    (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   high affinity mAbs - useful ir mediated allergic conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity 100.0%;
9; Conservative C
                                                                                                                                                                                                                                                                                                                                                               94WO-US010308
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                                                                                                                                                                                                                                                                                                                                                                                                        93US-00136783
                                                                                                                                                                                                                                           113. .121
/label= CDR
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               Mouse MAb 3B9 light chain.
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                     WO9507301-A1
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                                                                                                                                                                                                                                                                                                                                 16-MAR-1995
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                                                                                                                           Peptide
                                                                                    Mus sp
                                                                                                                                                          Region
                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                              Region
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This introlled teacher to the movel treatment. Specifically, it refers
to a peptide autoantigen that is linked to an antibody raised against an antibody presenting cell (APC) receptor. The present invention describes a method for treating diabetes mellitus by inducing an immune tolerance to an autoantigen, which can be chosen from glutamic acid decarboxylase (GAD), insulin or a heat shock protein (HSP), as well as epitopes derived from each thereof or beta cell antigens that are linked to an APC receptor antibody. In particular, the antibody recognises a receptor chesen from DC-SIGNR, MHC, toll receptor or mannose receptor amongst cohers, which is expressed on the surface of the APC. The antibody autoantigen construct then works to interfere with the interaction between the APC and immune cells such as autoreactive T cells, and hence inhibits T-cell proliferation. Accordingly, such compositions exhibit antidiabetic and immunosuppressive activities and can be used in the development of vaccines. Note that the single chain antibodies (scrWs) used in this specification contain both variable light and heavy chain cegions of the receptor is preserved. This peptide sequence is a heavy contain antine anti-human DC-SIGNR (hDC-SIGNR) CDR3 peptide of the
antibody/autoantigen construct containing an autoantigen linked to an antibody to a receptor of an antigen presenting cell and administering the construct to a subject.
                                                                                                   This invention relates to the novel treatment of an autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune disease; antibody; antigen presenting cell; APC; diabetes mellitus; immune tolerance; antidiabetic; immunosuppressive; vaccine; hDC-SIGNR; IgGlk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Light chain murine anti-hDC-SIGNR IgG1k antibody protein D10 Seq 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating an autoimmune disease comprises providing an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 47; DB 8;
Pred. No. 2e+06;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dakappagari
                                                                    Example 10; SEQ ID NO 123; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADT75056 standard; protein; 113 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAR-2003; 2003US-0451816P.
15-DEC-2003; 2003US-0529500P.
28-FEB-2004; 2004US-0548385P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QONNEDPPT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QQSNEDPPT
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Matches 8; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADT75056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus sp.
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ADT75056
ID ADT7
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                                                                                                                                                                                                                                                                                                                            This sequence represents the light chain of the murine 3B9 antibody of the invention. The antibody is a chimeric or humanised interleukin-4 (IL4) monoclonal antibody for the treatment of immunoglobulin B (1gB) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic astma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft versus host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine light chain CDR3 region IgG1k antibody binds hDC-SIGNR Seq 123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune disease; antibody; antigen presenting cell; APC; diabetes mellitus; immune tolerance; antidiabetic; immunosuppressive; vaccine; hDC-SIGNR; IgGlk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                    Recombinant IL4 antibodies useful for tratment of allergic rhinitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 50; DB 2; Length 132;
100.0%; Pred. No. 0.68;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating an autoimmune disease comprises providing an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dakappagari
                                                                                                                                                                                                                                                                   atopic ashthma and anaphylactic shock.
                                                                                                                                                                    Gross MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADT75077 standard; peptide; 9 AA.
                                                                                                                (SMIK ) SMITHKLINE BEECHAM PLC. (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                  Claim 24; Fig 1; 50pp; English.
                                                                  93US-00136783.
94WO-US010308.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-MAR-2003; 2003US-0451816P.
15-DEC-2003; 2003US-0529500P.
28-FEB-2004; 2004US-0548385P.
                                                 93US-00117366.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-MAR-2004; 2004WO-US006570.
                  95US-00483636
                                                                                                                                                                  Sylvester DR, Holmes SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 9; Conservative
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N-PSDB; AAX79519.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QQSNEDPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 132 AA;
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                  07-JUN-1995;
                                                   07-SEP-1993;
                                                                                   07-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADT75077;
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that utilises an antibody, autoantigen construct. Specifically, it refers
to a peptide autoantigen that is linked to an antibody raised against an
antigen presenting cell (APC) receptor. The present invention describes a
method for treating diabetes mellitus by inducing an immune tolerance to
an autoantigen, which can be chosen from glutamic acid decarboxylase
(GAD), insulin or a heat shock protein (HSP), as well as epitopes derived
from each thereof or beta cell antigens that are linked to an APC
chosen from DerSiGNR, MHC, toll receptor or mannose receptor amongst
chers, which is expressed on the auritace of the APC. The antibody/
autoantigen construct then works to interfere with the interaction
between the APC and immune cells such as autoractiver Tealls, and hence
inhibits T-cell proliferation. Accordingly, such compositions exhibit
antidiabetic and immunosuppressive activities and can be used in the
cell vaccines. Note that the single chain antibodies (serve)
used in this specification contain both variable light and heavy chain
regions connected by a linker, their short length makes these antibody
thinding to the the receptor is preserved which in the capacity for
thinding to the the preserved which and the capacity for
thinding to the the preserved which and the capacity for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     binding to the receptor is preserved. This polypeptide sequence is a light chain murine anti-human DC-SIGNR (hDC-SIGNR) IgG1k antibody protein
antibody/autoantigen construct containing an autoantigen linked to an antibody to a receptor of an antigen presenting cell and administering the construct to a subject.
                                                                                                              This invention relates to the novel treatment of an autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humanized antibody; antibody engineering; monoclonal antibody; MAb;
interleukin-4; IL-4; allergy; CDR; complementarity determining region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 8; Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47; DE Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Humanized antibody 3B9 light chain CDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sylvester DR;
                                                                           Example 10; Fig 11; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR70201 standard; protein; 9 AA.
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93US-00136783.
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Matches 8; Conservative
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93 QQNNEDPPT 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QQSNEDPPT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 113 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR70201;
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Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from

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                                                                                     A humanized antibody light chain variable region and signal sequence is given in AAR75355. The signal sequence is also provided in AAR70194. The sequences of the first 2 CDRs are identical to mouse anti-human IL-4 MAD. 3B9 light chain CDRs (given in AAR70195-96), but the third (AAR70201) differs by a single amino acid from the native mouse CDR (AAR70197). (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA molecules encoding recombinant antibodies useful for treating IL4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Light chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin E-mediated allergic reaction; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CDR) of the light chain variable region of murine interleukin-4 (IL-4) antibody 3B9. The specification describes chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin B-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host-versus-graft disease and renal disease. They
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present sequence represents a complementarity determining region
high affinity mabs - useful in treatment of {\rm IL-4-mediated} and {\rm IgB-mediated} allergic conditions.
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                                                                                                                                                                                                                                                 90.0%; Score 45; DB 2; Length 9;
100.0%; Pred. No. 2e+06;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDR of the light chain variable region of antibody 3B9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gross MS;
                                                      Disclosure; Page 28; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY23778 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Col 49; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SMIK ) SMITHKLINE BEECHAM CORP (SMIK ) SMITHKLINE BEECHAM PLC.
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94WO-US010308.
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                                                                                                                                                                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -mediated conditions.
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                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                      1 QQSNEDPP
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                                                                                                                                                                                                                Sequence 9 AA;
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14-OCT-1993;
07-SEP-1994;
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AAY23778
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RESULT 23 AAY18119

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differentiation (CD) positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the geparation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived complementarity determining region CDR-3 protein fragment which is used to illustrate the method of the invention
                                                                                                                                                                                                                                                                  Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hemacopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; complementarity determining region; CDR-3; light chain; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel device (I) for separating cluster
                                                                                                                                                                                                                                  Murine CD4/CD34 recognizing antibody light chain CDR-3 region #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 45; DB 3;
Pred. No. 2e+06;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Morimoto I, Miyamura K;
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                                                                                                                   AAY51138 standard; protein; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY59261 standard; peptide; 9 AA.
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(ASAH ) ASAHI MEDICAL CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-APR-2000 (first entry)
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Best Local Similarity
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1 QQSNEDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soka T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-MAY-1999;
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26-MAY-1998;
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                                                                                                                                                        AAY51138;
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                                                                             RESULT 24
                                                                                                   AAY51138
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                                                                                                                                                        요
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibody, interleukin-4; IL4; immunoglobulin B; IgB mediated disease; allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; actopic aethma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease; complementarity determining region; CDR.
are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans
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                                                                                                                                                        Gapa
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                                                                                                                   Length 9;
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2e+06;
                                                                                                                 Score 45; DB 2;
Pred. No. 2e+06;
                                                                                                   90.0%; Scor.
100.0%; Pred. No. 20.
0, Mismatches
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100.0%; Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Light chain CDR for hIL-4 specific antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gross MS;
                                                                                                                                                                                                                                                                                                                           AAY18119 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM PLC. (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 18; Col 47; 50pp; English.
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94WO-US010308.
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                      Conservative
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N-PSDB; AAX79518.
                                                                                                                                                                                          1 QQSNEDPP 8
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QOSNEDPP 8
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                                                                                                               Query Match
Best Local Similarity
Matches 8; Conserv
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                                                                         Sequence 9 AA;
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07-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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Gaps

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The invention relates to transforming a population of cells (e.g. plant cells), comprising using a library of two different polymuclectides encoding different immunoglobulin binding protein (IgBP) polypeptides that specifically bind to a ligand or form one or more disulphide bonds with polypeptides in transfected cells, to generate an IgBP that binds to a ligand, and transformed plant cells are selected, and preparing an IgBP array in plant cells. At least one peptide sequence has at least 7st sequence identity to a framework region (FR) of a native IgM, IgG, IgA, IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is useful for preparing an immunoglobulin binding protein array, preferably plant cells (e.g. insect cells or manalian cells). The CHBP is useful for cells or manalian cells). The CHBP is useful for preparing assays of IgBPs having desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or CD34 and their use for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   characteristics. The present sequence is a mammalian immunoglobulin derived peptide that may be incorporated into an IgBP of the invention
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protein polypeptides specific to ligand, selecting plant cells for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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100.0%; Pred. No. v.
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                                                                               Disclosure; Page 14; 129pp; English
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(ASAH ) ASAHI MEDICAL CO LTD
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Best Local Similarity
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                             preparing array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. Sequences AAX59259-61 represent the complementarity determining region (CDR)-1, CDR -2 and CDR-3 fragments in the L chain variable region of the antibody 4H5 respectively
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Pred. No. 2e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An antibody and the nucleic acid coding the antibody
                       4H5; drug; CDR;
                                                 region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 14; 25pp; Japanese.
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                                                                                                                                                                                                                                                                          98JP-00163034
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                                           determining
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                                                                                                                                                           JP11332563-A.
                       CD4 antigen;
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Matches
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31-MAR-2000 (first entry)
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                                                                                                                                                    Mus sp.
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single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents the L chain variable region of the antibody 4H5
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                                                                                                                                                                                                                                       1; Mismatches
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Pred. No.
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88.9%;
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N-PSDB; AAZ58662.
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QQSSEDPPT
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Best Local Similarity
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                                                                                                                                                                 Sequence 103
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Matches
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                                                         Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Devices containing antibodies recognising CD4
the separation of CD4 or CD34 positive cells.
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L; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 97-98; 111pp; Japanese.
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88.9%; Pred. No.
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Murine derived protein fragment #8.
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(ASAH ) ASAHI MEDICAL CO LTD
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QOSSEDPPT 101
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Contractor Contractor

present

Gaps

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us-10-723-872-20.rag

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The present invention relates to modified (e.g. deimmunised) antibodies are less immunogenic compared to the modified anti-PSWA antibodies are less immunogenic compared to the unmodified anti-PSWA antibodies. The modified antibodies comprise comprise complementarity determining regions (CDRs) from a non-human antibody (e.g. murine antibody J591,J415,J53 or E99), and framework sequences that are less immunogenic in humans (e.g. less antigenic than the murine frameworks in which a murine CDR naturally occurs). The modified antibodies bind with PWSA, preferably human PMSA, with high affinity and specificity. The anti-PMSA antibodies are useful for treating or preventing a prostatic or cancerous disorder, e.g. genitourinary inflammation, prostatitis, benign enlargement, prostatic cancer or testicular cancer, or solid tumours, soft tissue tumours or metastatic lesions, and its associated pain. The present sequence represents a variable region from a murine antibody
                                                                                                                                                                                                                                                                                                                                                                                                                      prostate specific membrane antigen; immunogenic; CDR; murine; complementarity determining respion; JS91, G415, JS31, E99; mouse; prostatic disorder; cancerous disorder; genitourinary inflammation; prostatitis; benign enlargement; prostatic cancer; testicular cancer; solid tumour; soft tissue tumour; metastatic lesion; pain; analgesic; antiinflammatory; cytostatic; framework region; variable heavy chain; variable light chain, VU; variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunoglobulins, useful for treating or preventing a prostatic or cancerous disorder, e.g. genitourinary inflammation, prostatitis, prostatic or testicular cancer.
                                                                                                                                                                                                                                                                                                                                                                                                        antibody; deimmunised antibody; anti-PMSA antibody;
 application for drugs. It is highly safe in human dose. The sequence represents a L chain fragment of the antibody 4H5
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                                                                                     Length 111;
                                                                                                                    0; Indels
                                                                                   Score 45; DB 3;
Pred. No. 4.3;
1; Mismatches
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20-SEP-2001; 2001US-0323585P.
08-MAR-2002; 2002US-0362810P.
                                                                                 90.0%;
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                                                                Query Match
Best Local Similarity 88.3...
Best Local Similarity 88.3...
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                                                    Sequence 111 AA;
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                                                                                                                                                                                                                Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and
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Pred. No. 4.3;
1; Mismatches 0; Indels
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                 99WO-JP002711.
                                                                                                                                                Soka T, Morimoto I,
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(ASAH ) ASAHI MEDICAL CO LTD
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N-PSDB; AAZ58690.
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               24-MAY-1999;
                                                25-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY59267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                Ono M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
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AAY59267
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse; murine; antibody; skin disorder; binding agent; PSMA; cytostatic; prostate specific membrane antigen; antibosoriatic; antiarthritic; dermatological; antiinflammatory; antiallergic; vaccine; dermal disorder; epidermal disorder; psoriasis; inflammatory disorder; epidermis; dermis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibodies have antipociatic, antiarchritic, dermatological, cytostatic, antinflammatory and antiallergic activities, and can be used in vaccines. M1 is useful for treating a skin disorder in a subject, by administering to the subject, an amount of an antibody which binds specifically to the extracellular domain of PSMA (the subject is a mammal, preferably human and is having, or at risk of, a skin disorder). The skin disorder is a dermal or an epidermal disorder, and is selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from psoriasis (preferably chronic stationary psoriasis, psoriasis vulgaris, eruptive (gluttate) psoriasis, psoriatic erythroderma, generalised pustular psoriasis (Von Zumbusch), annular pustular psoriasis exfoliative dermatitis, pityriasis rubra pilaris, pityriasis rubra pilaris, pityriasis rubra pilaris, pityriasis rubra pilaris, pityriasis rosacea, parapsoriasis, pityriasis lichenoiders, lichen planus, lichen nitidus, ichthyosiform dermatosis, keratodermas, dermatosis, and prokeratosis, preferably psoriasis. Ni is useful for treating a skin disorder such as an inflammatory or neoplastic disorder of the epidermis or dermis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ablating/killing aberrant prostate specific membrane antigen-expressing cells for treating skin disorders, by contacting the cell with an antibody that binds to the extracellular domain of prostate specific
                                                                                    Gaps
                                                                                    ö
                                        DB 6; Length 112;
                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Murine MuVL-3 antibody amino acid sequence SEQ ID NO:81.
                                                          4.3;
                                    90.0%; Score 45; DB 100.0%; Pred. No. 4.3 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 38; 225pp; English.
                                                                                                                                                                                                                                                                       ABR44694 standard; protein; 112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-SEP-2001; 2001US-0324100P. 08-MAR-2002; 2002US-0362612P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2002; 2002WO-US017204.
                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                 8; Conservative
                                                                                                                                                ||||||||||
QOSNEDPP 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neoplastic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-313319/30.
                                                                                                                        1 QQSNEDPP 8
                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  membrane antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003024388-A2.
Sequence 112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus.
                                                                                                                                                                                                                                                                                                                                                      25-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-2003.
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                                                                                                                                                                                                                                                                                                             ABR44694;
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                                                                                                                                                                                                                              RESULT 33
ABR44694
                                                                             Matches
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The invention relates to the use of an anti-prostate specific membrane antigen (anti-PSMA) antibody or antigen-binding fragment for treating prostate cancer, monitoring a patient receiving an anti-PSMA antibody to treat prostate cancer, or selecting a patient for treatment with an anti-PSMA antibody. Also included are a method of treating prostate cancer in a subject, a method of monitoring a patient receiving an anti-PSMA antibody to treat prostate cancer and a method of selecting a patient for treatment with an anti-PSMA antibody. Also disclosed are anti-PSMA antibody or antigen-binding fragment is a human antibody or antigen-binding fragment is a human antibody. Cor antigen-binding fragment. The modified antibody or antigen-binding fragment has one or more CDRs (complementarity determining region) from a mouse amonoclonal antibody. Complementarity determining region) from a mouse amonoclonal antibody or antigen-binding fragment has one or more CDRs (complementarity determining region) from a mouse amonoclonal antibody or selected from US91, J415, J533, or E99. The anti-PSMA antibody or antigen binding fragment is useful for treating prostate cancer, monitoring a patient receiving an anti-PSMA antibody to treat prostate cancer, or selecting a patient for treatment with an anti-PSMA antibody. The present sequence is a mouse kabat subgroup consensus sequence for a light or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of an anti-prostate specific membrane antigen (anti-PSMA) antibody or antigen-binding fragment for treating prostate cancer or monitoring a patient receiving an anti-PSMA antibody to treat prostate cancer.
preferably an epidermal precancerous or cancerous lesion. M1 is also metaful to treat or prevent disorders involving aberrant activity of PSMA-expressing cell, e.g. kidney, liver or brain cell. ACC69816 to ACC69837 and ABR44613 to ABR44733 represent sequences used in the exemplification
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody; antibody engineering; antibody therapy; prostate tumor; cytostatic; prostate specific membrane antigen; PSMA; heavy chain variable region; light chain variable region.
                                                                                                                                                                                                               ö
                                                                                                                                                                       Length 112;
                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse Kabat subgroup VKIII light chain variable region.
                                                                                                                                                                          . 9
                                                                                                                                                                     90.0%; Score 45; DB 100.0%; Pred. No. 4.3 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 81; 284pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         ADU67960 standard; protein; 112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-MAR-2004; 2004WO-US006586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2003; 2003US-00449379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-MAR-2003; 2003US-00379838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                               Ouery Match
Best Local Similarity 100...
8; Conservative
                                                                                      of the present invention
                                                                                                                                                                                                                                                                                                 93 QOSNEDPP 100
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                                                                                                                                                                                                                                                         8
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                                                                                                                                                                                                                                                         1 QOSNEDPP
                                                                                                                                Sequence 112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004098535-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-FEB-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ADU67960;
                                                                                                                                                                                                                                                                                                                                                                 RESULT 34
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AAR32123;
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                                                                                                                                                                                                                 Peptide
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              RESULT 36
                         AAR3212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method of treating or preventing an insulin-
related disorder in a subject which comprises administering an antibody
or its antigen-binding portion specific for prostate specific membrane
antigen (PSMA). The method is useful for treating an insulin-related
disorder, including obesity, hyperglycaemia, hypoglycaemia,
hyperinsulinaemia, insulin-resistence, impaired glucose colerance,
impaired fasting glucose. Type I diabetes mellitus, Type 2 diabetes
mellitus, and gestational diabetes. The present sequence represents Kabat
heavy chain variable region used to compare to a sequence from one of the mouse monoclonal antibodies listed above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of anti-prostate specific membrane antigen antibodies for treating or preventing insulin-related disorders, e.g. obesity, hyperglycemia, hyperinsulinemia, insulin-resistance, or Type 1 or 2 diabetes mellitus.
                                                                                                                                                                                                                                                                  obesity; hyperglycaemia; hypoglycaemia; hyperinsulinaemia; insulin-resistance; impaired glucose; the i diabetes mellitus; Type I diabetes mellitus; Type 2 diabetes mellitus; gestational diabetes;
                                                                          Gaps
                                                                                                                                                                                                                                                         insulin-related disorder; prostate specific membrane antigen; PSMA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.0%; Score 45; DB 8; Length 113; larity 100.0%; Pred. No. 4.4; Conservative 0; Mismatches 0; Indels
                                                     DB 8; Length 112;
                                                                          Indels
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                                                    Score 45; DB 8; Pred. No. 4.3; 0; Mismatches
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                                            90.0%; Scc...
100.0%; Pred
0; F
                                                                                                                                                                     ADQ90832 standard; protein; 113
                                                                                                                                                                                                                                                                                                                                                                                      17-OCT-2003; 2003US-00688015.
                                                                                                                                                                                                                                                                                                                                                                                                          30-OCT-2002; 2002US-0422396P.
                                                                                                                                                                                                                                     Kabat subgroup murine VKIII.
                                                                                                                                                                                                              (first entry)
                                                  Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                           93 QOSNEDPP 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subgroup murine VKIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-533338/51.
                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                 (BAND/) BANDER N H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                             1 QQSNEDPP
                               Sequence 112 AA;
                                                                                                                                                                                                                                                                                                                                             US2004136998-A1.
                                                                                                                                                                                                                                                                                         Type 1 diabetes antibody; mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 113 AA
                                                                                                                                                                                                                                                                                                                         Mus musculus.
                                                                                                                                                                                                                07-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                 15-JUL-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bander NH;
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                                                                                                                                                  RESULT 35
                                                                                                                                                          ADQ90832
ID ADQ
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This sequence is the light chain variable region of a preferred anti-CD4 monoclonal antibody for use in the claimed synergistic composition. MAD MT 3.10 is deposited as clone 3.101/SB10 (ECACC 90090702). The anti-CD4 antibody is used with at least one anti-ILZR alpha or beta antibody. Individually the antibodies are strongly inhibiting and when used together their immunosuppressive properties are improved; they synergistically inhibit T-helper cell proliferation to effectively inhibit transplant rejection at low doses without significantly reducing the general immune response. See also AAQ36608-Q36616. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synergistic antibody compsn. for use as immunosuppressant - comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R alpha- or anti-IL2R beta antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                        immunosuppression; tissue transplantation; graft, L chain; V region;
T-helper cell inhibition; transplant rejection; MAb;
interleukin-2 receptor.
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                                                                                                                                                                                             Anti-CD4 antibody MT 3.10 light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaluza B, Riethmueller G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45; DB
Pred. No. 5;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Variable
121. .131
/label= J1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BOEF ) BOEHRINGER MANNHEIM GMBH.
AAR32123 standard; protein; 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Page 11; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                      .. .20
'label= signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91DE-04143214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91DE-04124759.
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                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .120
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                                                                                            (revised)
(revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weidle U, Scheuer W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 QOSSEDPPT 121
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N-PSDB; AAQ36609.
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                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JUL-1991;
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                                                                                              25-MAR-2003
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                                                                                                                                            02-JUN-1993
                                                                                                                     10-MAR-2003
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RESULT 37

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OOSNEDPP

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Humanized

Peptide

Region

Region

Region

AAR75355;

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The present sequence represents the light chain variable region of a humanised murine interleukin-4 (IL-4) antibody 389. The specification describes chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, vestus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA molecules encoding recombinant antibodies useful for treating IL4 liated conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
                                                                                   Light chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin B-mediated allergic reaction; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthms; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.
                                                   Light chain variable region of humanised murine IL-4 antibody 3B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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Pred. No. 5;
; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Fig 5; 50pp; English.
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94WO-US010308.
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                 13-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sylvester DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
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112 QOSNEDPP 119
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N-PSDB; AAX85888.
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                07-JUN-1995;
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                                                                                                                                                                                                 Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A humanized antibody light chain variable region and signal sequence is given in AAR75355. The signal sequence is also provided in AAR70194. The sequences of the first 2 CDRs are identical to mouse anti-human IL-4 MAb 3B9 light chain CDRs (given in AAR70195-96), but the third (AAR70201) differs by a single amino acid from the native mouse CDR (AAR70197).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric and humanised \rm IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of \rm IL-4-mediated and \rm IgE-mediated allergic conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                             antibody; antibody engineering; monoclonal antibody; MAb;
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                                                                                                                                                                                                                                                                                                                                              "complementarity determining region"
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                                                                                                                                                                                                                                                         Location/Qualifiers
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/label= Sig_peptide
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AAR75355 standard; protein; 131 AA
                                                                                                                         Humanized antibody 3B9 light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 5; 97pp; English.
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93US-00136783.
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                                                                                                                                                                              interleukin-4; IL-4; allergy
                                                                                                                                                                                                                                                                                                              13. .57
'label= CDR
                                                                                                                                                                                                                                                                                                                                                                                  /label= CDR
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/label= CD
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                                                                      (revised)
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N-PSDB: AAO73986.
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Best Local Similarity
Matches 8; Conserv
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14-OCT-1993;
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20-SEP-1995
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Gaps

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AAY23771

RESULT 38 AAY23771

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This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the rollection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used to illustrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine.
                                                                                                                                               Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 305;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45; DB 3;
Pred. No. 11;
1; Mismatches
                                                       Morimoto I, Miyamura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soka T, Morimoto I, Miyamura K;
                                                                                                                                                                                                   Claim 22; Page 82-84; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 22; Page 80-82; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine derived protein fragment #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY51141 standard; protein; 305 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98JP-00163023.
 (ASAH ) ASAHI KASEI KOGYO KK.
(ASAH ) ASAHI MEDICAL CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.0%;
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(ASAH ) ASAHI MEDICAL CO LID
                                                                                                                                                                                                                                                                                                                                                                                                          the method of the invention
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Best Local Similarity 8b.,
Best Local Similarity 8b.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 QOSSEDPPT 256
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N-PSDB; AAZ44205.
                                                                                         2000-086720/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QOSNEDPPT
                                                                                        WPI; 2000-086720,
N-PSDB; AAZ44206
                                                     Soka T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 305 AA;
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                                                     Ono M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents the light chain of the humanised 3B9 antibody of the invention. The antibody is a chimeric or humanised interleukin-4 (IL4) monoclonal antibody for the treatment of immunoglobulin B (IgB) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft versus host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cluster differentiation, cell separation, antibody, CD4, CD34, leukemia; hematopoietic, undifferentiated, lymphocyte; bone marrow transplantation, HIV infection, autoimmune disease; murine.
atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gape
                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant IL4 antibodies useful for tratment of allergic rhinitis,
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100.0%; Pred. No. 5;
ive 0; Mismatches 0; Indels
                 autoimmune disease; graft versus host disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            atopic ashthma and anaphylactic shock
                                                                                                                                                                                                                                                                                                                                 Gross MS;
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                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM PLC. (SMIK ) SMITHKLINE BEECHAM CORP
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93US-00136783.
94WO-US010308.
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98JP-00163023
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Matches 8, Conservative
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14-OCT-1993;
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26-MAY-1998;
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                                                   Synthetic.
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Query Match

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AAY51142;

RESULT 40 AAY51142 Mus sp

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The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents the L chain sequence of the antibody 4H5
                                                                                                                                                                                                                                                                         An antibody and the nucleic acid coding the antibody.
                                                                      CD4 antigen; anti-human; antibody; 4H5; drug.
                                                                                                                                                                                                                                                                                              Disclosure; Page 17-18; 25pp; Japanese.
                                               Antibody 4H5 L chain sequence
                                                                                                                                                                  98JP-00163034.
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                       (first entry)
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N-PSDB; AAZ58664.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 305 AA;
                       17-APR-2000
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AAY59265;
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         differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and application for druga. It is highly selfe in human dose. The present sequence represents the H chain sequence of the antibody 4H5
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This invention describes a novel device (I) for separating cluster
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                                                                                                                                                      DB 3; Length 305,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An antibody and the nucleic acid coding the antibody
                                                                                                                                                                                                                                                                                                                                                                                CD4 antigen; anti-human; antibody; 4H5; drug
                                                                                                                                                     Score 45; DB:
Pred. No. 11;
1; Mismatches
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QOSSEDPPT 123
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Best Local Similarity
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Matches 8; Conserv
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                                                          ö
Score 45; DB 3; Length 305;
Pred. No. 11;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CD-4 antibody variable region; complementary peptide;
extra-corporeal blood circulation; cell filter material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD-4 antibody variable region complementary peptide
                                                                                                                                                                                                                                                                                                  AAR66145 standard; peptide; 17 AA.
     90.08;
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Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be us to form chimeric mouse-variable, human-constant region Abs suggested being useful as a vaccine to HIV. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                 New chimeric variants of murine antibody anti-leucine - contg. human antibody regions, and DNA encoding sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD14 receptor; monoclonal antibody; 28C5; hybridoma; antiseptic;
                                                                                           Anti-Leu 3a light chain variable region gene product, 206 Vx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 131,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB 2
Pred. No. 17;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monoclonal antibody 28C5 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
AAR04132 standard; protein; 131 AA.
                                                                                                                     HIV; AIDS; anti-Leu3A; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR64202 standard; protein; 215 AA.
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21. .35
--- "CDR1"
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/note= "FR.2"
51. .57
                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 2; 12pp; English.
                                                                                                                                                                                                                                                           88US-00260558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.0%;
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                                                                                                                                                                                                                                                                                     (BECT ) BECTON DICKINSON CO
                                                     (revised)
(first entry)
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Best Local Similarity 88.2
Ere 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ04039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 131 AA;
                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                           17-0CT-1988;
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                                                                                                                                                                                                                                11-OCT-1989;
                                                    25-MAR-2003
06-SEP-1990
                                                                                                                                                                                                      25-APR-1990.
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08-JUL-1995
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                                                                                                                                                                           EP365209-A.
                                                                                                                                                                                                                                                                                                                 Hinton R,
                          AAR04132;
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field.)
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be used to form chimeric mouse-variable, human-constant region Abs suggested as being useful as a vaccine to HIV. (Updated on 25-MAR-2003 to correct PF
                      AAR86140-R66146 are peptides complementary to the variable region of th CD-4 antibody, these peptides are fixed onto a claimed nonwoven fabric (average fibre dia. of 1-30 microns) coated with keto-alkyl halide functional groups. This material can be used as a filter for CD-4 positive cells in a medical treatment involving the extra-corporeal circulation of blood
                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New chimeric variants of murine antibody anti-leucine - contg. human antibody regions, and DNA encoding sequences.
                                                                                                                                                                                                                                                                                                                                                                                             Anti-Leu 3a light chain variable region gene product, KOL/206 Vl.
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Pred. No. 15;
0; Mismatches 1; Indels
                                                                                                                                             Score 42; DB 2; Length 17; Pred. No. 2.3; 1; Indels 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                 AAR04134 standard; protein; 115 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                        HIV; AIDS; anti-Leu3A; vaccine; ds.
Example 3; Page 8; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Fig 4; 12pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.0%;
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                                                                                                                                              84.0%;
88.9%;
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(first entry)
                                                                                                                                          Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 88.5
Matches 8; Conservative
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                                                                                                                                                                                                    1 QQSNEDPPT 9
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N-PSDB; AAQ04041.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 115 AA;
                                                                                                                  Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-0CT-1988;
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06-SEP-1990
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                                                                                                                                                                                                                                                                                                                           AAR04134;
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RESULT 45 AAR0413

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Gaps

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Region

RESULT 46 AAR04132

ઠે 셤 Jun O, Masahiko O, Hideyuki H, Tohru T;

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New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis,
                                                                                                                                                                                                                        Claim 9; Page 185; 292pp; English.
                               98AU-00059701.
                                                    97JP-00082953
                                                            97JP-00169088
                                                                                                                , Kimihisa I, Ju
Akio S, Shin Y;
                                                                                            (SANY ) SANKYO CO LTD
                                                                                                                                                WPI; 1998-543440/01.
                                                                                                                                                                                                    hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9 AA;
                                                   01-APR-1997;
25-JUN-1997;
08-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                30-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      light chain.
          08-OCT-1998
                                                                                                                Nobufusa S,
                                                                                                                            Hiroko Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB14746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                             activation - for detecting CD14 in a sample and to inhibit the binding of
                                                                                                                                                                                                                                                                                                                                Anti-human soluble CD14 receptor MAD 28C5 may be used to detect CD14 in cell samples, to Inhibit binding of LP8 to CD14 or a LP8/CD14 complex to a cell, to inhibit CD14-mediated activation of a cell expressing CD14 receptor, and for sepsis therapy. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune disease, Hashimoto's disease, systemic lupus erythematosus, graft versus host disease, Sjogren syndrome, pernicious anaemia; Addison's disease, scleroderma; Goodpasture syndrome, Crohn's disease, sterility, rheumatoid arthritis, autoimmune haemolytic anaemia; thrombopenia gravis, multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AlDS; transplant rejection; therapy; complementarity determing region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HFE7A; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                              Mathison JC;
                                                                                                                                                                                                                                                                  Hybridoma cell lines produce MAb which inhibit CD14-mediated cell
                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                    84.0%; Score 42; DB 2; Length 215;
88.9%; Pred. No. 27;
cive 0; Mismatches 1; Indels
                                                                                                                                                                                                              Tobias PS,
                                                                                                                                                                                                              Ulevitch RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-Fas MAb HFE7A light chain CDR-L3.
                                                                                                                                                                                                                                                                                                             Disclosure; Fig 3; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW83029 standard; peptide; 9 AA.
                        .98
. "CDR3"
                                                  99. .108
/note= "FR.4"
109. .215
note= "CDR2"
                    "FR.3"
                                                                                  /note= "CH-1"
                                                                                                                                                 94WO-US005898.
                                                                                                                                                                    93US-00070160
                                                                                                                                                                                                              Moriarty AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
(first entry)
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les 8; Conservative
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          .89
                     note=
                                          'note=
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P-PSDB; AAQ80292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QQSNEDPPT
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 215 AA;
                                                                                                       WO9428025-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                27-MAY-1994;
                                                                                                                                                                     28-MAY-1993;
                                                                                                                                                                                                                                                                                         to CD14.
                                                                                                                                                                                                              Leturcq DJ,
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15-MAR-1999
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Matches
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This is the amino acid of complementarity determining region 3 (CDR-L3) of the light chain (see AAW83042) of murine anti-human Fas monoclonal antibody HFS7A. The invention relates to antibodies, especially humanised antibodies see AAW83031-37), recognising the Fas antigen. Such antibodies preferably comprise a heavy chain and a light chain including comprise a heavy chain and a light chain including comprise a heavy chain and a light chain including companies are produced by CDR grafting. The antibodies are capable of inducing apoptosis in normal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells are used to chain increations, and also to treat such diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lugus erythematosus, Hashimoto's disease, graft versus host disease Sjogren syndrome, pernicious anaemia, Addison's disease, actorederma, Goodpasture syndrome, Crohn's disease, cheumatoid arthritis, autoimmune haemolytic anaemia, sterility, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AlbS and transplant rejection (all claimed). (Updated on 25-MAR-2003 to correct DR field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.0%; Score 41; DB 2;
88.9%; Pred. No. 2e+06;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB14746 standard; peptide; 9 AA.
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1 QOSNEDPRT 9
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les 8; Conserv
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29-SEP-1999;
                                                                                                                                                                                                                                                                                                                 The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Ras/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a tentaning regions) to antibody HFETA, via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autofimmune diseases, allergy, attentosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft captoduced by hybridoma HFETA (FERM-BP-5828)
                                                                                                                                                                                                                       Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas
                                                                                                                                                                                                                                                                                     Claim 10; Page 65; 139pp; Japanese.
                                                                                 99JP-00278301
                                                                                                                   98JP-00276883
                                                                                                                                                 (SANY ) SANKYO CO LID.
                                                                                                                                                                                   WPI; 2000-485645/43.
               JP2000169393-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9 AA;
                                                                                                                 30-SEP-1998;
                                                                                 30-SEP-1999;
                                               20-JUN-2000
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Gaps ö 1; Indels 82.0%; Score 41; DB 3; Length 9; 88.9%; Pred. No. 2e+06; 0; Mismatches Local Similarity 88.5 Φ Φ QQSNEDPRT 1 QQSNEDPPT Query Match Best Loc Matches ઠે 셤

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AAW90896 standard; peptide; 9 AA 08-AUG-2000 AAW90896; AAW9089 

Murine anti-Fas antibody peptide fragment #6. (first entry)

Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; nutinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome, Crohn's disease, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, allergy, insulin dependent diabetes mellitus, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis, transplant rejection.

EP990663-A2

05-APR-2000

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This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents capoptosis in cells with a normal system, by inhibiting binding between apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-antidabetic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosupressive, thyromimetic, antiviral, cantirheumatic, nephrotropic, antimifertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell aurface Fas or inhibit it by competitive cinhibition of ligand binding. (I) are used to treat and/or prevent cinhibition of ligand binding. (I) are used to treat and/or prevent cinhibition of ligand binding. (I) are used to treat and/or prevent cinhibition of ligand binding. (I) are used to treat and/or prevent disease, Sjorgen's syndrome, spermicious or hypoplastic versus host disease, Slorgen's syndrome, Scordpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, mysathenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B. Cor D) or alcoholic, and tranglant rejection. (I) selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in multiple addisease models. (I) act on the active site of Fas, i.e. they minic the native ligand, do not induce liyer disease, and have reduced risk of inducing a human anti-murine anti-base, and have reduced of examine anti-pas antibody response. This sequence represents a murine anti-pas antibody response.
                                                                                                                                                                                                                                                                                  New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems.
                                                                                                                                                                                   Takahashi T;
                                                                                                                                                                                Tamaki I,
                                                                                                                                                                                Nakahara K,
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Sequence 9 AA;

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A;Cross-references: UNIPARC:UP100001153EE; GB:S50265; NID:g260765; PIDN:AAB24320.1; PID: A;Note: this mouse sequence was hybridized and fused with a human constant region gene C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Superfamily: immunoglobulin regions heterotetramer; immunoglobulin F;1-20/Domain: signal sequence #status predicted <SIG>F;21-131/Product: Ig light chain V region #status predicted <MAT>F;36-114/Domain: immunoglobulin homology <IMM>
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KjGoshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
AjTile: Common structural features among monoclonal antibodies binding the same antigen.
AjReference number: A38601; WUID:91115823; PMID:1703527
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C;Species: Mus musculus (house mouse)
C;Date: 21-Uul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: B49442
E;Stura, E.A.; Stanffeld, R.L.; Fieser, G.G.; Silver, S.; Roguska, M.; Hincapie, L.M.; Sl Proteins 14, 499-508, 1992
A;Title: Crystallization, sequence, and preliminary crystallographic data for an antipepial A;Reference number: A49442; MUID:93066166; PMID:1438187
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A;Residues: 1-96 <STU>
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C;Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                        Score 45; DB 2; Pred. No. 0.2; 1; Mismatches
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88.9%; Pred. No. 1.3;
ive 0; Mismatches
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F;8-86/Domain: immunoglobulin homology <IMM>
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Best Local Similarity
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-65 <GOS>
                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig Appa chain V region (CD4 mAb clone M-T310 and others) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Si9973
R;Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
R;Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
R;Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
A;Description: Structural characterization of CD4 mAb.
A;Reference number: S19963
A;Ressidues: 1.12 <WEI>A;Ressidues: 1.12 <WEI>A;Ressidues: 1.12 <WEI>A;Ressidues: 1.12 <WEI>A;Ressidues: 1.12 <WEI
A;Ressidues: 1.12 <WEI
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A;Residues: 1.12 <WEI
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PH1226
EMB Chain precursor V region (M-T310) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
C;Accession: PH1226
EW Wis Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; Lenz Gene 121, 271-278, 1992
A;Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and on A;Reference number: PH1224; MUD:93077041; PMID:1446824
A;Accession: PH1226
A;Residues: 1-131 <WEI>
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QOSSEDPPT 101
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A, Molecule type: protein
A, Residues: 1-11 < WEI.
C, Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kay hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l. C, Superfamily: immunoglobulin v region; immunoglobulin homology
C, Reywords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology < IMM>
F;23-92/Disulfide bonds: #status predicted
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("Species: Mus musculus (house mouse)
("Species: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 09-Jul-2004
("Accession: A01936
R;McKean, D.J.; Bell, M.; Potter, M.
R;McKean, D.J.; Bell, M.; Potter, M.
A;Title: Mechanisms of antibody diversity: multiple genes encode structurally related m.
A;Reference number: A93822; NUID:79012520; PMID:99744
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C;Comment: This chain was isolated from a myeloma protein.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kag hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lc;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
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C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C;Accession: 80996
C;Accession: 80996
Bur. J: Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Eur. J: Immunol. 20, 771-777, 1990
Bur. J: Immunol. 20, 771-777, 1990
A;Fitle: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodi-A;Reference number: 809955; MUID:90269328; PMID:2347362
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                    Nature 276, 785-790, 1978

A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.

A;Reference number: A93204; MUID:79073152; PMID:103003

A;Accession: B01937
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R; Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood,
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Pred. No. 1.5;
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QOSNEDPYT 101
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A; Residues: 1-111 <REI>
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R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978

R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978

A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID: 79073152; PMID:103003

A;Rotense: DC3741

A;Reference number: A93204; MUID: 79073152; PMID:103003

A;Rotense: T.111 (*MEI)

A;Rotession: A93204

A;Molecule type: protein

A;Reference number: A93822; MUID: 79012520; PMID: 99744

A;Contents: T111

A;Accession: A93822

A;Molecule type: protein

A;Residues: L-111 (*MEX)

A;Accession: A93822

A;Molecule type: protein

A;Residues: L-111 (*MEX)

A;Contents: T11

A;Accession: A93822

A;Molecule type: protein

A;Residues: L-111 (*MEX)

A;Cross-references: UNIPARC;UPI000002A0FB

C;Complex: An immunoglobulin herecotetramer subunit consists of two identical light (*Rapid: Insunoglobulin vegion; immunoglobulin homology

C;Keywords: heterotetramer

F;16-94/Domain: immunoglobulin homology <IMM>
F;23-92/Disulfide bonds: #status predicted
                                                                                                                                   C;Accession: S26344
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e A;Title: Antibodies that are specific for a single amino acid interchange in a protein e A;Reference number: S26309; MUD:91341421; PMID:1908510
A;Accession: S26344
A;Residues: preliminary
A;Molecule type: mRNA
A;Catus: preliminary
A;Catus: J-107 - SSTNA
A;Catus: J-107
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                        j kappa chain V region - mouse
;Species: Mus musculus (house mouse)
;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
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Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004
Accession: A93204; A93822; A01934
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C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: B01937, A01937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 1.5;
0; Mismatches
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Best Local Similarity 88.9%;
Matches 8; Conservative
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les 8; Conserv
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Best Local S
Matches 8
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A;Cross-references: UNIPROT:P01667; UNIPARC:UPI000002A102
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kag hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;16-94/Domain: immunoglobulin homology <IMM'>
F;23-92/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:P01665; UNIPARC:UP1000002A100
R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Bur, J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec A;Reference number: S42176; MUID:94009207; PMID:7691608
A;Accession: S42187
A;Molecule type: DNA
A;Residues: 10-99 <MOJ>
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A;Note: V-kappa-21E; anti-collagen
A;Accession: S42191
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A,Cross-references: UNIPARC:UP1000011655C; EMBL:225452; NID:g407840; PIDN:CAA80939.1; PI
A,Note: V-kappa-21E ; anti-collagen
A,Accession: S42192
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A;Residues: 12-99 «KOW»
A;Gross-references: UNIPARC:UPI000011655E; EMBL:Z25458; NID:g407844; PIDN:CAA80945.1; PI
A;Note: V-kappa-21E; anti-collagen
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A,Note: V-kappa-21E; anti-collagen
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A;Accession: S42194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Rearrangement of genetic information may produce immunoglobulin diversity. A;Reference number: A93204; MUID:79073152; PMID:103003 A;Accession: A01937
        A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
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C;Species: Mus musculus (house mouse)
C;Date: 01-Sep-1981 #sequence revision 01-Sep-1981 #text change 09-Jul-2004
C;Accession: A01937; S42187; S42194; S42190; S42189; S42188; S42191; S42192
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
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Pred. No. 2.4;
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                                                                                                                                                                                                                                                                                                                                                                                     78.0%;
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Best Local Similarity 88.5.
Best Local Similarity 88.5.
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                                                              A;Accession: C01937
A;Molecule type: protein
A;Residues: 1-111 <WEI>
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A;Residues: 13-99 <MOF>
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A; Residues: 15-99 < MOA>
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A; Residues: 12-99 <MOZ>
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A;Residues: 10-99 <MOO>
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Ig kappa chain V region (VM201) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C;Accession: A33936
R;Meek, K,; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989
A;Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene
A;Reference number: A33936; MUID:89282831; PMID:2471975
A;Resession: A33936
A;Status: prellminary
A;Molecule type: mRNA
A;Residues: 1-111 cMERA
A;Residues: 1-111 cMERA
A;Residues: 1-111 cMERA
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology <IMM>
F;14-94/Domain: immunoglobulin homology <IMM>
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S26343
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26343
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e A;Title: Antibodies that are specific for a single amino acid interchange in a protein e A;Reference number: S26343
A;Reference number: S26343
A;Restud: prellminary
A;Molecule type: mRNA
A;Residues: 1-107 <STA>
A;Coss-references: UNIPARC:UPI0000115F8A; EMBL:X59207; NID:952334; PIDN:CAA41917.1; PIL C;Superfamily: immunoglobulin immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-93/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: C01937, A01937
E;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
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     Score 40; DB 2; Length 111;
Pred. No. 1.5;
0; Mismatches 1; Indels
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Pred. No. 1.5;
0; Mismatches 1; Indels
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        80.0%;
88.9%;
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Best Local Similarity 88.9.
Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                              93 QQSNEDPYT 101
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75 QQSNEDP 81

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A;Cross-references: UNIPARC:UP1000011655C; EMBL:225454; NID:g407842; PIDN:CAA80941.1; PI

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anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 109) - mouse ('Species: Mus musculus (house mouse)
C'Species: Mus musculus (house mouse)
C'Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C'Accession: D45/22
I Virol. 67, 489-496, 1993
A'Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hy A'Reference number: A45722; MUID:93100833; PMID:7677958
A'Accession: D45/22
A'Status: preliminary; not compared with conceptual translation
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Mreaidues: 1-652 < FADJ.
A; Reaidues: 1-652 < FADJ.
A; Cross-references: UNIPROT: P24482; UNIPARC: UP10000052F0B; EMBL: U25842; NID: 9786312; PI:
A; Araki, H.; Hamatake, R.K.; Johnston, L.H.; Sugino, A.
R; Araki, H.; Hamatake, R.K.; Johnston, L.H.; Sugino, A.
A; Araki, H.; Hamatake, R.K.; Johnston, L.H.; Sugino, A.
A; Aritle: DPB2, the gene encoding DNA polymerase II subunit B, is required for chromosom.
A; Reference number: A39698; MUID: 91271241; PMID: 2052544
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A;Residues: 'MELEAS',1-460,'Y',462-523,'R',525-567,'F',569-586,'Q',588-646,'I',648-692
A;Cross-references: UNIPARC:UP100001691DE; GB:M61710; NID:g171411; PIDN:AAA34576.1; PID
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NiAlternate names: DNA polymerase epsilon chain B; protein P9705.7; protein YPR175w
C;Species: Saccharomyces cerevisiae
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
C;Accession: S59833; A39698
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Keywords: DNA binding; heteropentamer; nucleotidyltransferase; nucleus
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A;Croses-references: UNIPARC;UP10000176D43
A;Note: sequence extracted from NCB1 backbone (NCB1P:120592)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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A; Description: The sequence of S. cerevisiae cosmid 9705.
A; Reference number: S59829
A; Accession: S59833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38; DB 2;
Pred. No. 3.7;
1; Mismatches
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Pred. No. 41;
2; Mismatches
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A;Cross-references: SGD:S0006379; MIPS:YPR175w
A;Map position: 16R
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F;16-94/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Matches 6; Conservative
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425 QKLNDDPPT 433
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Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispate: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
Cisate: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
Cisatesion: Bol937; Aol937
Riveigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A; Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A; Reference number: A93204; MUID: 79073152; PMID: 103003
A; Accession: Bol937
A; Accession: Bol937
A; Residues: 1-111 *WED:
A; Residues: 1-111 *WED:
A; Cross-references: UNIPPROT: PO1669; UNIPARC: UPI000002A104
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as 18A and 19M, the subunits associate into la C; Superfamily: immunoglobulin homology vimhology vimhology immunoglobulin homology vimhology vim
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G/Species: Mus musculus (house mouse)

C/Species: Musculus (house mouse)

R/Mo, J.A.; Bona, C.A.; Holmdahl, R.

Eur. J. Immunol. 23, 2503-2510, 1993

A/Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
A/Reference number: S42176; MulD:94009207; PMID:7691608

A/Reference prolimary

A/Rolecule type: DNA

A/Rol
A,Note: V-kappa-21E, anti-collagen
C,Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
Aain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>
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Pred. No. 2.4;
0; Mismatches
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Pred. No. 2.4;
0; Mismatches
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Similarity 88.9%;
8; Conservative (
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Best Local Similarity
Matches 8; Conserv
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RESULT 18 KVMSM6

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Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. Guss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C. Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q18518; UNIPARC:UPI000008034A; EMBL:Z50027; PIDN:CAA90332.1; A;Experimental source: clone C39B10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:082263; UNIPARC:UP1000017A722; GB:AE002093; NID:93738308; Pl
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A;Status: preliminary
A;Molecule Firm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: X
A;Introns: 17/2; 70/3; 107/2; 156/2; 172/1; 226/1; 269/1; 287/3; 310/1; 351/1
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                                                                                                                                                                                                                      hypothetical protein C39B10.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19840
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A;Molecule type: DNA
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Pred. No. 46;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, July 1995
A;Reference number: Z19186
A;Accession: T19840
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                                                                                     113 QQNNEDPWT 121
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Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
Matches 6, Conserv
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A;Map position: 2
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Consequence of the precursor vegicus (WG), AR22, PC9245, PC4050) - mouse Consequence to the precursor vegicus (WG), AR22, PC9245, PC4050) - mouse Checkers, 19074-1922 sequence registon 02-Mys-1922 sequence registon 02-Mys-1923 sequence registon 02-Mys-1923 sequence registon 02-Mys-1923 sequence registon 02-Mys-1923 sequence vegicus (WG), PC92-1923 sequence registon 02-Mys-1923 sequence vegicus (WG), PC92-1923 sequence vegicus
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Pred. No. 11;
1; Mismatches 1; Indels
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77.8%;
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Best Local Similarity 77.8
Matches 7; Conservative
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Gaps

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Gaps

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Ig kappa chain V region (1G3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C;Accession: A33601
R;Goshorn, S.C.; Retzel, B.; Jemmerson, R.
Biol. Chem. 266, 2134-2142, 1991
A;Title: Common structural features among monoclonal antibodies binding the same antiger A;Reference number: A38601; MUID:91115823; PMID:1703527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-93 <GOS>
A;Residues: 1-93 <GOS>
A;Zross-references: UNIPARC:UP10000115175; GB:M57978; NID:g196402; PIDN:AAA63359.1; PID C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Superfamily: immunoglobulin cy.Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig light chain V region (clone 202.38m) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1079
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
A;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
A;Tille: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
A;Reference number: PH9971; MUID:92381444; PMID:1512540
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C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S19972
R;Waissenhorn, W_; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
R;Maissenhorn, W_; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
A;Description: Structural characterization of CD4 mAb.
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A;Cross-references: UNIPARC:UP100001767CE
A;Cross-references: UNIPARC:UP100001767CE
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-94/Domain: immunoglobulin homology <!MM>
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Pred. No. 11;
0; Mismatches
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Matches 7; Conservative
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                    QSNEDPLT 54
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A;Molecule type: mRNA
A;Residues: 1-112 <WEI>
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                    47
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Dev. Biol. 142, 1-12, 1990
A;Title: Multiple proteins are produced from the dec-1 eggshell gene in Drosophila by all A;Reference number: A44766; MUID:9103253; PMID:1699826
A;Accession: A44766
A;Status: preliminary
A;Rolecule type: mRNA
A;Residues: 1-1123 «WAR>
A;Cross-references: UNIPROT:P18169; UNIPARC:UPI0000128F37; GB:M35887; NID:g157181; PID:g
A;Genetics: FlyBase:dec-1
A;Cross-references: FlyBase:FBgn0000427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: C44766
R; Waring, G.L.; Hawley, R.J.; Schoenfeld, T.
Dev. Biol. 142, 1-12, 199
A; Title: Multiple proteins are produced from the dec-1 eggshell gene in Drosophila by all A; Reference number: A44766; MUD:91032553; PMID:1699826
A; Accession: C44766
A; Accession: C47766
A; Residues: preliminary
A; Molecule type: mRNA
A; Residues: 1-1589 cWAR>
A; Residues: 1-1589 cWAR>
A; Cross-references: UNIPARC:UP1000017BE86; GB:M35889; NID:g157185; PID:g157186
C; Genetics:
A; Cross-references: FlyBase:FBgn0000427
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CiDate: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
CiDate: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
CiAccession: B38601 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
CiAccession: B38601 #sequence_revision R.
J. Biol: Chem. 2566 2114-2142, 1991
A.Atlitle: Common structural features among monoclonal antibodies binding the same antigen A.Reference number: A38601; MUID:91115823; PMID:1703527
A.Accession: B38601
A.Accession: B38601
A.Accession: B38601
A.Residues: 1-65 -GOS>
A.Residues: 1-65 -GOS>
A.Residues: 1-65 -GOS>
CiSuperfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  defective chorion-1 fc177 protein precursor - fruit fly (Drosophila melanogaster)
C,Species: Drosophila melanogaster
C,Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 24-Sep-1998
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Pred. No. 1.1e+02;
2; Mismatches 1; Indels
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Pred. No. 7.7;
0; Mismatches 1; Indels
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Pred. No. 1.6e+02;
2; Mismatches 1;
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Best Local Similarity 66.7%;
Matches 6; Conservative 2
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Best Local Similarity 87.5
Matches 7; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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CjAccession: B84668
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Kaul, S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: B84668
A;Accession: B94668
A;Accession: L584 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-586 «MIL»
A;Residues: 1-586 «MIL»
A;Cross-references: UNIRROT:P90788; UNIPARC:UPI00007FDC1; EMBL:Z73906; PIDN:CAA98115.1;
A;Experimental source: clone D2030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Residues: 1.597 <WIL>
A,FRESIDUES: 1.557 <WIL>
A,CTOSS-references: UNIPROT:062338; UNIPARC:UPI0000164002; EMBL:281106; PIDN:CAB03223.1;
A,Experimental source: clone R06C1
                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: UNIPROT: Q9SLHO; UNIPARC: UP1000000BFC4; GB: AE002093; NID: 93885335; PI
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20353
R;Wilkinson, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C'Species: Caenorhabditis elegans
C'Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
C'Accession: T23961
R'Kershaw, J.
Submitted to the EMBL Data Library, October 1996
A'Reference number: Z19824
A'Reference T23961
                            ethylene-insensitive3-like1 (EIL1) [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein D2030.2 - Caenorhabditis elegans
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A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, June 1996 A;Reference number: Z19261 A;Accession: T20353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Introns: 27/2; 90/1; 224/3; 474/3; 553/2
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Best Local Similarity
Matches 6; Conserv
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A;Gene: CESP:D2030.2
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A;Map position: 2
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N;Alernate names: protein F344.140
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 31-Dec-2004
C;Accession: T45859
R;Barques, M; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; May submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23007
A;Reference number: Z3007
A;Retaus: preliminary
A;Molecule type: DNA
A;Retaus: preliminary
A;Molecule type: UNA
A;Retaus: preliminary
A;Molecule cype: UNIPROT:Q9SN12; UNIPARC:UPI00000033C92; EMBL:AL132978
A;Experimental source: cultivar Columbia; BAC clone F3A4
C;Genetics:
A;Mote: F3A4.140
C;Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 28
S71285
myb-related protein, 33.2K - Arabidopsis thaliana
c; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 31-Dec-2004
C; Accession: S71285
R; Kirik, V.; Baumlein, H.
submitted to the EMBL Data Library, September 1995
A; Description: Characterization of two cDNAs encoding MYB-related proteins in Arabidopsi
A; Recession: S71285
A; Molecule type: mRNA
A; Residues: 1-304 < KIR>
A; Accession: S7285
A; Molecule type: mRNA
A; Residues: UNIPROT: (039155; UNIPARC: UPI000009D1EE; EMBL: Z54137; NID: G1263096; PI
C; Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
C; Keywords: DNA binding; duplication
F; 1-52, Domain: myb DNA-binding repeat homology < MYBD.
F; 1-32, Domain: myb DNA-binding repeat homology < MYBD.
F; 1-32, Domain: myb DNA-binding repeat homology < MYBD.
A;Cross-references: UNIPARC:UPI0000116032; EMBL:X65094; NID:g52290; PIDN:CAA46222.1; PID (Subgerfamally: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin P:16-94/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 301; 40;
                                                                                                                                           2; Length 112;
                                                                                                                                                                                                  1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 2
Pred. No. 40;
1; Mismatches
                                                                                                                                      Score 35; DB Pred. No. 14; 1; Mismatches
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Best Local Similarity 85./1
Loca 6; Conservative
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Best Local Similarity 85.
                                                                                                                                   Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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197 SSEDPPT 203
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197 SSEDPPT 203
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Length 584;

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Length 586;

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Science 251, 936-939, 1991
A;Title: A heparin-binding growth factor secreted by macrophage-like cells that is relat A;Reference number: A38432; MUID:91157008; PMID:1840698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-208 <HIG.>
A;Residues: 1-208 <HIG.>
A;Cross-references: UNIPROT: 099075; UNIPARC: UPI0000035E3F; GB: M60278; NID: g183866; PIDN
R;Higashiyama, S:; Lau, K.; Besner, G.E.; Abraham, J.A.; Klagsbrun, M.
B. Balol. Chem. 267, 6205-6212, 1992
A;Title: Structure of heparin-binding EGP-like growth factor. Multiple forms, primary st
A;Reference number: A37300; MUID: 92210596; PMID: 1556128
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R; Abraham, J.A.; Damm, D.; Bajardi, A.; Miller, J.; Klagsbrun, M.; Ezekowitz, R.A.B.
Biochem. Biophya. Res. Commun. 190, 125-133, 1993
A; Title: Heparin-binding EGF-like growth factor: Characterization of rat and mouse cDNA A; Reference number: JC1409; MUID:93135756; PMID:7678488
A; Accession: JC1409
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                                                                                                                                                                                                                                         heparin-binding EGF-like growth factor precursor - human
C;Species: Homo sapions (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A38432, A37300
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Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
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A,Map postition: 5G23-5G23
C,Superfamily: heparin-binding EGF-like growth factor; EGF homology
C,Keywords: heparin binding; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34; DB 1; Length 208; Pred. No. 42; 0; Mismatches 1; Indels
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A,Residues: 63-74,'X',76-84,'X',86-148 <HI2>
A,Cross-references: UNIPARC:UP10000173352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;108-143/Domain: EGF homology <EGF>
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                                                                       273
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Best Local Similarity
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A; Residues: 1-208 < ABR>
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267 EOSNEDP
   1 QQSNEDP
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A; Residues: 1-1522 < PRM>
A; Cross-references: UNIPARC: UPI000005328B; EMBL: Z69381; NID:g1183970; PID:e221807; PID:g
R; Pandolfo, D.; de Antoni, A.; Lanfranchi, G.; Valle, G.
A; D1-11076, 1996
A; Title: The DNA sequence of cosmid 14-5 from chromosome XIV reveals 21 open reading fra
A; Reference number: S72073; MUID:97051596; PMID:8896273
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A;Molecule type: DNA
A;Residues: 1-1592 <PAF>
A;Cross-references: UNIPARC:UPI000005328B; EMBL:Z69381; NID:g1183970; PIDN:CAA93356.1;
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
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hypothetical protein YNL242w - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                     Score 35; DB 2; Length 597;
Pred. No. 85;
1; Mismatches 2; Indels
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                                                             A;Map position: 1
A;Introns: 8/2; 75/2; 141/1; 180/2; 230/2; 288/2; 405/3
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Pred. No. 2.5e+02;
1; Mismatches 0;
                                                                                                                                                                     70.0%; Score 35; 66.7%; Pred. No.
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Best Local Similarity 85.7%;
Matches 6; Conservative
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A;Cross-references: SGD:S0005186
A;Map position: 14L
                                                                                                                                                                                                                                         6; Conservative
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263 QEDNEDQPT 271
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Best Local Similarity
Matches 6; Conserv
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C,Genetics:
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C;Accession: C85440
R;Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: C85440
A;Accession: C85440
A;Anolecule type: DNA
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A; Residues: 1-497 < SAM>
A; Residues: 1-497 < SAM>
A; Cross-references: UNIPROT: P13285; UNIPARC: UP100000CDBC; GB: M24212; NID: G522186; PIDN: A; Accession: B30178
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 120-497 < SA2>
A; Cross-references: UNIPARC: UP1000061589
B; Laux, G.; Perricaudet, M.; Farrell, P.J.
B; Laux, G.; Perricaudet, M.; Farrell, P.J.
B; MBD J. 7, 769-774, 1988
A; Title: A spliced Epstein-Barr virus gene expressed in immortalized lymphocytes is crest A; Reference number: $00392; MUID:88283646; PMID:2840285
A; A; Accession: $00392.
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A;Residues: 1-497 <LAU>
A;Cross-references: UNIPARC:UPI00000CDBC; EMBL:Y00835; NID:959183; PIDN:CAA68762.1; PID.
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Cibate: 31-Dec-1989 #sequence revision 31-Dec-1989 #text_change 09-Jul-2004
Cibate: 31-Dec-1989 #sequence revision 31-Dec-1989 #text_change 09-Jul-2004
Cibate: 31-06-1989 #source for the first f
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C,Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
                                                                            myb-related protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2004
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F;120-497/Product: membrane protein LMP-2B #status predicted
F;120-1497/Product: membrane #status predicted <TMA>
F;120-166/Domain: transmembrane #status predicted <TMB>
F;178-198/Domain: transmembrane #status predicted <TMC>
F;208-235/Domain: transmembrane #status predicted <TMC>
F;242-259/Domain: transmembrane #status predicted <TME>
F;242-289/Domain: transmembrane #status predicted <TME>
F;267-288/Domain: transmembrane #status predicted <TMF>
F;300-316/Domain: transmembrane #status predicted <TMG>
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Pred. No. 67;
0; Mismatches
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N;Contains: membrane protein LMP-2B
C;Species: human herpesvirus 4, Epstein-Barr virus
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Best Local Similarity 85.7%;
Matches 6; Conservative
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RESULT 36
T151678
myb-related transcription factor MYB73 [imported] - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 31-Dec-2004
C;Accession: T51678
R;Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.; J. Paz-Ares, J.; Weishaar, B.
Plant J. 16, 263-276, 1998
A;Title: Towards functional characterisation of the members of the R2R3-MYB gene from Az A;Reference number: Z14349; MUID:9839469; PMID:9839469
A;Accession: T51678
A;Accessi
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A;Cross-references: UNIPROT:09SBF6; UNIPARC:UPI0000A4D20; EMBL:AF062906; PIDN:AAC83628.
A;Experimental source: cultivar Columbia
C;Genetics:
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A;Map position: IV
C;Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
C;Keywords: transcription factor
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Pred. No. 55;
0; Mismatches
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Similarity 85.7%;
6; Conservative
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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137 SGEDPPT 143

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A;Status: translated from GB/EMBL/DDBJ
A;McJecule type: DNA
A;Rcsidues: 1-66 aROU7
A;Cross-references: UNIPROT:O80971; UNIPARC:UPI000009E30D; EMBL:AC004705; NID:g3252804;
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPARC:UP1000009530D; GB:AE002093; NID:g3252808; PIDN:AAC24178.1; (
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: F87713
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Gwinn, M.L.; Haft, D.H.; Kolor
N, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Reference number: A87249; MUID:21173698; PMID:11259647
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A;Cross-references: UNIPROT:Q9A222; UNIPARC:UPI0000C7BA9; GB:AE005673; NID:g13425516; E
C;Genetics:
A;Gene: CC3744
                                                                                   hyporhetical protein At2g14810 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein F26C24.5
Species Arabidopsis thaliana (mouse-ear cress)
C;Becies Arabidopsis thaliana (mouse-ear cress)
C;Becies 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02595; G84521
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, Bubmitted to the EMBL Data Library, June 1998
A;Becription: Arabidopsis thaliana chromosome II BAC F26C24 genomic sequence.
A;Reference number: 214680
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Pred. No. 52;
1; Mismatches
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83.3%;
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Best Local Similarity 71...
Set Local Similarity 71...
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Best Local Similarity 83.3
Matches 5; Conservative
4 NEDPPT 9
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KSNQDPP 39
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C; Ac; Regan, T.; Hudson-Taylor, D.; Miller, L.H.; Baruch
MOL. Biochem. Parasitol. 97, 133-148, 1998
A; Title: Analysis of adhesive domains from the A4VAR Plasmodium falciparum erythrocyte m
A; Reference number: Z20486; MUID:99094502; PMID:9879893
A; Reference number: Z20486; MUID:99094502; PMID:9879893
A; Residues: 1-3026 <SMI>A; Residues: 1-3026 <SMI>A; Residues: 1-3026 <SMI>A; Residues: 1-3026 <SMI>A; Residues: Varences: UNIPROT:Q26030; UNIPARC:UPI000007B327; EMBL:L42244; NID:g3540144; PI
C; Genetics: Varence varences: Varence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disported imported - Mycoplasma pulmonis (strain UAB CTIP)
C;Species Mycoplasma pulmonis
C;Species Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: E90591
C;Accession
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                                F)355-373/Domain: transmembrane #status predicted <TWI>
P)392-411/Domain: transmembrane #status predicted <TWJ>
P;419-443/Domain: transmembrane #status predicted <TWK>
P;410-443/Domain: transmembrane #status predicted <TWK>
P;450-470/Domain: transmembrane #status predicted <TWL>
P;27,320,417/Binding site: carbohydrate (Asn) (covalent) #status predicted
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         predicted
F;321-339/Domain: transmembrane #status P;355-373/Domain: transmembrane #status
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Matches 6; Conservative
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50 RESNEEPP 57
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A;Genetic code: SGC3
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Best Local S
Matches 5
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RESULT JQ2347

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C;Accession: $22520
R;Shinozaki, K.; Vamaguchi-Shinozaki, K.; Urao, T.; Koizumi, M.
Balat Mol. Biol. 19, 493-499, 1992
A;Title: Nucleotide sequence of a gene from Arabidopsis thaliana encoding a myb homologu
A;Reference number: $22520; MUID:92322982; PMID:1623193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
XResidues 1-39 xSHI.
A;Cross-references: UNIRROT:042575; UNIPARC:UPI00009F710; EMBL:D10936; NID:g217858; PIC
A;Experimental source: strain Columbia
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R;Shen, M.; Kawamoto, T.; Yan, W.; Nakamasu, K.; Tamagami, M.; Koyano, Y.; Noshiro, M.; Rishen, M.; Kawamoto, T.; Yan, W.; Nakamasu, K.; Tamagami, M.; Koyano, Y.; Noshiro, M.; Asiochem. Biophys. Res. Commun. 236, 294-298, 1997
A;Title: Molecular characterization of the novel basic helix-loop-helix protein DEC1 exp. A;Reference number: JC5547; MUID:97382424; PMID:9240428
A;Accession: JC5547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              carboxy-terminal processing proteinase homolog lmo1851 [imported] - Listeria monocytogen
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: ACI306
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
R;Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
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AjGene: mybl
AjGene: mybl
Ajntrons: 112/1
C;Superfamily: Arabidopsis myb-related protein 1; myb DNA-binding repeat homology
C;Superfamily: Arabidopsis myb-related protein 1; myb DNA-binding; cyreywords: DNA binding; duplication; nucleus; transcription regulation
F;50-101/Domain: myb DNA-binding repeat homology <WYB1>
F;102-152/Domain: myb DNA-binding repeat homology
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
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C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
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Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 1;
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Best Local Similarity 55.0°
Post Local Si Conservative
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232 RQDDKDPPT 240
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279 KQESEEPPT 287
                                                                                                       249 OGNEDPAT 256
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                  2 QSNEDPPT
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hypothetical 23.6K protein - turkey herpesvirus
NyAlternate names: ORF2 protein
C;Species turkey herpesvirus
C;Species turkey herpesvirus
C;Species turkey herpesvirus
C;Species turkey herpesvirus
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
C;Accession: JQ2347
A;Zelnk, V; Datteil, R; Audonnet, J.C.; Smith, G.D.; Riviere, M.; Pastorek, J.; Ross, J. Gen. Virol. 74, 2151-2162, 1993
A;Title: The complete sequence and gene organization of the short unique region of herpe A;Reference number: JQ2346; MUD:94014999; PMID:8409940
A;Reference number: JQ2346; MUD:94014999; PMID:8409940
A;Residues: 1-209 <ZEL>
A;Reperimental source: strain FOL26
C;Superfamily: Marek's disease virus minor virion protein
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RING-H2 finger protein RHF2a [imported] - Arabidopsis thaliana
RING-H2 finger protein RHF2a [imported] - Arabidopsis thaliana
RING-H2 finger protein RHF2a [imported] - Arabidopsis thaliana
RING-H2 (Species Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: T51854
R;Jensen, R.B; Jensen, K.L.; Jespersen, H.M.; Skriver, K.
FEBS Lett. 436, 281-7, 1998
A;Fitle: Widespread occurrence of a highly conserved RING-H2 zinc finger motif in the mc
A;Reference number: Z13771; MUID:98452956; PMID:9781696
A;Accession: T51854
A;Accession: T51854
A;Accession: T51854
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: mRNA
A;Residues: 1-375 <JEN>
A;Residues: 1-375 <JEN>
A;Cross-references: UNIPROT:Q9Z742; UNIPARC:UP100000AC55E; EMBL:AF079182; PIDN:AAC69856.
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T45301
T45301
Domoserine o-acetyltransferase [imported] - Mycobacterium leprae
C; Species Mycobacterium leprae
C; Species Mycobacterium leprae
C; Accession: T45301
C; Accession: T45301
C; Accession: T45301
A; Reference number: Z22864
A; Residues: Jasa cPAR>
A; Residues: Jasa cPAR>
A; Residues: L382 cPAR>
A; Rasidues: 
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112 QNNEEPP 118
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Search completed: February 23, 2006, 09:51:20 Job time : 28.7385 secs
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A;Map position: 3
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R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker. J. Dusniquez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karet, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Recession: Aci678
A;Tile: Comparative genomics of Listeria species.
A;Accession: Aci678
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-496 cGLA>
A;Cross-references: UNIPROT: Q92AP7; UNIPARC:UP10000CC6F5; GB:AL592022; PIDN:CAC97195.1;
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin1965
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acidic protein - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 02-Nov-2001

C;Accession: D8853.

R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog

A;Reference number: A75000; MUID:99069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C elegans/ and www_sanger.ac.uk/Projects/C_ele

A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A;Status: preliminary

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-705 <STO>

A;Cross-references: UNIPARC:UP1000017A083; GB:chr_III; PIDN:AAA27898.1; PID:g156195; GSF
                   A Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.Title: Comparative genomics of Listeria species.
A.Reference number: AB1077; MUID:21537279; PMID:11679669
A.Accession: AC1306
A.Accession: AC1306
A.Status: preliminary
A.Status: preliminary
A.References: UNIPROT:Q87649; UNIPARC:UP1000005545E; GB:NC_003210; PIDN:CAC99929.1
A.Cross-references: UNIPROT:Q87649; UNIPARC:UP1000005545E; GB:NC_003210; PIDN:CAC99929.1
A.Staperimental source: strain EGD-e
C;Genetics:
A;Gene: lmo1851
C;Superfamily: carboxyl-terminal processing proteinase
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Pred. No. 1.7e+02;
1; Mismatches 1
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Best Local Similarity 75.0
Matches 6; Conservative
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Science 294, 849-852, 2001
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Best Local Similarity
Matches 6; Conserv
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Length 705;
                                                     Score 33; DB 2; Length 705
Pred. No. 2.4e+02;
1; Mismatches 1; Indels
                                                       66.08;
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Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                        290 EQNEDPP 296
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Gaps

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Q5v2w7 haloarcula Q5icn4 cytophaga j Q7py08 anopheles g Q5sn12 arabidopsis Q39155 arabidopsis		gloe caen caen esch	mus muscul mus muscul caenorhabd	Qysinu arabidopsis P90788 caenorhabdi O4s280 tetraodon n	Q6g165 xenopus tro Q6p8i1 mus musculu	Q5r151 mus musculu Q7uv96 rhodopirell	Q4X1US aspergilius Q60d35 solanum dem Q7qti3 giardia lam P53855 saccharomyc	Q61zq1 caenorhabdi Q75jh8 dictyosteli Q9f293 yersinia Q7x310 uncultured	human human human	Q66552 numan nerpe Q66553 human herpe Q66554 human herpe	human	human	human	human	human	Q66566 human herpe	human	human	human	Q66573 human herpe Q66574 human herpe	Q6rkn8 human herpe Q6rkn0 human herpe	O6rkp2 human herpe		M 4	aegilops human her	Q4xw74 plasmodium Q99075 homo sapien	Q06186 mus musculu Q06175 rattus norv	- F	burkhol
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GenCore version 5. Copyright (c) 1993 - 2006 Bi protein search, using sw model	February 23, 2006, 09:29:53 ; S (wit 81.8	US-10-723-872-20 50 1 QQSNEDPPT 9	BLOSUM62 Gapop 10.0 , Gapext 0.5	2166443 segs, 705528306 residues	hits sa	length: 0 length: 2000000000	<pre>## Minimum Match 0% ## Maximum Match 100% Listing first 1000 summaries</pre>	<pre>UniProt_05.80:* 1: uniprot_sprot:* 2: uniprot_trembl:*</pre>	is the number of results predicater than or equal to the score	analysis of the total		sh Length DB	82.0 655 2 Q4H3K9_CIOIN 80.0 111 1 KV3H MOUSE 80.0 111 1 KV3L MOUSE	0.01111	0 111 1	380	0 511 2	376 2	1111	692 1	.0 101 2 .0 131 1	.0 428 2	.0 443 2 Q72LZ6	0 443 2	.0 562 2 Q6CFIS	.0 1590 1	.0 107	0.0 147 2	10
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10.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.0	10.00   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.000	074c 08in 054r 071y	08y6 092a 0598	04 P7 08 WX	07zt 08x0 09y7	05tv	0941 0846	P342	051e 07t2	075p 05f3	04x0 04i2	075p 0780	0481 06£1	05ra 0488	Q5b1	09d4 07n6	063h	P354 0406	08iy 091y	06nv 06cv	07mi 0480	09br 0150	05r7 0529	094i 06ph	052f 08db	09v8	0817	0943	06pn	0/22 08h1	08h1	08d 08t4
10.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.0	10.00   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.000																															
10.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.0	10.00   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.0000   20.000																															
10.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.0	10.00   20.000000000000000000000000000000	PROME DROME DVIN	ISMO	DRYSA JSTMA TUMAN	SRARE VEUCR VEUCR	MEUCR	ROME	SEL	SNTHI	SRYLA SHICK	SIBZE	ORYLA VEUCR	TETNG	PONPY	SMENI	HOLL	NOGA	FEL	HUMAN	AOUSE CLULA	/IBVY FETNG	TUMAN	PONPY	ORYSA 4OUSE	WAGGR	OROME	PLAF7	ASHGO	MOUSE	HARE TELE	TELE DICDI	SYNEL
10.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.0	10.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.00   20.0	CFO E	7.89 I 7649 I 7AF7 I 3SJ9 C	0.003 1.087 1.107	77C0 77A8 7	VF2	MX1 I	A CAI	EG6 1	3W8_C	1210_C	30F3_C	1171 187_0	VAI4_E 3813_7	3145 1ZF1_	1649 E	35 F3 7	IR AND	Y63_F	TV83	MI14 7	3R70 1	27X2 195 RE	1152 (PHM6 N	FA6 P	/SPO_I	1004	7JF9 1 52F6 7	NCO N	12.61 11.P4	1107	74Y7
10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.0	10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.0																															
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Column   C		
11.0   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.000000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.000000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.000000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.000000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.000000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.000000   0.000000   0.000000   0.000000   0.000000   0.000000   0.000000   0.000000   0.000000   0.000000   0.00000000	helicoverpa helicoverpa helicoverpa helicoverpa helicoverpa homo sapten dictyosteli ustilago ma beptatretus oryza sativ neurospora leptospira leptospira leptospira rattus norv mus musculu yersinia ps yersinia gs drosophila horococcus rhodococcus	
115   2 OPECE   20050   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   20150   2015	07711y8 0894026 0894026 0894026 0894026 0894026 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403 089403	P46627 P30553 P30552 P56481 Q8bkf6
115   2 OPECE WINDS   2004   2001   2002   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004   2004	CCC CCC CCC CCCC CCCC CCCCC CCCCCCCCCC	SSB 33B
115   2   076016   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014   076014	07 7 1 1 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2	GASR_RABIT GASR_RAT GASR_CANP GASR_MOUSE QBBKF6_MOU
155   2   078162   078051   078018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018   079018		
1.55   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00   2.00	000000000000000000000000000000000000000	
11.0   2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2   0011/2	2222 222 222 222 222 222 222 222 222 2	•
15.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0   10.0		
15.   1.55   2.   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.00012   0.0001	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	685 685 687 688
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Q8mqw5 drosophila 016587 caenorhabdi Q95r60 drosophila Q95rn3 drosophila Q81ku3 plasmodium 056301 human herpe	Q86af2 dictyosteli Q6pdg5 mus musculu Q5a3i9 candida alb Q12276 saccharomyc	dictyost drosophi mus musc	drosophila drosophila drosophila	drosophila rice tungr	U/qoks anopheles g Q8t6g6 dictyosteli Q5b1r6 aspergillus	Q6cun4 kluyveromyc Q4qik1 leishmania O7toil rattus norv	Q9zvf0 arabidopsis Q8im56 plasmodium	Q55ez4 dictyosteli Q9vai2 drosophila	Q6qu66 drosophila Q8is13 dictyosteli		Q6duh4 rattus norv Q5kmx9 cryptococu	dictyoste mus muscu			mycobacte entamoeba	O60293 nomo sapien Q7s784 neurospora O9nhx6 drosophila	drosophil drosophil	drosophila	Q4wu4/ aspergiilus Q86bh2 drosophila O41wx4 burkholderi	Q6gyp7 mus musculu Q6gyq0 homo sapien	Q8mxl2 leishmania Q9u9s7 dictyosteli	Q8ievl plasmodium Q4q795 leishmania	Ö96296 plasmodium Q8i495 plasmodium	Q8i515 plasmodium Q9w2u7 drosophila	Q484K5 tetraodon n Q5t1r5 homo sapien	idae Ollon
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Q54in8 dictyosteli         908           Q87lw2 vibrio para         909           Q4ibx2 gibberella         910           Q74h1 anopheles         911           Q51ux6 magnaporthe         913           Q60h58 brachydanio         913	drosophila plasmodium homo sapien homo sapien	homo sapien schizosacch oryza sativ hrachwianio	i z z c	Kluyveromyc candida alb	baccharomyc haemophilus candida alb	xenopus lae homo sapien mus musculu	dictyosteli mus musculu	oryza sativ arabidopsis	nocardia fa brachydanio brachydanio	caenorhabdi anopheles g	saccharomyc homo sapien	rickettsia 94 brachydanio 94	tetraodon n mus musculu corynebacte	leishmania aspergillus	96.5	plasmodium dictyosteli brachydanio	mus musculu ustilago ma	drosophila drosophila	nomo sapien entamoeba h	neurospora tetraodon n	dictyosteli rattus norv	mus musculu mus musculu	dictyosteli 97 drosophila 97	ואסי	ustilago ma drosophila	asimya goss
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21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 04, Last annotation update)
19 kappa chain V-III region CBPC 101.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                          PROTEIN SEQUENCE (FEEC 111).

MEDDINEA 9012520; PubMed-29744;

MCKean D.J., Bell M., Potter M.;

"Mechanisms of antibody diversity; multiple genes encode structurally related mouse kappa variable regions."

Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).

-I- MISCELLANEOUS: The PC 3741 and TEPC 111 sequences are identical.
                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                    PROTEIN SEQUENCE (PC 3741).
MEDLINE=99073152; PubMed=10303;
MEDLINE=99073152; PubMed=10303;
Weigert M., Gatmaiten L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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Complementarity-determining-1.
Framework-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A93204; KVMS37.

HSSP, P01665; 1QNZ.

Ensembl; SNSWGS000000006064; Mus musculus.

InterPro; INR007110; Ig-like.

InterPro; IPR0031596; Ig-v.

SMART; SM0406; IGv; I.

DROSITE; PS50815; IG_LIKE; I.

Direct protein sequencing; Immunoglobulin domain;
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Pred. No. 12;
0; Mismatches
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
18 kappa chain V-III region PC 3741/TEPC 111.
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                  PROTEIN SEQUENCE (TEPC 111)
                                                                                                                                                                                                                                                                                                          Nature 276:785-790(1978).
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                                                                                                                                                              NCBI_TaxID=10090;
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ID KV31_MOUSE

AC PO1664;

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                                                      Q4wn65 aspergillus
Q8wxq6 homo sapien
Q96p79 homo sapien
Q96p79 homo sapien
Q8lkq plasmodium
Q4rxm3 tetraodon n
Q1186 epstein-bar
Q77744 human herpe
Q6nvd0 mus musculu
G5szk8 homo sapien
Q6-216 yarrowia li
Q91pp5 r genome po
P25464 cephalospor
Q47LC8 tetraodon n
Q41C8 tetraodon n
Q41C8 tetraodon n
                                          aspergillus
aspergillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ciona intestinalis.
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
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Imai K.S., Hino K., Yagi K., Satoh N., Satou Y.;
"Genomewide surveys of developmentally relevant genes in Ciona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomewide surveys of developmentally relevant genes in Ciona
Q5t1r4
Q9hc17
Q5bb54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Satou Y.;
"Expressed genes in Ciona intestinalis.";
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AB210413; BAE06418.1; -; mRNA.
SROHENCE 655 AA; 72268 MW; 99E9DDB73E0D61B7 CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Transcription factor protein.
Name=Ci-ets/pointed1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=12736827; DOI=10.1007/800427-003-0330-z; Satou Y., Satoh N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           655 AA
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0; Mismatches
                                                                            QBWXQ6_HUMAN
Q96JP6_HUMAN
Q96P79_HUMAN
                                                                                                                                                            Q8IKQ6 PLAF7
Q4RXM3 TETNG
TEGU EBV
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FREM2 MOUSE
FREM2 HUMAN
                O9HCL7 HUMAN
O5BB54 EMENI
O4WN65 ASPFU
                                                                                                                                                                                                                                                                                Q8V2A4 9GAMA
Q6C2L6 YARLI
                                                                                                                                                                                                                                                                                                                                                                     Q4RLC8_TETNG
Q51X35_MAGGR
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Q4H3K9;
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nes 8; Conservative
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NCBI_TaxID=7719;
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ID KV3H MOUSE
AC P01660;
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  HSSP; P01665; 1QNZ.
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                                                                                                 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                    MEDLINE=79012520; PubMed=99744; McKean D.J., Bell M., Potter M.; McKean D.J., Bell M., Potter M.; Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions."; Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
-1- MISCELLANEOUS: This chain was isolated from a myeloma protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchoncoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=79073152; PubMed=103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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                                                                                                                                                                                                                                                                                                   Complementarity-determining-1. Framework-2.
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Framework-4.
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Pred. No. 12;
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                                                                                                                                                                                                                                                                                                                                                                                            E2B1AD98AD965962 CRC64;
                                                                                                                                                                                                                                                               Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Ig kappa chain VIII region PC 7183.
                                                                                                                                                                               HSSP, POIGES, 1QNZ.
SMR; POIGES, 10NZ.
SMR; POIGES, 1-111.
Ensembl; ENSWUSGO0000053225; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv.
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin dol
Immunoglobulin V region.
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                                                                                                                                                                                                                                                                                                                                                                                            11964 MW;
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les 8; Conservative
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P01666;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Anti-human Fc gamma receptor III 3G8 kappa light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Fragment).
Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria, Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae, Murinae, Mus.
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Bruenke J., Fischer B., Barbin K., Schreiter K., Wachter Y., Mahr K., Titgemeyer F., Niederweis M., Peipp M., Zunino S.J., Repp R., Valerius T., Fey G.H., "A recombinant bispecific single-chain Fv antibody against HLA class II and FcgammaRIII (CD16) triggers effective lysis of lymphoma
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Pred. No. 12;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11952 MW; 2058BB50CE306D31 CRC64;
SMR; P01666; 1-111.
Ensembl; ENSMUSGO0000053225; Mus musculus.
EnterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv.
PROSITE; PS50835; IG_LIKE; 1.
Picct protein sequencing; Immunoglobulin domain;
Immunoglobulin 1 23 Framework-1.
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88.9%; Pred. No. 12;
iive 0; Mismatches
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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EMBL, AX173024; AA018226.1; -; mRNA.
HSSP, P01665; 10NZ.
SWR; Q911U6; 1-111.
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KV30 MOUSE
P01667;
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  Matches
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                                                                                                                                                                                                                                                                                        MEDLINE=94009207; PubMed=7691608;
Mo J.A., Bona C.A., Holmdahl R.;
"Variable region gene selection of immunoglobulin G-expressing B cells
with specificity for a defined epitope on type II collagen.";
Eur. J. Immunol. 23:2503-2510(1993).
                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                          STRUCTURE BY NMR OF 1-111.

MEDLINE=20264305; PubMed=10801487; DOI=10.1016/S0969-2126(00)00119-2;
Tugarinov V., Zv1 A., Levy R., Hayek Y., Mateushita S., Anglister J.;
"NMR structure of an anti-gpl20 antibody complex with a V3 peptide
reveals a surface important for co-receptor binding.";
Structure 8:385-395(2000).
                                                                                                                                                                                                                   Weigert M., Garmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct_protein sequencing, Immunoglobulin domain; v region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complementarity-determining-1.
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Framework-4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7ASFCB586C306D29 CRC64;
                                                                                           21-JUL-1986 (Rel. 01, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
IIG kappa chain V-III region PC 7043.
Mus musculus (Mouse).
                                                          111 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ensembl; ENSMUSG0000053225; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Framework-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, 225444; CAA80931.1; -; mRNA.
EMBL, 225446; CAA80933.1; -; mRNA.
EMBL, 225496; CAA80935.1; -; mRNA.
EMBL, 225452; CAA80937.1; -; mRNA.
EMBL, 225452; CAA80937.1; -; mRNA.
EMBL, 225454; CAA80931.1; -; mRNA.
                                                                                                                                                                                              PROTEIN SEQUENCE.
MEDLINE=79073152; PubMed=103003;
                                                                                (Rel. 01, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12002 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z25454; CAA80941.1; -; EMBL; Z25458; CAA80945.1; -; PIR; A01937; KVMS43.
                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE OF 10-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.0%;
                                                                                                                                                                                                                                                       Nature 276:785-790(1978).
                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDB; 1QNZ; NMR; L=1-111
92 QQSNEDPYT 100
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111 AA;
                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3D-structure;
                                                                                21-JUL-1986
                                                         MOUSE
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SEQUENCE
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Best Local Similarity

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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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Gaps
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MEDLINE=79073152; PubMed=103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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Complementarity-determining-1.
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PROSITE; PSS0835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KV3Q_MOUSE STANDARD; PRT; 111 AA. P01665.

P01665.

P01667.

P01667.

P0167.

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                                                                                                                                                                                                                                                                                                                                                                                                 111 AA.
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Mismatches
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SMR; PO1665; 1-111.
SMR; PO1667; 1-111.
InterPro; IPR007110; IG-like.
InterPro; IPR003596; IG-V.
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8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                   93 QOSNEDPPT 101
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8; Conserv
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ID KV3Q_M
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Bukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
NCBI_TaxID=283643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi, Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
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Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D., Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E., Bosdet I.E., Brent M.R., Chiu R., Dooring T.L., Donlin M.J., D.'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J., Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I., Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FTRAIN=B-3501A,
Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
Wickes B.L., Fu J., Davis R.W.;
"Cryptococcus neoformans serotype D sequencing.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
--- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=JEC21;
Loftus B., Amedeo P., Roncaglia P., Vamathevan J., Utterback
Van Aken S., Fraser C.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB 2; Length 511;
Pred. No. 1.1e+02;
0; Mismatches 1; Indels
                        Indels
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Hypothetical protein.
SEQUENCE 511 AA; 56762 MW; 21468107971233BD CRC64;
                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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Last annotation update)
                          1;
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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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      ed. No. 76;
Mismatches
      Pred. No.
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13-SEP-2005 (TrEMBLrel. 31, 6
13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 78.0%;
Local Similarity 87.5%;
nes 7; Conservative
  87.5%;
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10-MAY-2005 (TrEMBLrel. 30,
10-MAY-2005 (TrEMBLrel. 30,
10-MAY-2005 (TrEMBLrel. 30,
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                        7; Conservative
                                                                                                                                                                                                                                                                                                   Hypothetical protein.
ORFNames=CNBE3830;
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                                                                                                 11 OASNEDPP 18
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NUCLEOTIDE SEQUENCE.
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    Best Local Similarity
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                                                            OOSNEDPP
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                        Matches
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QSKGF1_CR1
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                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J., Smith D., Collins M., Fosker N., Harris D., Oliver K., O'Neil S., Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.; Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.

EMBL; CT005268; CAJ08414.1; -; Genomic_DNA.
                                                                                                                                    Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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Framework-2.
Complementarity-determining-2.
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Complementarity-determining-3.
Framework-4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
3,2-trans-enoyl-CoA isomerase, mitochondrial, putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12011 MW; 6FAA345279356829 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42876 MW; 3D7DA5DC8D7B531C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 19;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                     PIR; E01937; KVMS69.
HSSP; P01665; 1QNZ.
SMR; P01669; 1-111.
Ensembl; ENSMUSGO0000053225; Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Framework-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                 MEDLINE=79073152; PubMed=103003;
                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                040636_LEIMA PRELIMINARY;
040636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 85.
                                                                                                                                                                                                Nature 276:785-790(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 OOSNEDPWT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORFNames=LmjF31.2250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QQSNEDPPT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
STRAIN=Friedlin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               380 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 AA;
                                                         NCBI_TaxID=10090
                                                                                               PROTEIN SEQUENCE
                                                                                                                                                                           diversity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON TER
SEQUENCE
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Saccharomycetales; mitosporic Saccharomycetales; Candida.
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KV3J MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARAIN-56601 / Sergiroup Icterohaemorrhagiae / Serovar lai;

MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;

Ren S.-X., Pu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,

Zhang Y.-X., Xtong H., Iu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,

Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,

Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Rang S.-Y., Ma W.,

Yoo Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,

Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,

Xu J.-G., Zhao G.-P.,
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Mathewson C.A., Mitchell T.G., Pertea M., Riggs F.R., Salzberg S.L., Scholin J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A., Shu B.B., Tenney A., Utcerback T.R., Wickes B.L., Wortman J.R., Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W., Praser C.M., Hyman R.W.;

"The genome of the basidiomycetous yeast and human pathogen Cryptococcus neoformans.";
                                                                                                                                                                                                                                                                                                                                                                                       Leptospira interrogans.
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypochetical protein MNR2.
Name-wNR2; ORFNames-Ca019.13112, Ca019.5667;
Candida albicans SCS314.
Eukaryota; Pung1; Ascomycota; Saccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Unique physiological and pathogenic features of Leptospira interrogans revealed by whole-genome sequencing."; Nature 422:888-893(2003).
                                                                                                                                                      Score 39; DB 2; Length 511; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.0%; Score 38; DB 2; Length 376; 66.7%; Pred. No. 1.2e+02;
                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE011360; AAN49060.1; -; Genomic_DNA.
GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPRO0379; Ser_estrs.
Complete proteome; Hydrolase.
SEQUENCE 376 AA; 42295 MW; 3BD6B83967FF3971 CRC64;
                                                                                                                              511 AA; 56762 MW; 21468107971233BD CRC64;
                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               797 AA.
                                                                                                   EMBL; AE017345; AAW43670.1; -; Genomic_DNA.
Complete proteome.
                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                      78.0%;
                                                                                         Science 307:1321-1324(2005).
                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
OrderedLocusNames=LA1861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OS9UQ3 CANAL PRELIMINARY;
Q59UQ3;
                                                                                                                                           Query Match
Best Local Similarity 87.5'
                                                                                                                                                                                                                                                                                              QBF526_LEPIN PRELIMINARY;
Q8F526;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |: | ||||
102 QEKNSDPPT 110
                                                                                                                                                                                                                                 229 QOFNEDPP 236
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                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Matches
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C59003 CAN
D59000 AC
D7 10-MA
D7 10-MA
D7 10-MA
DF Hypot
GN Name=
GN Name=
GN Candi
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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"Mechanisms of antibody divershity: multiple genes encode structurally
related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                              PubMed=15123810; DOI=10.1073/pnas.0401648101;
Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
Paris R.W., Scherer S.;
"The diploid genome sequence of Candida albicans.";
Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                               Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O., Roberts J., Person K., Donnelly S., Favoreto S., Tzung K.-W., Jones T., Scherer S., Agabian N.; "Annotation of the Genome of Candida albicans."; Submitted (APR-2004) to the EMBL/GenBan/DDBJ databases. EMBL; AACQ01000129; EAK94231.1; -; Genomic_DNA. EMBL; AACQ01000128; EAK94278.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- MISCELLANEOUS: The ABPC22 and PC9241 sequences are identical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.0%; Score 38; DB 2; Length 797; 66.7%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypochetical protein.
SEQUENCE 797 AA; 90614 MW; 5F9B1DB5F4559746 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Rappa chain V-III region ABPC 22/PC 9245.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 AA.
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SWR; PO1662; 1-111.
Sasembl; ENSWUSGO00000000060064; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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MEDLINE=79073152; PubMed=103003;
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MEDLINE=79012520; PubMed=99744;
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                                                                 NUCLEOTIDE SEQUENCE
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NCBI_TaxID=237561;
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7; Conservative
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
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                                               Framework-1.
Complementarity-determining-1.
Framework-2.
Complementarity-determining-2.
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Framework-2.
Complementarity-determining-2.
                                                                                                         Complementarity-determining-3.
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                                                                                                                                                                                DB 1; Length 111;
                                                                                                                                                                                                       Indels
                                                                                                                                                         12041 MW; D7DF0609303453CE CRC64;
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                         Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
19 kappa chain V-III region PC 4050.
                                                                                                                                                                                                                                                                                                             111 AA
                                                                                                                     Framework-4.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity.
                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                               Score 37; DB
Pred. No. 45;
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SMR; PO1663, 1-11.
EMB: PO1663, 1-11.
EMB: PO163, 1-11.
InterPro; IPR003596; Ig-1ike.
InterPro; IPR003596; Ig-v.
SMRAT; SM00406; IGV; II-
PROSITE; PS50835; IG_LIKE; I.
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                                                                                               Framework-3
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                                                                                                                                                                               74.0%;
77.8%;
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE;
Direct protein sequencing;
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Immunoglobulin V region.
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                                                                                                                                                                                                       Conservative
                                      Immunoglobulin V region.
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93 QONNEDPYT 101
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                                                                                                                                                                 Query Match
Best Local Similarity
7; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                         111 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN SEQUENCE.
                                                                                                                                                                                                                                                                                                          KV3K_MOUSE
P01663;
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SEQUENCE
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SEQUENCE
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Score 37; DB 1; Length 111; Pred. No. 45;

74.0%;

Query Match Best Local Similarity

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge W., Araujo R., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge W., Araujo R., Borman S., Barrell B.G., Badcock K., Enes V.,
Botstein D., Bowman S., Brueckner M., Carpenter J., Cherry J.M.,
An Elistrich F.S., Delius H., Diagolo T., Dubois B., Dubsterinoeft A.,
Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,
Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.W.,
Anicke-Smith S., Hyman R.W., Johnston M., Kalman S., Kleine K.,
Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,
Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Mosetl D.,
Marathe R., Massenguy F., Mewes H.-W., Mirtipati S., Mosetl D.,
Neller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D.,
Petel F.X., Pohl T.M., Purnelle B., Rajandream M.A., Rechmann S.,
Rieger M., Riles L., Roberts D., Schaefer M., Scharfe M., Scharfe M., Schrens B.,
Schramm S., Schroeder M., Sdicu A.-M., Tettelin H., Urrestarazu L.A.,
Ushinsky S., Vierendeels F., Vissers S., Voss H., Walsh S.V.,
Mambutt R., Wang Y., Wedler E., Wedler H., Winnett B., Zhong W.-W.,
M. Zollner A., Vo D.H., Hani J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The nuclectide sequence of Saccharomyces cerevisiae chromosome XVI.", Nature 387:103-105(1997).
-!- FUNCTION: DNA polymerase II participates in chromosomal DNA replication. DPB2 is essential for cell growth. May have a role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISCELLANDOUS: In eukaryoces there are five DNA polymerases: alpha, beta, gamma, delta, and epsilon which are responsible for different reactions of DNA synthesis. SIMILARITY: Belongs to the DNA polymerase epsilon subunit B
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SUBUNIT: Consists of five subunits (200 kDa, 80 kDa, 34 kDa,
                                                                                                                                                                                                                                                                                                 subunit B).
Name=DPB2; OrderedLocusNames=YPR175W; ORFNames=P9705.7;
Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                            (DNA polymerase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: Deoxynucleoside triphosphate + DNA(n)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Araki H., Hamatake R.K., Johnston L.H., Sugino A.; "DPBS, the gene encoding DNA polymerase II subunit B, chromosome replication in Saccharomyces cerevisiae."; Proc. Natl. Acad. Sci. U.S.A. 88:4601-4605(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M61710; AAA34576.1; ALT_INIT; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                            P244E2; Q06622;
01-MAR-1992 (Rel. 21, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
03-SEP-2005 (Rel. 48, Last annotation update)
DNA polymerase epsilon subunit B (EC 2.7.7.7)
                                                                                                                                                              692 AA
                                                                                                                                                           PRT;
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SUBCELLULAR LOCATION: Nuclear.
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MEDLINE=91271241; Pubmed=2052544;
                                                                                                                                                              STANDARD;
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93 OONNEDPLT 101
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OOSNEDPPT
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QSAZV6 EME
ID QSAZV
AC QSAZV
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                                                                                               Ensembl; YPT75W; Saccharomyces cerevisiae.

R Ensembl; YPT75W; Saccharomyces cerevisiae.

RGC; S000006379; DPB2.

RGC; GO:00005634; C:CYCpolasm; IDA.

RGC; GO:0005634; C:Croplication DNA polymerase complex; IDA.

RGC; GO:0005637; C:replication fork; TAS.

RGC; GO:0005637; P:pesilon DNA polymerase activity; TAS.

RGC; GO:0006293; P:mainanch repair; TAS.

RGC; GO:0006299; P:miclectide-excision repair; TAS.

REPAITHER; PTRR12708; DNA pol E B.

R Pfam; PF04042; DNA_pol E B; 1.

M Complete proteome; DNA replication; DNA-binding;

M DNA-directed DNA polymerase; Nuclear protein; Nucleotidyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypothetical protein.
Schistosoma japonicum (Blood fluke).
Eukaryota, Metazoa; Platylelminthes; Trematoda, Digenea, Strigeidida, Schistosomatoidea; Schistosomatidae; Schistosoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Pred. No. 63;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 1; Length 692;
Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78704 MW; SC01647BD2B6A39A CRC64;
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(Rel. 01, Last sequence update)
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EMBL; U25842; AAB68109.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (NOV-2004) to the EMBL/Gen!
EMBL; AY815032; AAW26764.1; -; mRNA.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   461
524
568
587
647
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425 QKLNDDPPT 433
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                            859833.
                                                                           GermOnline; 144440;
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
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Q5DBP2 SCH
Q5DBP AC
Q5DBP DT 10-MA
DT 10-MA
DT 10-MA
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DT 8-MA
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                                                                                                                                                                                                               PROTEIN SEQUENCE OF 1-35.
MEDILINE-7823.5887; Pubmed=98179;
Burstein V., Schechter I.,
"Primary structures of N-terminal extra peptide segments linked to the
                                                                                                                                                                                                                                                                                                                        variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled expression of immunoglobulin genes."; Biochemistry 17:2392-2400(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=79012520; PubMed=99744;
MCKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally related maps of antibody forestated regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia, Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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McKean D.J., Potter M., Hood L.E.;
Mouse immunoglobulin chains. Pattern of sequence variation among
kappa chains with limited sequence differences.";
Biochemistry 12:760-771(1973).
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Complementarity-determining-1.
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PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.0%; Score 36; DB 1;
77.8%; Pred. No. 84;
tive 1; Mismatches
10-MAY-2005 (Rel. 47, Last annotation update)
Ig kappa chain V-III region MOPC 63 precursor.
Mus musculus (Mouse).
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Interpro; IPR007110; Ig-1ike.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGV; 1.
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QSAZV6;
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58
73
112
1121
1131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR, B90412; KVMSM6.
HSSP, P01665; 1QNZ.
SMR; P01661; 21-131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 AA;
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nes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE REVISION.
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Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
Goldsmith A.D., Lee J.M., Quach H.L., Torriuni M., Yu G., Bowser L.,
Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YUCLEOTIDE SEQUENCE.
Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
Kaminya A., Karlin-Neumann G., Kawai J., Kim E., Lin J.,
Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.
                                                                                                                                                            Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E., Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I., Czreszy T.H., Buell C.R., Town C.D., Nierman W.C., Fraser C.M., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name-phob; OrderedLocusNames=LIC13397;
Leptospira interrogans (serogroup Icterohaemorrhagiae / serovar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.0%; Score 36; DB 2; Length 442
66.7%; Pred. No. 3.46+02;
.ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W
Theologis A.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC005309; AAC53650.2; -; Genomic_DNA.
EMBL; AC006072; AAM15133.1; -; Genomic_DNA.
EMBL; AX7048334; AAL56748.1; -; mRNA.
EMBL; AX713973; AAL57264.1; -; mRNA.
                                                                    to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                         Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ecker J.R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              442 AA; 49290 MW; D6E987FA3D95BE30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   072L26 LEPIC PRELIMINARY; PRT; 443 AA. 072L26.
072L26.
072L26.
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; F84921; F84921.
InterPro; IPR010378; DUF974.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF06159; DUF974; 1. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : | |||||
246 EDSTEDPPT 254
                                       Town C.D., Kaul S.;
Submitted (FEB-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                  NUCLEOTIDE SEQUENCE.
         NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Theologis A.;
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1D 077
AC 077
DT 05
DT 05
DE Ph
GN N<sup>2</sup>
OS L<sup>2</sup>
CC CC
             셤
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Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
Burkgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
Butler J. Callywore A., Cooke P., Cookum B., DeArellano K.,
A. Choepel Y., Collywore A., Cooke P., Cookum B., DeArellano K.,
Buz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
Brickson J., Faros S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
Bactyna S., Grerre S., Graham L., Grand-Pietre N., Hafez N.,
Bactyna S., Grerre S., Graham L., Grand-Pietre N., Hafez N.,
Anthews C., Maucels T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
Anthews C., Maucels E., Macdend C., Macdonald P., Major J., Manning J.,
Matthews C., Maucels E., Macarthy M., Meldrim J., Meneus L.,
Mielsen C.B., Norbu C., O'Comor T., OrDonnell P., O'Neil D.,
Anthews C., Muchypy T., Naylor J., Nguyen C., Nicol R.,
Rachupka A., Ramasamy U., Raymond C., Retera R., Rise C., Rogov P.,
Rachupka A., Ramasamy U., Raymond C., Retera R., Rise C., Soncro S.,
Schupback R., Seaman S., Schupback R., Seaman S., Severy P., Smirnov S.,
Anthe C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
Alalamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
Ander E.,
And
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
14-MORCHAICAL procein.
ORFNames=AN6174.2;
Aspergillus ridulans FGSC A4.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Burotiomycetes; Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome Sequence of Aspergillus nidulans.";
Submitted (JAN-2004) to the BMBL/Genbank/DBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.0%; Score 36; DB 2; Length 428; 75.0%; Pred. No. 3.2e+02; rive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preliminary data.

EMBL: AACD01000105; BAAS7960.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 428 AA; 46824 MW; 18CFD565DBF8F787 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      082263_ARATH PRELIMINARY; PRT; 442 AA.
082265; Q944K4;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-FBB-2005 (TrEMBLrel. 29, Last annotation update)
Expressed protein (Hypothetical protein At2g47960)
(At2g47960/T9J23.10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 75.0
les 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 QSQNEDPP 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QQSNEDPP 8
                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                     NCBI_TaxID=227321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                          STRAIN=FGSC A4;
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Q6CFIS YAR
ID Q6CFI
AC Q6CFI
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                                                                   WUCLEOTIDE SEQUENCE.

STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;

MEDLINB=22598143; PubMed=12712204; DOI=10.1038/nature01597;

Ren S.-X., Fu G., Zeng H., Du G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,

Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,

Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Xin H.-F.,

Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,

Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,

Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,

XIU J.-G., Zhao G.-P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leptospira interrogans.
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
    Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Unique physiological and pathogenic features of Leptospira interrogans revealed by whole-genome sequencing."; Nature 422:888-893(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.0%; Score 36; DB 2; Length 443; 85.7%; Pred. No. 3.4e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      443 AA; 51489 MW; 89B4A7D462327F50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    443 AA; 51548 MW; D8A13873080C33CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Phosphodiesterase/alkaline phosphatase D (EC 3.1.3.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE011577; AAN51444.1; -; Genomic_DNA.
GO: GO:00040315; F:alkaline phosphatase activity; IEA.
GO; GO:000152; P:etabolism; IEA.
InterPro; IPR001952; Alk_phosphtse.
InterPro; IPR000413; Integrin_alpha.
Pfam; PF00145; Alk_phosphatase; I.
PROSITE; PS00245; Alk_phosphatase; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam, PF00245; Alk phosphatase; 1.
PROSITE; PS00242; INTEGRIN_ALPHA; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     443 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Query Match
Best Local Similarity 85.7°,
Best Local Similarity
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 LEPIN
QEYG8 LEPIN PRELIMINARY;
QBEYG8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OrderedLocusNames=LA4246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 ŚNEDPPS 133
                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 SNEDPPT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome
SEQUENCE 443 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome
SEQUENCE 443 AA
                  NCBI_TaxID=44275;
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WormBase; WEGENEGOOGOS2; C39BIO.2.
WormBase; C39BIO.2; CE36632.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005230; F:extracellular ligand-gated ion channel acti. . .; IEA.
GO; GO:0004890; F:GABA-A receptor activity; IEA.
GO; GO:0005216; F:ion channel activity; IEA.
GO; GO:000531; F:ion channel activity; IEA.
GO; GO:0005811; P:ion transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGREAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
Complete proteome; Hypothetical protein: Ion transport; Ionic channel;
Postsynaptic membrane; Transmembrane; Transport.
SEQUENCE 460 AA; 52798 MW; 9C4E95B292E86409 CRC64;
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The C. elegans sequencing consortium; "Genome sequence of the nematode C. elegans; a platform for
                              Length 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.0%; Score 36; DB 2; Length 460
77.8%; Pred. No. 3.5e+02;
tive 0; Mismatches 2; Indels
                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein C39B10.2.
ORFNames=C39B10.2;
Caenorhabditis elegans.
                      72.0%; Score 36; DB 2; I 85.7%; Pred. No. 3.4e+02; tive 1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1] TNCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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                                                                                                                                                                                                                                                                                             460 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family.
EMBL; ZSO027; CAA90332.3; -; Genomic_DNA.
PIR; T19840; T19840.
Ensembl; C39810.2; Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR006028; GABAA, recept.
InterPro; IPR006029; Neu channel memb.
InterPro; IPR006202; Neur chan LBD.
InterPro; IPR006201; Neur channel.
Pfam; PF02931; Neur chan LBD; 1.
Pfam; PF02932; Neur chan LBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00253; GABARECEPTR.
PRINTS; PR00252; NRIONCHANNEL.
Query Match
Best Local Similarity 85.73,
1.10cal 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IS YARLI
QECPIS YARLI PRELIMINARY;
QECPIS;
                                                                                                                                                                                                                                                                  Q18518 CAEEL
ID Q18518 CAEEL PRELIMINARY;
AC Q18518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 77.8 tes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 QQSNTRPPT 44
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                                                                                                                                                                     127 SNEDPPS 133
                                                                                                                        σ
                                                                                                                        3 SNEDPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
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EMBL; M35887; AAA28446.1; -; mRNA.
EMBL; AE003442; AAN09215.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=FC106;
            Abril J.F.,
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                                                                                                                                                                                                                                  NUCLECATIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

NUCLECOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

PubMed=15229592; DOI=10.1038/nature02579;

Notable 1. Sherman D., Fischer G., Durrens P., Casaregola S.,

Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,

Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,

Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,

Bospons L., Fabre E., Fairhead C., Ferry-Dumacet H., Groppi A.,

Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,

A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,

Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,

Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,

Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,

Zeniou-Meyer M., Zuvanovic Y., Bolotin-Fukuhara M., Thierry A.,

Mincker P., Souciet J.-L.;

Wincher P., Souciet J.-L.;

"T. "Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20196006; Pubmed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburnar M., Henderson S.N., George R.A., Lewis S.E., Richards M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similarities with tr/gOUVE Yarrowia lipolytica Pal2 protein.
OrderedLocusNames-YALIOBO6710g,
Yarrowia lipolytica (Candida lipolytica).
Bukaryota, Fungi, Ascomycota, Saccharomycetina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE, AND ALTERNATIVE SPLICING.
MEDLINE=91032553; PubMed=1699826;
Waring G.L., Hawley R.J., Schoenfeld T.;
"Multiple proteins are produced from the dec-1 eggshell gene in Drosophila by alternative RNA splicing and proteolytic cleavage
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.0%; Score 36; DB 2; Length 562; 100.0%; Pred. No. 4.4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         562 AA; 61494 MW; F3F69CECE74CDBD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DECII DROME STANDARD; PRT; 1208 AA. P18169; QBIRR1; 01-NOV-1990 (Rel. 16, Created) 10-OCT-2003 (Rel. 42, Last sequence update) 10-MAY-2005 (Rel. 47, Last annotation update) Defective chorion-1 protein, FC125 isoform precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; CR382128; CAG82808.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 430:35-44 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      547 NEDPPT 552
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SEQUENCE 562 AA
                                                                                                                                                                                                    NCBI_TaxID=4952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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A Ballew R.M., Bauu A., Baxendale J., Baycaktaroglu L., Beasley E.M., Ballew R.M., Bauu A., Barendale J., Baycaktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Bockchan M.R., Bouck J., Brokstein P., Botchten P., Caleiu E., Center A., Chandra I., R. Buttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., R. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Bucken B. Delfort A., Deng Z., Mays A.D., Dew I., Dietz. S.M., R. Bablos B. Delfort A., Dugan-Rocha S., Dunkov B.C., Dunn P. Burbin K.J., Bvangelista C.C., Ferraz C., Ferriera S., Fleischmann W., R. Podien K.J., Brangelista C.C., Ferraz C., Ferriera S., Pleischmann M., Rodson K., Gony F., Gorrell J.H., Gu Z., Guan P., Harris M.

R. Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., Brandler C., Gabrielian A.E., Garg N.S., Galbart W. M., Classer K., Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Julu X., Mattei B., McIntosh T.C., McLood M.P., McPherson D., Lu X., Mattei B., McIntosh T.C., McLood M.P., McPherson D.L., R. Melson D.R., Murphy E., Murphy L., Murzhy D.M., Nelson D.R., Nelson D.R., Nelson D.R., Nelson M., Strong R., Sun H., Kannigton K., Sunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kamos I. Simpson M., Strong R., Sun S., Yao Q.A., Mary D.M., Wasserman D.A., Weissenbach J., Wang Z.-Y., Wassarman D.A., Weinsch K., Zhan M., Zhong G., Zhao Q., Zhan G., Zhon S., Zhan M., Zhong G., Zhao Q., Zhan G., Sheng S., Shu K., Sheng S., Zhon S., Zhon S., Zhu S., Zhu S., Zhu X., Shu S., Zhu X., Shu S., Zhu X., Shu S., Zhu S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEVELOPMENTAL STACE: Expression peaks at embryonic stage 10A, is slightly reduced by stage 10B, and undetected in stage 11.
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MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=P18169-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=P18170-1; Sequence=External;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=P18171-1; Sequence=External;
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IsoId=P18169-1; Sequence=External;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lewis S.E.;
       ö
PIR; A44766; A44766.

Bnsembl; CG2175; Drosophila melanogaster.

FlyBase; FBGH000427; dec-1.

GO; GO:0042600; C:chorion; IDA.

GO; GO:0005576; C:extracellular region; IDA.

GO; GO:000513; F:structural constituent of chorion (sensu In. . .; IMP.

GO; GO:0007306; P:insect. chorion formation; IMP.

InterPro; IPR006729; DEC-1.

InterPro; IPR006719; DEC-1.

InterPro; IPR006718; DEC-1.

InterPro; IPR006718; DEC-1.

InterPro; IPR006718; DEC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A -> V (in Ref. 1).
Q -> E (in Ref. 1).
Q -> E (in Ref. 1).
A -> T (in Ref. 1).
PENEGTARHKVDALGVGGNKRKKSKSKSAPP -> AGERRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RQAQSRCPGSWRQQAQEVQVQVGAA (in Ref. 1).
QRPVVQSYGTSYGG -> SVRWFRVTEQATAE (in Ref.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          9 (approximate).
10 (approximate).
11 (approximate).
12 (approximate).
12 X 26 AA approximate tandem repeats, Glu, Met-rich.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91032553; PubMed=1699826; Maring G.L., Hawley R.J., Schoenfeld T.; "Multiple proteins are produced from the dec-1 eggshell gene in Drosophila by alternative RNA splicing and proteolytic cleavage
                                                                                                                                                                                                                                                    Potential. Defective chorion-1 protein, FC125
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Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 1; Length 1208;
Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1208 AA; 137444 MW; 2D8D140756FFFDEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DECI3 DROME STANDARD; PRT; 1590 AA.
P18171; Q9W3P3;
01-NOY-1990 (Rel. 16, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Defective chorion-1 protein, FC177 isoform precursor.
                                                                                                                                                                                                                               Chorion; Repeat; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                           (approximate). (approximate).
                                                                                                                                                                                                                                                                                                                                                                                         (approximate)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.0%;
                                                                                                                                                                            Pfam; PF04624; Dec-1; 12. —
Pfam; PF04626; DBC-1, 1.
Alternative splicing; Chori
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dev. Biol. 142:1-12(1990).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219
347
382
877
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680
696
720
733
788
788
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QQSNEDPPT 9
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REPEAT
REPEAT
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REPEAT
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       SOT PETT TE FETT TE FE
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Feleffer B.D., RA Bardon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Randon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Randon R.V., Basud A., An H.-J., Andrews-Ffannkoch C., Baldwin D., Ra Beeson K.Y., Bence P.V., Barman B.P., Bhandari D., Bolshakov S., Bortchan M.R., Bouck J., Broketein P., Brothier P., Raman B.P., Bhandari D., Bolshakov S., Bortchan M.R., Bouck J., Broketein P., Brothier P., Abrits R.A., Cawley S., Dahlke C., Davemport L.B., Davies P., Andrews M., Dubler A., Dablke C., Davemport L.B., Davies P., Andrews M., Dubler A., Davies M., Dietz S.M., Ra Burtis N.C., Evangelista C.C., Ferraz C., Ferraz C., Ferraz C., Ferras C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F. Gorrell J.H., Wei M.-H., Iboeyam C., Jasko P., Lei Y., Harvey D.A., Heinam T.J., Wei M.-H., Iboeyam C., Jasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Merkulow G., Milshina N.V., Moharry C., Morris J., Woshrefi A., Welkere B., Moharry C., Morris J., Woshrefi A., Welker B.C., Siden-Kiames I., Simpser D.D., Nang A., Shue B.C., Siden-Kiames I., Simpser D., Shup D., Walle B.C., Siden-Kiames I., Simpser D., Shup D., Walle B.C., Siden-Kiames I., Shup B., Shue B.C., Shup D., Shup G., Shup D., Shup C., Shup D.,
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MEDLINE=22426069; PubMed=12537572;
Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                   STRAIN=Berkeley;
MEDLINB=20196006; PubMed=10731132; DOI=10.1126/8cience.287.5461.2185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hawley R.J., Waring G.L.;
"Cloning and analysis of the dec-1 female-sterile locus, a required for proper assembly of the Drosophila eggshell.";
else Boby 1349(1988).
--- FUNCTION: Required for proper assembly of the eggshell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=3;
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=P18171-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=88243015; PubMed=3378704;
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Carlton J.M., Angluoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Sheterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cuckenbush J., Sedegah M., Shoaibi A., Cummings L.M., Preiser P.R., III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., van Lin L.H., Janse C.J., Maters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J., "Genome sequence and comparative analysis of the model rodent malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A., Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K., James K., Rutherford K., Harris B., Harris D., Churcher C., Quail M.A., Ormond D., Doggett J., Trueman H.E., Mandoza J. Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C. Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.; "A comprehensive survey of the Plasmodium life cycle by genomic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     parasite Plasmodium yoshii "",
Nature 419:512-519 (2002).
-!- CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine = AMP +
diphosphate + protein N-ubiquityllysine.
-!- PATHWAY: Ubiquitin conjugation; second step.
-!- SIMILMATTY: Belongs to the ubiquitin-conjugating enzyme family.
-!- SIMILMATTY: Belongs to the ubiquitin-conjugating enzyme family.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preliminary data.

R EMBL, Ababul000856; EAA22551.1; -; Genomic_DNA.

HSSP; P52490; 1JAT.

SWR; Q7RK78; 1-106.

R GO; GO:0016874; F:ligase activity; IEA.

R GO; GO:0004840; F:luiquitin corle; IEA.

R GO; GO:0006812; P:ubiquitin corle; IEA.

R InterPro; IPR000608; UBQ-conjugat_E2.

R Pfam; PF00179; UQ_con; 1.

R ProDom; PD000461; UBQ_conjugat_E2.

R PROSITE; PS00133; UBIQUITIN_CONJUGAT_1; 1.

R PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.

W Ligase; UDl_conjugation_pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=73239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium berghei.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBI_TaxID=5821;
                                                                                                                                                                  MEDLINE=22255706; PubMed=1236865; DOI=10.1038/nature01099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.0%; Score 35; DB 2; Length 107; 66.7%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 AA; 11811 MW; ED9F62F412B49B99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Ubiquitin-conjugating enzyme e2, putative (Fragment).
ORFNames=PB000336.03.0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q4YR21_PLABE PRELIMINARY;
     Plasmodium yoelii yoelii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | |:||||
QDLNKOPPT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QQSNEDPPT 9
                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                           STRAIN=17XNL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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04YR21 PLAD
04YR2
AC 04YR2
DT 13-SE
DT
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     ਨੇ
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                                              This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                             IntAct; P18171; ...
Ensembl; CG2175; Drosophila melanogaster.
FlyBase; FBG0000447; dec-1.
FlyBase; FBG0000450; C:chorion; IDA.
GO; GC:0004560; C:chorion; IDA.
GO; GO:0005576; C:extracellular region; IDA.
GO; GO:0005513; F:structural constituent of chorion (sensu In. . .; IMP.
GO; GO:0007306; P:insect chorion formation; IMP.
InterPro; IPR006719; DEC-1_C.
InterPro; IPR006719; DEC-1_REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> AGERRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 (approximate).
7 (approximate).
8 (approximate).
8 (approximate).
10 (approximate).
11 (approximate).
12 (approximate).
12 X 26 AA approximate tandem repeats, Glu, Met-rich.
A -> V (in Ref. 1).
D -> H (in Ref. 1).
A -> T (in Ref. 1).
A -> T (in Ref. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PENEGTARHKVDALGVGGNKRKKSKSKSAPP -> AGERRI
RQAQSRCPGSWRQQAQEVQVQVGAA (in Ref. 1)
QRPVVQSYGTSYGG -> SVRWFRVTEQATAE (in Ref.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potential.
Defective chorion-1 protein, FC177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
-!- DEVELOPMENTAL STAGE: Expressed during embryonic stage 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 1590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1).

R -> Q (in Ref. 1).

SV -> C (in Ref. 1).

Q -> P (in Ref. 1).

E -> D (in Ref. 1).

B -> D (in Ref. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
11-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative ubiquitin-conjugating enzyme (Fragment).
Name-PY03025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 1; I
Pred. No. 1.4e+03;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chorion; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 AA.
                                                                                                                                                                                                                    EMBL; M35889; AAA28448.1; -; mRNA.
EMBL; AE003442; AAF46278.2; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    995 995
1051 1052
1296 1296
1299 1299
1590 AA; 179188 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF04624; Dec-1; 12. —
Pfam; PF04626; DEC-1_C; 1.
Pfam; PF04625; DEC-1_N; 1.
Alternative spliting; Chori
SIGNAL
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QTRK78 PLAYO PRELIMINARY;
Q7RK78;
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Best Local Similarity 66.7
Matches 6; Conservative
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960 QKSNSNPPT 968
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Probom; PD000461; UBQ_conjugat; 1.
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                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydran R.W., Fung E., Conway A., Kurdi O., Mao J., Miranda M., Nakao B., Rowley D., Tamaki T., Wang F., Davis R.W.; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

--- CATALYICA ACTIVITY: ATP + ubiquitin + protein lysine = AMP + diphosphate + protein N-ubiquityllysine.
--- PATHWAY: Ubiquitin conjugation; second step.
--- SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family. EMBL; ABC19444; AAN36127.1; -; Genomic_DNA.
                                                    preliminary data.
-!- CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine = AMP + diphosphate + protein N-ubiquitylylaine.
-!- PATHWAY: Ubiquitin conjugation; second step.
-!- SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.
EMBL; CAALO1002860; CH99536.1; -; Genomic_DNA.
InterPro; IPR000608; UBQ-conjugat_E2.
ProDom; PD0009461; UBQ_con; 1.
SMART; SM00212; UBCC; -1.
          Science 307:82-86(2005).
-1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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GO; GO:0004840; F:ubiquitin conjugating enzyme activity; IEA.
GO; GO:0006512; P:ubiquitin cycle; IEA.
InterPro; IPR00608; UBQ-conjugat_E2.
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Ubiquitin-conjugating enzyme e2, putative.
ORFNames-PFL0190w;
Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TAXID=36329;
                                                                                                                                                                                                                                                                                70.0%; Score 35; DB 2; Length 139; 66.7%; Pred. No. 1.4e+02; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                           PROSITE, PSOOI83, UBIQUITIN_CONJUGAT_1; 1.
PROSITE; PSSO127, UBIQUITIN_CONJUGAT_2; 1.
Ligase, Ubl conjugation pathway.
NON TER 1 1 1 1 SEQÜENCE 139 AA; 15597 MW; 5DE03B5E857E8C43 CRC64;
transcriptomic, and proteomic analyses.";
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QBIG07;
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                                                                                                                                                                                                                                                                                                             6; Conservative
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Best Local Similarity
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Hall N., Karras M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
James K., Rutherford K., Harris B., Harris D., Churcher C.,
James K., Rutherford K., Harris B., Harris D., Churcher C.,
Churcher C.,
Bidwell S.L., Rajandream M.A., Carucci D.J. Yates J.R., Kafatos F.C.,
Bidwell S.L., Rajandream M.A., Carucci D.J. Yates J.R., Kafatos F.C.,
Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
"A comprehensive survey of the Plasmodium life cycle by genomic,
T. Transcriptomic, and proteomic analyses.",
Science 307:82-86(2005).
-I-CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
prellminary data.
-I-CATALYITC ACTIVITY: ATP + ubiquitin + protein lysine = AMP +
diphosphate + protein N-ubiquitin-conjugating enzyme family.
Hamis CAAJ1000659; CAH75150.1, -; Genomic_DNA.

EMBL; CAAJ0100659; CAH75150.1, -; Genomic_DNA.

PREMB; CAAD000469; UBQ-conjugat_EZ.

PRANDEN, PRO0179; UQ_con; 1.

RANDEN, SMADT. S
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NCBI_TaxID=5825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 147;
                                                                                                                                                                                                                                                          Length 147;
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SMART; SM00212; UBCC; 1. PROSTIE; P800183; UBIQUITIN CONJUGAT 1; 1. PROSTIE; PS00183; UBIQUITIN CONJUGAT 2; 1. Ligase; Ubl conjugation pathway.
SEQUENCE 147 AA; 16539 MW; 233FBD5A8481B085 CRC64;
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PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
Ligame; Ubl conjugation pathway.
EEQUENCE 147 AA; 16539 MW; 233FBD5A8481B085 CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Ubiquicin-conjugating enzyme e2, putative.
ORFNames=PC000554.00.0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 AA.
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Q4Y6R0;
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ODLNKOPPT 19
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InterPro; IPR003448; Mb_biosynth_MoaE.
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QTPYOB;
01-MAR-2004 (TYEMBLYEL: 26,
01-MAR-2004 (TYEMBLYEL: 26,
01-MAR-2004 (TYEMBLYEL: 26,
                                                                                                                                                                                                                                                                                                                                                                              QSICN4 CYTJO PRELIMINARY;
QSICN4;
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                                                                                                                    Complete proteome. SEQUENCE 275 AA;
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Best Local Similarity
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Q7PY08 ANO
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PubMed=15520287; DOI=10.1101/gr.2700304;
Baliga N.S., Bonneau R., Facciotti M.T., Pan M., Glusman G.,
Deutsch E.W., Shannon P., Chiu Y., Weng R.S., Gan R.R., Hung P.,
Date S.V., Marcotte E., Hood L., Ng W.V.;
"Genome sequence of Haloarcula marismortui: a halophilic archaeon from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome Sequence of Aspergillus nidulans.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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EMBL. AYS56297; AAV46135.1, - ; Genomic_DNA.
GO; GO:0005525; F:GTP binding; IEA.
GO; GO:0006777; P:Mo-molybdopterin cofactor biosynthesis; IEA.
               Aspergillus nidulans FGSC A4.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.0%; Score 35; DB 2; Length 267; 66.7%; Pred. No. 2.9e+02; ative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AACD01000135; EAA59629.1; -; Genomic DNA.
SEQUENCE 267 AA; 30232 MW; 5841E7EB112B77BB CRC64;
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Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=moaB; OrderedLocusNames=rrnAC1186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last seq
01-FEB-2005 (TrEMBLrel. 29, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Halobacteriaceae; Haloarcula
NCBI_TaxID=2238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QSV2W7 HALMA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 OSSNESPPS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QQSNEDPPT 9
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                                                                                                                NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 6; Conserv
ORFNames=AN7975.2;
                                                                          NCBI_TaxID=227321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the Dead Sea.";
                                                                                                                                    STRAIN=FGSC A4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HALMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 32
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Modification Sectionary.

Modification Sectionary.

Modification I: Mayer C., Rybkine T., Collatz E., Podglajen I: Modification Sectionary.

Tan unusual primary sigma factor in the Bacteroidetes phylum.";

Mol. Microbiol. 56:888-90(2005).

BMBL; AY781293; A4W50927.1; -; Genomic DNA.

GO; GO:0003700; F:ranscription factor activity; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

GO; GO:0006352; P:regulation initiation; IEA.

RO; GO:0006352; P:regulation initiation; IEA.

RO; GO:0006352; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR00942; Sigma70_r1.

R InterPro; IPR007624; Sigma70_r3.

R InterPro; IPR00943; Sigma70_r3.

R InterPro; IPR00943; Sigma70_r3.

R InterPro; IPR00943; Sigma70_r3.

R InterPro; IPR001991; Ming hix DNA_bd.

Pfam; PF00140; Sigma70_r12; I.
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA-directed RNA polymerase; Nucleotidyltransferase; Sigma factor;
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                                                                                                                                                                                                                                      Length 275;
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Pred. No. 3.2e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytophaga johnsonae.
Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                         275 AA; 30435 MW; 32546495775A07BB CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
                                                                                                                                                                                                                               Score 35; DB 2;
Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297 AA
                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
InterPro; IPR004435; MoDB_reg. —
PANTHER; PTRID311; Mb_biosynth_MoaE; 1.
Pfam; PP02391; MoaE; 1.
Pfam; PF03205; MobB; 1.
TIGRFAMS; TIGR00176; mobB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Flavobacteriaceae; Flavobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00140; Sigma70_r1_2; I
Pfam; PF04542; Sigma70_r2; I.
Pfam; PF04543; Sigma70_r3; I.
Pfam; PF04545; Sigma70_r4; I.
PRINTS; PR00046; SIGMA70FCT.
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HSSP; P01104; 1H8A.

TRANSFAC; T02590; -.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0045449; P:regulation of transcription; IEA.
InterPro; IPR012287; Homeodomain-rel.
InterPro; IPR01208; Myb DNA bd.
Pfam; PF00249; Myb DNA-binding; 2.
SMART; SM00717; SANT; 2.
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Best Local Similarity 85...
6; Conservative
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SEQUENCE 301 AA; 3311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSEDPPT 203
                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
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Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
ENSANGP0000011561 (Fragment).

ORFNames=ENSANGG0000009072;

Anopheles gambiae str. PEST.

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;

Anophelinae; Anopheles.

NCBI_TAXID=180454;
                                                                                                                                                                                                                                                          Anopheles Genome Sequencing Consortium;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!-CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is RGJ; GO:000515; F:protein binding; IEA.

RGO; GO:0005215; F:protein binding; IEA.

RGO; GO:0005870; F:zinc ion binding; IEA.

RGO; GO:0006870; F:zinc ion binding; IEA.

RGO; GO:0006886; P:intracellular protein transport; IEA.

InterPro; IPR000306; Znf_FYVE.

R PROSITE; PSSO916; RABBD; 1.

R PROSITE; PSSO916; RABBD; 1.

R PROSITE; PSSO916; ZFFYVE; 1.
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01-MAY-2000 (TrEMBLrel. 29, Last sequence update)
01-MAY-2000 (TrEMBLrel. 29, Last annotation update)
01-FBB-2005 (TrEMBLrel. 29, Last annotation update)
NERR3-MYB transcription factor (13950060/F3A4_140).
Name=F3A4.140; ORFNames=At3g50060;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; cosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brogues M., Collado M.C., Navarro P., Terol J., Perez-Alonso M., Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.0%; Score 35; DB 2; Length 297; 66.7%; Pred. No. 3.3e+02; ive 1; Mismatches 2; Indels
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Kim C.J., Chen H., Cheuk R., Shinn P., Banh J., Bowser L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EU Arabidopsis sequencing project;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 AA; 33344 MW; ED430BD3654E8941 CRC64;
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Q9SN12;
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Best Local Similarity
6, Conserva
                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
STRAIN=PEST;
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SEQUENCE
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Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kaniya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Ondera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamama K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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MEDLINE=98341717; PubMed=9678577; DOI=10.1023/A:1006011002499;
Kirik V., Kolle K., Misera S., Baumlein H.;
Two novel MYB homologues with changed expression in late embryogenesis-defective Arabidopsis mutants.";
Plant Mol. Biol. 37:819-827(1998).
-- SUBCELLUIAR LOCATION: Nuclear (By similarity).
EMBL; Z54137; CAA90810.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.0%; Score 35; DB 2; Length 301; 85.7%; Pred. No. 3.4e+02; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                    Ou L., Gu H.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: Nuclear (By similarity).

EMBL; AL1123978; CAB62114.1; -; Genomic_DNA.

EMBL; AF424588; AAL11582.1; -; mRNA.

EMBL; AY214828; AAS10068.1; -; mRNA.

EMBL; AY214828; AAM70537.1; -; mRNA.

PIR, 745859; T45859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0045449; P:regulation of transcription; IEA.
GO; GO:0045449; P:regulation of transcription; IEA.
InterPro; IPR012087; Homeodomain-rel.
InterPro; IPR012087; Homeodomain-rel.
Fam; PF00249; Myb DNA-binding; 2.
SWART; SM00717; SANT; 2.
PROSTIE; PS00037; MYB 1; UNKNOWN 1.
PROSTIE; PS00334; MYB 2; 2.
PROSTIE; PS50090; MYB 3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 AA; 33111 MW; 9CCD5863E9D06DEC CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
1-NOV-1996 (TrEMBLrel. 26, Last annotation update)
MYB-related protein.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304 AA.
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1 QOSNEDPPT 9
          NUCLEOTIDE SEQUENCE.
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91 QQANEDP 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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PubMed=15894715;
                                       STRAIN=B-3501A;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Romero I., Fuertes A., Benito M.J., Malpica J., Leyva A., Paz-Ares J.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-58P-2005 (TrEMBLrel. 31, Created)
13-58P-2005 (TrEMBLrel. 31, Last sequence update)
13-58P-2005 (TrEMBLrel. 31, Last sequence update)
13-58P-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein.
ORFNames=CNBA3050;
Cryptococcus neoformans var. neoformans B-3501A.
Bukaryota; Pungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
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                                                                                                                                                                                                           Gaps
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                                                                                                                                                    70.0%; Score 35; DB 2; Length 304; 85.7%; Pred. No. 3.4e+02; ive 1; Mismatches 0; Indels
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                                                                                                     33292 MW; EFA25289C3FD5A21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO: 0005634; C:nucleus; IEA.
GO; GO: 0005674; F: DNA binding; IEA.
GO; GO: 0004547; F: DNA binding; IEA.
GO; GO: 0004547; F: DNA binding; IEA.
InterPro; IPR012287; Homeodomain-rel.
InterPro; IPR01005; Myb DNA bd.
Pfam; PF00249; Myb DNA-binding; 2.
SWART; SM00171; SANT; 2.
PROSITE; PS00037; MYB 1; UNKNOWN_1.
PROSITE; PS00037; MYB 2; 2.
PROSITE; PS000937; MYB 2; 2.
PROSITE; PS00099; MYB 2; 2.
Nuclear Protein; Repeat.
SEQUENCE 304 AA; 33296 MW; SJAE63F19CC24B42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33296 MW; 53AE63F19CC24B42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1994 (TrEMBLrel. 26, Last annotation update)
R2R3-MPB transcription factor.
Name-ALMYB77;
                                                                                                                                                                                                                                                                                                                                                                                                                                      304 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
PROSITE; PS00037; MYB_1; UNKNOWN_1.
PROSITE; PS00334; MYB_2; 2.
PROSITE; PS50090; MYB_3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Y14208; CAA74604.1; -; mRNA.
HSSP; P01104; 1H8A.
                                                                                                                                                                                                                                                                                                                                                                                                                            049745_ARATH PRELIMINARY;
                                                                                                                                            Query Match 70.0
Best Local Similarity 85.7
Matches 6; Conservative
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QS60DS;
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                                                                              Nuclear protein; Repeat
SEQUENCE 304 AA; 332
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197 SSEDPPT 203
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049745 ARP
10 049745
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DT 01-JU
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CO BURAX
COC BURAX
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Rehmany A.P., Gordon A., Rose L.E., Allen R.L., Armstrong M.R., Whisson S.C., Kamoun S., Tyler B.M., Birch P.R., Beynon J.L.; "Differential Recognition of Highly Divergent Downy Mildew Avirulence Gene Alleles by RPPI Resistance Genes from Two Arabidopsis Lines."; Plant Cell 17:1839-1850(2005).

EMBL; AY973541; AAY58908.1; -; Genomic DNA.

SEQUENCE 328 AA; 36445 MW; B7D65F4A4589D330 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hyaloperonospora parasitica.
Eukaryota, stramenopiles, Oomycetes, Peronosporales, Peronosporaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M., Wickes B.L., Fu J., Davis R.W.;
"Cryptococcus neoformans serotype D sequencing.",
Submitted (JUL-2004) to the BMBL/GenBank/DDBJ databases.
--- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Mus musculus 6 days neonate skin cDNA, RIKEN full-length enriched library, clone:A030004P03 product:similar to OVARC1001010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=4933434L15Rik;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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6; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                            preliminary data.

BMBL; AREY0100001; EAL23658.1; -; Genomic_DNA.
GO; GO:0000548; C:chromatin; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0006333; P:chromatin binding; IEA.
GO; GO:0006333; P:chromatin assembly or disassembly; IEA.
Hypothetical protein; Nuclear protein.
SEQUENCE 315 AA; 36950 MW; 4863P2C56366D68E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Putative methylene tetrahydrofolate dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.0%; Score 35; DB 2; I
55.6%; Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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Q4VDG8;
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QBBYY6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
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207 EEGDEDPPT 215
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Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konoo H., Adachi J., Fukuda S., Alazawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fluischmann W., Gasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubi F., Suzuki R., Tomita M., Wagner L., Washio T., Asakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakameto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whithaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Mormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Murcidea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/63; TISSUE=Skin;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayattsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hori P., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Skin;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=Skin;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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STRAIN-JEC21;
Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D., Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E., Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J., D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J., Huang J.C., Janbon G., Jones S.J.M., Krzywinski M.I., Kwon-Chung J.K., Lengeler K.B., Maiti R., Marra M.A., Marra R.E., Mathewson C.A., Mitchell T.G., Perrea M., Riggs P.R., Salzberg S.L., Shvartsbeyn A., Schein J.E., Shin H., Specht C.A., Suh B., Tenney A., Utterback T., Stys B.L., Waye N.H., Kronstad J., Lodge J.K., Heitman J., Davis R.W., Fraser C.M., Hyman R.W.; "The genome and transcriptome of Cryptococcus neoformans, a basidiamycete fungal pathogen of humans.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Fungi, Basidiomycota, Hymenomycetes, Heterobasidiomycetes;
Tremellomycetidae, Tremellales, Tremellaceae, Filobasidiella.
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Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami P. Tagawa A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; EmBL, AK037169; BAC29731.1; -; mRNA.
EmBL, AK037169; BAC29731.1; -; mRNA.
EmBL, AK037169; BAC397341.1; -; mRNA.
EMBL, AK037169; BAC397341.1Sik. Mus musculus.
MGI; MGI:1914803; 49334411Sik.
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Loftus B., Amedor P., Roncaglia P., Vamathevan J., Utterback T.,
Ard Aken S., Fraser C.; Fraser C.s. Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                       Length 330;
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Last annotation update)
                                                                                                                                                                                                                                                     70.0%; Score 35; DB 2; I 66.7%; Pred. No. 3.7e+02;
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Best Local Similarity 66...
6; Conservative
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QSKPD8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
ORFNames=CNA03150;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIRALINE_2297040; PubMed=14621292; MEDLINE_2297040; PubMed=14621292; Makamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T., Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N., Shimpo S., Takeuchi C., Yamada M., Tabata S.; Tomplete genome structure of Gloeobacter violaceus PCC 7421, a cyanobacterium that lacks thylakoids."; DNA Res. 10:137-145(2003).

-! CATALYTIC ACTIVITY: L-Glutamate 1-semialdehyde + NADP(+) + FRNA (Glu) = L-Glutamy1-tRNA (Glu) + NADPH.
-!- PATHWAY: Porphyrin biosynthesis by the C5 pathway; first step. Involved in chlorophyll biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                        29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Glutamyl-tRNA reductase (EC 1.2.1.70) (GluTR).
Mame=hemA; OrderedLocusNames=glr1218;
Gloeobacter violaceus.
Bacteria; Cyanobacteria; Gloeobacteria; Gloeobacter.
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HAWAP; MF 00087; -; 1.
InterPro; IPR000343; Glutr.
InterPro; IPR000518; Shikimate_DH.
InterPro; IPR000584; Thir NAD_FAD_bd.
Pfam; PF00745; Glutr Cdimer; 1.
Pfam; PF05201; Glutr N, 1.
Pfam; PF01488; Shikimate_DH; 1.
TIGRFAM9; TIGR01035; hemā; 1.
Chlorophyll biosynthesis; Complete proteome; NADP; Oxidoreductase;
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99 Proton acceptor (By similarity).
48136 MW; 5491B16BF167B368 CRC64;
                                                                                                                                                                                  70.0%; Score 35; DB 2; Length 334; 55.6%; Pred. No. 3.8e+02; tive 3; Mismatches 1; Indels
                                                                                                                        PROSITE; PSS0013; CHROWO 2; 1.
Complete proteome; Hypothetical protein; Nuclear protein.
SEQUENCE 334 AA; 39200 MW; E1E20A7092538F15 CRC64;
            EMBL, AE017341; AAW40937.1; -; Genomic_DNA.
GO; GO:000785; C:chromatin; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005624; C:nucleus; IEA.
GO; GO:0005633; P:chromatin binding; IEA.
InterPro; IPR009953; Chromo.
PFan; PF00138; Chromo; 1.
SMART; SM00298; CHROMO; 1.
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                                                                                                                                                                                                                                                                                                                                                430 AA
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Science 307:1321-1324 (2005)
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nes 5; Conservative
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ACT_SITE 50 50
ACT_SITE 99 99
SEQUENCE 430 AA; 4813
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Q7NLA8;
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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Rhabditidae; Peloderinae; Caenorhabditis.
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The C. elegans sequencing consortium,
"Genome sequence of the nematode C. elegans: a platform for
Investigating biology.";
Science 282:2012-2018 (1998).
REMBL; Z81106; CAB01323: 3; -; Genomic DNA.
REMBL; AL033536; CAD45609.2; -; Genomic DNA.
REMBL; AL033536; CAD45609.2; -; Genomic DNA.
REMBL; Z81106; CAD45609.2; JOINED; Genomic DNA.
REMBL; Z81106; CAD45609.2; JOINED; Genomic DNA.
REMBL; Z83961; T23961.
REMBC; CAD45609.2; JOINED; Genomic DNA.
REMBC; CAD46609.2; JOINED; Genomic DNA.
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Score 35; DB 1; Length 430;
Pred. No. 5e+02;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1998 (TrEMBLrel. 07, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
13.SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein R06Cl.6.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein D2030.2b.
ORFNames=D2030.2, D2030.2B;
Caenorhabditis elegans.
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STRAIN-Bristol N2;
MEDLINE-99069613; Pubmed-9851916;
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science 282:2012-2018(1998).
EMBL; 273906; CAB45047.1; -; Genomic_DNA.
HSSP; 025926; 1UM8.
   70.0%;
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6; Conservative
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Carrainestrian Sergeare.

Strain-CSTBL/65; Tissue-Retina;

MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

A Arakawa T., Ahinagawa A., Shibata K., Yoshino M., Itch M., Ichkind S.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruhl P., Lewis S., Matsud Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Puruno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Bromstein M.J., Bult C., Fletcher C., Fullid M., Mazzarelli J., Nombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nymbaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Havashiraki V., V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the RIKEN Genome Exploration Research Group Phase I & II Team; Manalysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=Retina;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUE=Retina;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sunin N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Sumamoto R., Mateumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoke W., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Mateuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RikEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
MUS musculus adult retina cDNA, RIKEN full-length enriched library,
clone:A9330013F09 product:similar to OVARC1001010 PROTEIN.
Name=4933434L15Rik;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection.";
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The FANTOM Consortium,
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NUCLEOTIDE SEQUENCE
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A WEDILINE=22388244; PubMed=12471157; DOJ=10.1073/pnas.252529799;
A WEDILINE=22388244; PubMed=12471157; DOJ=10.1073/pnas.252529799;
A Mayhew G.F., Burland V., Plunkett G. III, Redford P., Roesch P.,
A Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
A Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
T. "Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli.",
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
R RBL; Asto1670; AAN80398 1; -; Genomic_DNA.
R GO; GO:0008270; F:zinc ion binding; IEA.
R GO; GO:0006209; P:zinc ion binding; IEA.
R InterPro; IPR006025; Pept M.Z. BS.
R ROSITE; PS00142; ZINC_PROTEASE; I.
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Escherichia coli 06.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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55.6%; Pred. No. 5.6e+02;
Lionatches 1; Indels
472 AA; 52843 MW; F5758ECF8BD0393A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     51239 MW; 682775F2C9FC4C11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Protein hipA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CFT073 / ATCC 700928 / UPEC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ilarity 66.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 46
Q8BXR2 MOUSE
ID Q8BXR2_MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QBFHF4_ECOL6 PRELIMINARY;
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hes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 QQSNNQPPS 115
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453 EONNHEPPT 461
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                     470 AA;
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                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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RESULT 45
OGERH84 ERO
10 08FH84
DT 01-MA
RA Welch
RA Melch
RA Melc

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542 AA

PRT;

Matches

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94 QESSEHPPT 102
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SEQUENCE
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Q61EX9_CAEBR
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GO; GO:000875; F:S-adenosylmethionine-dependent methyltransf. . .; IEA.
GO; GO:010740; F:transferase activity; IEA.
InterPro; IPR000051; SAM_DA
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CS7BL/6J; TISSUB=Thymus; MEDLINE=98279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus adult male thymus CDNA, RIKEN Ull-length enriched
library, clone:5830430H09 product:similar to OVARC100100 PROTEIN
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Methyltransferase; Transferase.
SEQUENCE 542 AA; 60617 MW; 7A17C6478393FC49 CRC64;
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Genome Res. 10:1757-1771(2000).
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Q9CTV2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 70.0
Best Local Similarity 66.7
Matches 6; Conservative
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164 QESSEHPPT 172
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Mus musculus (Mouse)
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Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Imotani K., Ishii Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomuza K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Subakited (Auc. 2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AKO20021; BAB31969.1; -; mRNA.
EMBL, AKO20021; BAB31969.1; -; mRNA.
REBERDI, EMSMUSGO000028018; Mus musculus.
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InterPro; IPR000051; SAM_bd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The FANTOM CONSORTIUM, the RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                     Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUE=Thymus;
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Matches 6; Conservative
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MEDLINE=20083487; PubMed=10617197; DOI=10.1038/45471;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6238;
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                                                                                                                                                                                                                                                                                                                                                                                                 The C.briggsae Sequencing Consortium;
The C.briggsae Sequencing Consortium;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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095LH0; O21114;
10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-MX-2005 (Rel. 47, Last annotation update)
ETHYLENE-INSENITY-3-1ike 1 protein.
Name-EILI; OrderedLocusNames=At2g27050; ORFNames=T20PB.10;
Arabidopsis thaliana (Mouse-ear cress).
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Pred. No. 7e+02;
1; Mismatches 2; Indels
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ATP-binding; Hypothetical protein; Nucleotide-binding.
                                                                                           (TrEMBLrel. 28, Last sequence update) (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; CAACO1000058; CABG6568.1; -; Genomic_DNA.000; GO:0005524; F:ATP binding; IEA.00; GO:0005824; F:ATP binding; IEA.00; GO:0006887; F:MTP are activity; IEA.00; GO:000166; F:metal ion binding; IEA.00; GO:0001066; F:mucleotide binding; IEA.00; GO:0001087; F:unfolded protein binding; IEA.00; GO:00051082; F:unfolded protein binding; IEA.00; GO:0005131; P:protein folding; IEA.InterPro; IPR004487; ClpX.
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                                                                                                                                                         protein CBG11883 (Fragment).
                                                              (TrEMBLrel. 28, Created)
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Q61EX9 CAEBR PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                   Name=CBG11883;
Caenorhabditis briggsae.
                                                                                                                     25-OCT-2004 (TrEMBLrel Hypothetical protein Cl
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Best Local Similarity
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Southrick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
Chao Q., Choy N., Enju A., Goldmith A.D., Gurjal M., Hansen N.F.,
Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,
Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBJUNT: Acts as homodimer to bind the primary ethylene response element (By similarity).
-1- SUBCELLULAR LOCATION: Nuclear (By similarity).
-1- MISCELLANBOUS: LOSS-Of-function mutations (ELLI-1 and ELLI-2) in the gene show a weak ethylene-insensitive phenotype.
-1- SIMILARITY: Belongs to the EIN3 family.
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Activator; Coiled coil; DNA-binding; Nuclear protein; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Solano R., Stepanova A.N., Chao O., Ecker J.R.;
"Nuclear events in ethylene signaling: a transcriptional cascade
mediated by ETHYLENE-INSENSITIVE3 and ETHYLENE-RESPONSE-FACTORI.";
Genes Dev. 12:3703-3714 (1998).
Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                      'Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                STRAIN=cv. Columbia;
MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;
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EMBL; B1003344; AAC29962.1; -; mRNA.
PIR; B84668; B84668.
SMR; Q9SLHO; 180-303.
TRANSPAC; 102650; -.
GO: GO:0003700; F:transcription factor activity; TAS.
GO; GO:0009873; P:ethylene mediated signaling pathway; TAS.
Pfam; PF04873. Priv.
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EMBL; AC005623; AAC77863.1; -; Genomic_DNA.
EMBL; AY065191; AAL38367.1; -; mRNA.
                                                                                                                                                                                                                                                                         [3]
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
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                                                                                                                                                                                                                                 Nature 402:761-768(1999).
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01-JAV-1998 (TrEMBLrel. 05, Last sequence update)
01-JAV-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 20, Last annotation update)
0RFNames=D2030.2, D2030.2a.
Caenorhabditis elegans.
Caenorhabditidae; Retazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
The C. elegans sequencing consortium;
"Genome sequence of the nematode C. elegans: a platform for
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                                                                  70.0%; Score 35; DB 1; Length 584; 75.0%; Pred. No. 7.1e+02; ative 1; Mismatches 1; Indels
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74 74 E -> G (in Ref. 1).
584 AA; 66495 MW; 471E1715D1483B11 CRC64;
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ATP-binding; Complete proteome; Hypothetical protein;
Nucleotide-binding; Transport.
SEQUENCE 586 AA; 63606 WW; DFF205957A53A805 CRC64;
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Science 282:2012-2018(1998).
Science 282:2012-2018(1998).
EMBL; 273966; CAA980115.1; -; Genomic_DNA.
PIR; PASP; O25926; 1UWB.
Braembl; D2030.2; Caenorhabditis elegans.
WormBeep; D2030.2; Caenorhabditis elegans.
WormPep; D2030.2; Caenorhabditis elegans.
WormPep; D2030.2; PATP binding; IEA.
GO; GO:00016897; F:ATP binding; IEA.
GO; GO:00016897; F:ATP and binding; IEA.
GO; GO:000166; F:nucleotide binding; IEA.
GO; GO:000166; F:nucleotide binding; IEA.
GO; GO:000166; F:nucleotide binding; IEA.
GO; GO:0001802; F:unfolded protein binding; IEA.
GO; GO:0015031; P:protein transport; IEA.
InterPro; IPR0034891; AAA ATPase.
InterPro; IPR0034891; AAA, ATPASE.
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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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3B9 was positive. CDNA clones of the 3B9 light and heavy chains were cloned into pGEMYf+ and transformed into E. coli DH5-alpha. A heavy chain cDNA clone was sequenced (AAQ83491) that encoded the protein given in AAR70190. 3 CDNB (AAR70198-200) were identified. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 7 AA;

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## ALIGNMENTS

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Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated and IgE-mediated allergic conditions.
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                                                                             AAR70198 standard; protein; 7 AA
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93US-00136783.
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                                                                                                                                                                                                                                   25-MAR-2003
20-SEP-1995
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                                                                                                                                                          AAR70198;
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AAR70198
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Spleen cells from mice immunized with human IL-4 were used to prepare hybridomas, which were screened for anti-IL-4 MAD secretion. Only clone

Disclosure, Page 56; 97pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New DNA molecules encoding recombinant antibodies useful for treating IL4
                                                                                                                                                                                                                                                                                                                  Heavy chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanísed antibody; IL-4 mediated allergic reaction; Immunoglobulin B-mediated allergic reaction; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy; complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a complementarity determining region (CDR) of the heavy chain variable region of murine interleukin-4 (IL-4) antibody 3B9. The specification describes chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunosjobulin B-mediated allergic reactions e.g. allergic reninitis, conjunctivitis, atopic dermatitis, atopic acthma, anaphylactic shock, rheumatoid arthritis, host-versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans
                                                Gaps
                                                ..
             100.0%; Score 34; DB 2; Length 7; 100.0%; Pred. No. 2e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                         CDR of the heavy chain variable region of antibody 3B9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gross MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Col 45; 50pp; English.
                                                                                                                                                                                          AAY23775 standard; peptide; 7 AA
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93US-00136783.
94WO-US010308.
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                                                                                                                                                                                                                                                           13-SEP-1999 (first entry)
Query Match
Best Local Similarity 100.
7; Conservative
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                                                                                              TSGMGVS 7
                                                                              TSGMGVS
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14-OCT-1993;
07-SEP-1994;
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Best Loc Matches

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AAY18111 ID AAY RESULT

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New polynucleotide encoding a complementarity- or framework-determining region of an anti-idiotypic antibody that binds to human or primate antihuman immunodeficiency virus (HIV) antibodies, for use in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     idiotypic antibody complementarity-determining region (CDR) or framework-determining region (FR). The antibody binds to human or primate antihuman immunodeficiency virus (HIV) antibodies and can be used in the treatment of HIV infection. The present sequence is a region of the IF7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monoclonal antibody; 10D5; complementarity determining region; CDR; mouse; humanised antibody; antibody; Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to coding sequences of the murine 1F7 anti-
                                                                                                                                         Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR; complementarity determining region; framework-determining region; FR; heavy chain; light chain; HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 34; DB 5; 100.0%; Pred. No. 2e+06;
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                                                                                                          Murine Mab 1F7 heavy chain CDR1 region.
   AAO18530 standard; peptide; 7 AA.
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                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Muller S, Kohler H;
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1 TSGMGVS 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7 AA;
                                                                        11-OCT-2002
                                                                                                                                                                                                                                                                                        18-JUL-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                against HIV.
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                                     AA018530;
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ID ABP
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                                                                                                                                                                                                                                                                                                                                         Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease; complementarity determining region; CDR.
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                                       Gaps
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Score 34; DB 2; Length 7;
Pred. No. 2e+06;
0; Mismatches 0; Indels
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Pred. No. 2e+06;
Mismatches 0
                                                                                                                                                                                                                                                                                                     Heavy chain CDR for hIL-4 specific antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atopic ashthma and anaphylactic shock.
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                                                                                                                                                                                                 AAY18111 standard; peptide; 7 AA
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100.0%; Pri
cive 0; 1
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 100.0%;
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93US-00136783.
94WO-US010308.
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                                                                                                                                                                                                                                                                      (first entry)
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Best Local Similarity 100.
Matches 7; Conservative
                                     Conservative
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                Local Similarity
nes 7; Conserv
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14-OCT-1993;
07-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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 Query Match
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Gaps ;

07-NOV-2002

RESULT 4 AAO18530

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Benson JM;

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(MERC/) MERCKEN M.
(BENS/) BENSON J M.
                                     Mercken M,
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                                                                                                                                                                                                         The present sequence is that of complementarity determining region (CDR) antibodies of the heavy chain of murine monoclonal antibody 10D5. Novel humanised antibodies of the invention have CDRs from 10D5 and human framework sequences. These humanised antibodies have binding affinities (affinity and epitope location) approximately the same as those of the mouse 10D5 antibody. The invention includes antibodies, single chain antibodies, and their fragments, as well as nucleotide sequences, vectors, transformed host cells, and methods of using the humanised antibody to treat, prevent, alleviate, reverse or otherwise ameliocate symptoms and/or pathology associated with Down's syndrome, (pre-)clinical Albheimer's disease or (pre-)clinical cerebral amyloid angiopathy, and to inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amyloid, antibody engineering; antibody production; allergy; anyloid-associated disorder; Alzheimers disease; cancer; allergy; autolimune disease; Parkinsons disease acquired immune deficiency syndrome; multiple sclerosis; migraine; acquired immune deficiency syndrome; multiple sclerosis; migraine; dementia; infection; nootropic; neuroprotective; cytostatic; antiallergic; Immunosuppressive; antiparkinsonian; antimigraine; antimicrobial; anti-HIV; heavy chain; complementarity determining region.
                                                                                                                                   New humanized 10D5 antibody, useful for the manufacture of a medicament for treating Down's syndrome, clinical or pre-clinical Alzheimer's disease or cerebral amyloid angiopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 34; DB 6; Length 7; llarity 100.0%; Pred. No. 2e+06; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalian amyloid antibody, heavy chain CDR SEQ ID No:53.
                                                                                                                                                                                                                                                                                                                                                     formation or reduce Abeta plaque in the brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADZ08828 standard; peptide; 7 AA.
                                                                                                                                                                                       Claim 2; Page 29; 52pp; English.
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28-MAR-2003; 2003US-0458474P.
28-MAR-2003; 2003US-0458509P.
28-MAR-2003; 2003US-0458510P.
           26-APR-2002; 2002WO-US011854
                                    30-APR-2001; 2001US-0287653P
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                                                             (BLIL ) LILLY & CO ELI
                                                                                     Hinton PR, Vasquez M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CENZ ) CENTOCOR INC
                                                                                                             WPI; 2003-183836/18.
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Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TSGMGVS 7
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                                                                                                                                                                                                                                                                                                                                                                           Sequence 7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADZ08828;
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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The invention relates to at least one isolated mammalian amyloid antibody comprising at least one heavy comprising at least one isolated mammalian amyloid antibody that binds to the same region of an amyloid polypeptide as an antibody comprising at least cone heavy chain complementarity determining at least cone heavy chain caid sequence of at least one of SEO ID NO: 79.78, (ii) having the amino acid sequence of at least one of SEO ID NO: 79.78, (iii) having the amino acids 2-7, 3-8, 33-42, or 34-40 of a fully defined sequence of 42 amino acids (SEO ID NO: 50), (iii) an isolated nucleic acid encoding at least one of may of the isolated mammalian amyloid antibody. (iii) an isolated nucleic acid encoding at least one of sEO ID NO: 50, (iii) an isolated nucleic acid encoding at least one muman complex of sequence of SEO ID NO: 51, 52, 61, 62, 71, 72, 81 and 82, (iv) an isolated nucleic acid encoding an amyloid antibody, (vi) a protatypolic or entatypoid antibodis. (vi) a method of an isolated nucleic acid encoding an amyloid antibody (vi) a method of comprising an isolated nucleic acid encoding an amyloid antibody (vi) a method of comprising an isolated nucleic acid encoding an amyloid antibody (vi) a method of the amyloid antibodise mentioned, and at least one pharmaceutical carrier or animal, (vi) a method of diagnosing or treating an amyloid antibodise mentioned, where the device comprising a contracting or administering a comprising at least one amyloid antibodise mentioned, where the device comprising at least one amyloid antibodise mentioned, where the device comprising a contracting or administering as anyloid antibodise mentioned, where the device comprising a contracting or administering as anyloid antibodise mentioned, where the device comprising a contracting or administering as anyloid antibodise mentioned, where the device c
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                                                                                                                amyloid-associated disorders, such as Alzheimer's disease, cancer, allergies, autoimmune disease, Parkinson's disease, multiple sclerosis, migraine and dementia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune disease, Parkinson's disease, AIDS, multiple sclerosis, migraine, dementia and infantia.
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                                                                                 New isolated mammalian anti-amyloid antibodies useful for treating
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                                                                                                                                                                                                                                                                                                Claim 6; SEQ ID NO 53; 306pp; English
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WPI; 2005-242565/25.
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ID AAY2
XX
AC AAY2
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Recombinant IL4 antibodies useful for tratment of allergic rhinitis,
                                                                                                                                                                                                                                                                       atopic ashthma and anaphylactic shock.
                                                                                                                                                                                                                                                                                               Example 3; Col 65-66; 50pp; English.
                                                                                                                                                                                                Gross MS;
                                                                                                                                                           PLC.
CORP.
                                                                                                           93US-00117366.
93US-00136783.
94WO-US010308.
                                                                                    95US-00483636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine Mab 1F7 heavy chain.
                                                                                                                                                           (SMIK ) SMITHKLINE BEECHAM (SMIK ) SMITHKLINE BEECHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                Sylvester DR, Holmes SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IMMP-) IMMPHERON INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Muller S, Kohler H;
                                                                                                                                                                                                                     WPI; 1999-370482/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 TSGMGVS 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                   N-PSDB; AAX79527.
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200255668-A2.
                                                                                    07-JUN-1995;
                                                                                                            07-SEP-1993;
14-OCT-1993;
                                                                                                                                      07-SEP-1994;
                                     US5914110-A.
                                                              22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JUL-2002.
               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA018528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                       The specification describes chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin B-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host-versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans. The present sequence represents the heavy chain variable region of Ig NEW, and is used in the course of the
                                                                                                                                                                                                                                                                                                                                                                              New DNA molecules encoding recombinant antibodies useful for treating IL4 -mediated conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease.
                                             Light chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin B-mediated allergic reaction; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic dermatitis; aropic dermatitis; antipic asset; renal disease; allergy; rheumatoid arthritis; host-versus-graff disease; renal disease; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 34; DB 2; Length 121; 100.0%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heavy chain sequence for humanised 3B9 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                      Heavy chain variable region of 1g NEW.
                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Col 65-66; 50pp; English
                                                                                                                                                                                                                                                                                                                      Gross MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY18122 standard; protein; 121 AA
                                                                                                                                                                                                                                                                                SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                           SMIK ) SMITHKLINE BEECHAM PLC
                                                                                                                                                                                                                                           93US-00136783.
94WO-US010308.
                                                                                                                                                                                                                                 93US-00117366.
                                                                                                                                                                                                          95US-00483632
 (first entry)
                                                                                                                                                                                                                                                                                                                    Sylvester DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                            WPI; 1999-429500/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 TSGMGVS 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TSGMGVS 7
                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAX85929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 121 AA;
                                                                                                                                                                                                         07-JUN-1995;
                                                                                                                                                                                                                                 07-SEP-1993;
                                                                                                                                                                                                                                            14-OCT-1993;
07-SEP-1994;
13-SEP-1999
                                                                                                                                                         US5928904-A
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                                                                                                                                                                                 27-JUL-1999
                                                                                                                                                                                                                                                                                                                    Holmes SD,
                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY18122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                       Ig NEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
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This sequence represents the heavy chain of the humanised 1B9 antibody of the invention. The antibody is a chimeric or humanised interleukin-4 (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic asthma and anaphylactic shock. The antibodies are also useful for requiating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft versus host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR; complementarity determining region; framework-determining region; FR; heavy chain; light chain; HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 34; DB 2; Length 121; 100.0%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA018528 standard; protein; 121 AA.
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Gaps

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0; Indels

5; Length 121;

Score 34; DB Pred. No. 36; Mismatches

100.0%;

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infections. ABG67186-ABG67189 represent variable regions of human 1gG1
                                                                                                                                                                                                                                                                                                        antibody; CD30; anti-CD30 antibody; cytostatic; gene therapy; cancer
                                                                                                                                                                                                                                                                                Anti-CD30 monoclonal antibody VH variable region T105 SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                      ADG25814 standard; protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                            09-JUN-2003; 2003WO-US018373.
                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-2002; 2002US-0387293P.
16-SEP-2002; 2002US-0411032P.
                                                                                                                                                                                                                                                       (first entry)
                                                                                         Conservative
              antibody heavy chain
                                                   31 TSGMGVS 37
                                                                                                               1 TSGMGVS
                                       Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                          WO2003104432-A2
                                                                                                                                                                                                                                                       11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kreitman R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pastan IH,
                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                               ADG25814;
                                                                                                                                                                               RESULT 11
                                                                                                                                                                                            ADG25814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a hepatitis C virus (HCV) vaccine comprising different groups of peptides each group being capable of raising, in an infected individual, an antibody able to bind to the hypervariable 1 (HVR1) region of the envelope protein E2 of the infecting HCV strain. The different groups of peptides are administered sequentially to raise antibodies, helper T-lymphocytes, and cytotoxic T-lymphocytes which are cross-reactive to the HVR1 region of the infecting HCV. The vaccines are useful for preventing and treating chronic HCV
                                                                                                                                      The present invention relates to coding sequences of the murine 1F7 antidictypic antibody complementarity-determining region (CDR) or framework-determining region (FR). The antibody binds to human or primate antihuman immunodeficiency virus (RIV) antibodies and can be used in the treatment of HIV infection. The present sequence is the 1F7 heavy chain
                                                New polynucleotide encoding a complementarity- or framework-determining region of an anti-idiotypic antibody that binds to human or primate anti-human immunodeficiency virus (HIV) antibodies, for use in vaccines
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        helper
                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus vaccine; HCV; hypervariable region 1; HVR1; envelope protein E2; antibody; helper T-lymphocyte; IgGl; cytotoxic T-lymphocyte; HCV infection; virucide; heavy chain.
                                                                                                                                                                                                                                          100.0%; Score 34; DB 5; Length 121; 100.0%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus (HCV) vaccines able to raise antibodies, lymphocytes and/or cytotoxic T lymphocytes able to bind to hypervariable 1 region of the infecting HCV strain.
                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human IgGl antibody heavy chain variable region 15H4VH.
                                                                                                                                                                                                                                                                   Mismatches
                                                                                                              Disclosure, Page 18-19; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  ABG67188 standard; protein; 121 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; Fig 2; 52pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-DEC-2000; 2000GB-00030102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Piccolella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-DEC-2001; 2001WO-GB005421
                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                             Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-508540/54.
           WPI; 2002-590668/63.
N-PSDB; AAL48652.
                                                                                                                                                                                                                                                                                                                    31 TSGMGVS 37
                                                                                                                                                                                                                                                                                            1 TSGMGVS 7
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C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ALLA/) ALLAIN J
                                                                                                                                                                                                                  Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200245743-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                    24-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-JUN-2002
                                                                                        against HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Allain J,
                                                                                                                                                                                                                                                                                                                                                                                                           ABG67188;
                                                                                                                                                                                                                                                                                                                                                          RESULT 10
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The present invention describes an isolated antibody that binds specifically to a stalk of CD30 of a cell, or to an epitope destroyed upon cleavage of soluble CD30 (sCD30) from intect CD30. Also described:

(1) a composition comprising the acid encoding an antibody that binds therapeutic part; (2) a nucleic acid encoding an antibody that binds comprising the nucleic acid encoding an antibody that binds specifically to a stalk of CD30 of a cell, or to an epitope destroyed upon cleavage of SCD30 from intact CD30; (3) an expression vector comprising the nucleic acid operably linked to a promoter; (4) inhibiting growth of a CD30+ cancer cell; (5) detecting the presence of a CD30+ cell as sample; (6) a host cell expressing the isolated nucleic acid encoding the antibody having variable heavy and variable light can a biological sample comprising a container and an anti-CD30 antibody.

An anti-CD30 antibody has cytostatic activity, and can be used in gene therapy. The anti-CD30 antibody that binds specifically to a stalk of contact CD30 is useful for the manufacture of a medicament for inhibiting the exemplification of the present invention.
                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                         New antibody that binds specifically to a stalk of CD30 of a cell, or t
an epitope destroyed upon cleavage of soluble CD30 (sCD30) from intact
CD30, useful for inhibiting the growth of a CD30+ cancer cell.
    Beers R;
Numata Y, Santora K,
                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 38; SEQ ID NO 14; 102pp; English
    Onda M,
Nagata S,
Sinha A;
                                                                                                                                       WPI; 2004-062352/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 121 AA;
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DB 8; Length 121;

100.0%; Score 34;

Query Match

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This invention relates to novel antibodies that bind to the G protein coupled receptor protein identified as GRR64, namely GRR64-1, GRR64-16, GRR64-18, GRR64-18, GRR64-19, GRR64-19, GRR64-19, GRR64-18, GRR64-18, GRR64-18, GRR64 anti-GRR64 antibodies as selective cytotoxic agents against GRR64 expressing tumour cells such as those associated with ovarian cancer, uterine cancer and Ewing's sarcoma. The present invention describes epitope mapping of those antibodies that show high affinity binding to GRR64 through competitive binding analyses, such that the antibodies can be assessed for GRR64 dependent cell death in vitro. Accordingly, they can be used to develop cytostatic compositions for gene therapy or immunotherapy that inhibit cellular proliferation of an ovarian cancerous call and furthermore can diagnose and inhibit growth of tumour cells. This polypeptide is encoded by a heavy chain variable region DNA sequence of a murine anti-human GRR64 antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                    New antibody that inhibits binding of a GPR64 polypeptide to an antibody comprising GPR64-18, GPR64-81, GPR64-93 or GPR64-101, useful in preparing a composition for diagnosing or treating ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse; human; humanised antibody; antibody; Alzheimer's disease;
Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
         uterine cancer; Ewing's sarcoma; cell death; cytostatic; gene therapy; immunotherapy; cellular proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monoclonal antibody, 10D5, complementarity determining region; CDR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanised 10D5 antibody heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 34; DB
100.0%; Pred. No. 37;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                            Dubridge R, Bhaskar V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; SEQ ID NO 17; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP58283 standard; protein; 123 AA.
                                                                                                                                                                                                                                                     (PROT-) PROTEIN DESIGN LABS INC
                                                                                                                                                                              19-DEC-2003; 2003WO-US040820
                                                                                                                                                                                                                   20-DEC-2002; 2002US-0435618P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
                                                                                                                                                                                                                                                                                                                               WPI; 2004-525780/50.
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                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ADQ09621
                                                                                                                                                                                                                                                                                          Law D, Wang Q,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 122 AA;
                                                                                                     WO2004058171-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus sp.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-OCT-2003
31-MAR-2003
                                                                                                                                           15-JUL-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                  Мив вр.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an engineered CD44 antibody for inducing the differentiation and wither of leukemia cells, the gene in the heavy chain and light chain variable region of monclonal antibody H144a of CD44, the polypeptide coded by said gene, the carrier containing said gene, and the application of said gene and polypeptide in preparing medicines for diagnosing and treating leukemia and disclosed. The present sequence represents the amino acid sequence of the mouse CD44 antibody V segment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Variable heavy chain protein of murine anti-human GPR64-18 antibody ID17.
                                                                                                                                                                                                                                                                                                                                               antibody engineering; CD44; leukemia; hematological disease; neoplasm;
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Engineering antibody against CD44 for inducing leukemia cell differentation and necrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 34; DB 9; Length 121; 100.0%; Pred. No. 36; Sive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 murine; mouse; antibody; GPR64; cytotoxic; ovarian cancer;
                             Indels
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HEMA-) HEMATOLOGY INST CHINESE MEDICINE ACAD.
           Pred. No. 36;
100.0%; Prea. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; SEQ ID NO 2; 19pp; Chinese.
                                                                                                                                                                                            AEA37667 standard; protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADQ09631 standard; protein; 122 AA.
                                                                                                                                                                                                                                                                                                         Mouse CD44 antibody V segment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-DEC-2003; 2003CN-01107583
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                                                                                                                                                                                                                                                                      (first entry)
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Best Local Similarity luv...
7; Conservative
                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2005-173920/19.
                                                                                                  31 TSGMGVS 37
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       Best Local Similarity
                                                            1 TSGMGVS 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Song G;
                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-OCT-2004
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                                                                                                                                                                                                                                                                                                                                                                  cytostatic
                                                                                                                                                                                                                                 AEA37667;
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                           Matches
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The present sequence is that of a preferred heavy chain variable region of a humanised antibody of the present invention. In this sequence, the complementarity determining regions (CDRs) originate from murine monoclonal antibody 10D5 and the framework region originates from human germline VH segment DP-28 and J segment JH4. Novel humanised antibodies of the invention have CDRs from 10D5 and human framework sequences. These humanised antibodies have binding affinities (affinity and epitope location) approximately the same as those of the mouse 10D5 antibody. The invention includes antibodies, single chain antibodies, and thair fragments, as well as nucleotide sequences, vectors, transformed host cells, and methods of using the humanised antibody to treat, prevent, alleviate, reverse or otherwise ameliorate symptoms and/or pathology associated with Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral amyloid anglopathy, and to inhibit formation or center of the brain. (Updated on 23-OCT-2003 to standardise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New humanized 10D5 antibody, useful for the manufacture of a medicament for treating Down's syndrome, clinical or pre-clinical Alzheimer's disease or cerebral amyloid angiopathy.
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                                                                                                                                                                                                                                                  label= Met, Ile, Leu
                                                                                                                                                                                                                                                                               label= Asn, Ser, Thr
                                                                                                                                                                                                                                                                                                              label= Met, Val, Leu
                                                                                                                                                        label= Lys, Arg
                                                                                                                                                                                     label= Ser, Thr
                                                                                                                                                                                                                    label= Thr, Ser
/label= Gln, Glu
                            label= Val, Ala
                                                                                                                          label= Ser, Thr
                                                                                                                                                                                                                                                                                                                                                                         /label= Leu, Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 8; 52pp; English.
                                                             "CDR1"
                                                                                           note= "CDR2"
                                                                                                                                                                                                                                                                                                                            .00. .112
'note= "CDR3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-APR-2002; 2002WO-US011854.
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Best Local Similarity 100.
Matches 7; Conservative
                                                                        .67
                                             11. .35
'note= "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hinton PR, Vasquez M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-183836/18.
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                                                                                                           Misc-difference
                                                                                                                                                                       Misc-difference
                Misc-difference
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                                                                                                                                                                                                     Misc-difference
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                                                                              Region
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The present sequence is that of a particularly preferred heavy chain variable region of a humanised antibody of the present invention. In this sequence, the complementarity determining regions originate from murine monoclonal antibody 10D5 and the framework region originates from murine germline VH segment DP-28 and J segment JH4. Novel humanised antibodies of the invention have CDRs from 10D5 and human framework sequences. These humanised antibodies have binding affinities (affinity and epitope clocation) approximately the same as those of the mouse 10D5 antibody. The invention includes antibodies, single chain antibodies, and their framents as well as nucleotide sequences, vectors, transformed host cells, and methods of using the humanised antibody to treat, prevent, alleviate, reverse or otherwise ameliorate symptoms and/or pathology associated with Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical Alzheimer's disease or (pre-)clinical amyloid angiopathy, and to inhibit formation or ceduce Abeta plaque in the brain. (Updated on 23-0CT-2003 to standardise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                        Monoclonal antibody; 10D5; complementarity determining region; CDR; mouse; human; humanised antibody; antibody; Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New humanized 10D5 antibody, useful for the manufacture of a medicament for treating Down's syndrome, clinical or pre-clinical Alzheimer's disease or cerebral amyloid angiopathy.
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                                                                                                                         Humanised 10D5 antibody heavy chain variable region.
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
ABPS8285 standard; protein; 123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 9; 52pp; English.
                                                                                                                                                                                                                                                                                                                  .35
                                                                                                                                                                                                                                                                                                                                                     52. .67
/note= "CDR2"
                                                                                                                                                                                                                                                                                                                                                                                          100. .112
/note= "CDR3"
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                                                                     (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200288307-A2.
                                                                                                                                                                                                                                  Mus sp.
Homo sapiens.
Chimeric.
                                                                   23-OCT-2003
31-MAR-2003
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                                    ABP58285;
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TSGMGVS 37 TSGMGVS 7

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The present sequence represents the heavy chain variable region of murine interleukin.4 (IL-4) antibody 3B9. The sequences are used in the production chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin B-mediated allergic reactions e.g. allergic rehinitis, conjunctivitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New DNA molecules encoding recombinant antibodies useful for treating 1L4-mediated conditions.
                                                                                                                                                                                     Heavy chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin B-mediated allergic reaction; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic aesthma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                    Heavy chain variable region of murine IL-4 antibody 3B9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heavy chain sequence for murine 3B9 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 34; DB
100.0%; Pred. No. 42;
ive 0, Mismatches
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                                      AAY23768 standard; protein; 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-00117366.
93US-00136783.
94WO-US010308.
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                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Conservative
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N-PSDB; AAX85885.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995;
                                                                                                               13-SEP-1999
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                                                                            AAY23768;
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                                                                                                                                                                                                                                                                                                      Mus sp.
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   RESULT 17
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                         4AY23768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spleen cells from mice immunized with human IL-4 were used to prepare hybridomas, which were screened for anti-IL-4 MAb secretion. Only clone 3B9 was positive. cDNA clones of the 3B9 light and heavy chains were cloned into pGEM7f+ and transformed into B. coll DH5-alpha. The clones were sequenced (AAQ83490-91), and used for antibody engineering. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated and IgE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                             Chimeric antibody; humanized antibody, antibody engineering; monoclonal antibody; MAb; interleukin-4; IL-4; allergy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      "complementarity determining region"
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                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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/label= Sig_peptide
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                                                                                         AAR70190 standard; protein; 140 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mediated allergic conditions.
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93US-00136783.
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/label= CDR
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/label= CDR
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/label= CDR
                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                          Mouse MAb 3B9 heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                   (revised)
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31 TSGMGVS 37
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20-SEP-1995
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Key Peptide Mus sp

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N-PSDB; AAQ83493.
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25-MAR-2003
20-SEP-1995
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14-OCT-1993;
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Peptide
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$2 X C C C C C C X S X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents the heavy chain of the murine 3B9 antibody of the invention. The antibody is a chimeric or humanised interleukin-4 (IL4) monoclonal antibody for the treatment of immunoglobulin E (1gE) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic dermartisis, atopic asthma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft versus host disease
                Antibody, interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allargic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant IL4 antibodies useful for tratment of allergic rhinitis, atopic ashthma and anaphylactic shock.
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interleukin-4; IL-4; allergy.
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100.0%; Pred. No. 42;
ive 0; Mismatches 0; Indels
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/label= Sig_peptide
51. .57
/label= CDR
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94WO-US010308.
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Matches 7; Conservative
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                                                                                                                                                      US5914110-A.
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07-SEP-1994;
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20-SEP-1995
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A humanized antibody heavy chain variable region and signal sequence is given in ARR70192. The signal sequence is also provided in ARR70193. The CDR sequences of the construct are identical to the native CDRs of mouse anti-human II-4 MAD 389 (AAR70198-200). (Updated on 25-WAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated and IgE-mediated allergic conditions.
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                    /note= "complementarity determining region"
120. .130
(label= CDR
/note= "complementarity determining region"
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0; Mismatches
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/label= Sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
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/label= CDR
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/label= CDR
/label= CDR
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Matches 7; Conservative
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Peptide

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The present sequence represents the heavy chain variable region of a humanised murine interleukin-4 (IL-4) antibody 3B9. The specification describes chimeric and humanised IL-4 monoclonal antibodies. The appecification antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans
                                                                                                                                                                                                                     New DNA molecules encoding recombinant antibodies useful for treating IL4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heavy chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin B-mediated allergic reaction; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic aethma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.
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100.0%; Pred. No. 42;
tive 0; Mismatches 0; Indels
                                                                                                                           Gross MS;
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                                                                (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
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93US-00136783.
94WO-US010308.
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94WO-US010308.
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(first entry)
                                                                                                                           Sylvester DR,
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                                                                                                                                                                                                                                          -mediated conditions
                                                                                                                                                              WPI; 1999-429500/36.
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                                                                                                                                                                                 N-PSDB; AAX85887
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Homo sapiens.
Chimeric.
         14-OCT-1993;
07-SEP-1994;
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14-OCT-1993;
07-SEP-1994;
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                                                                                                                         Holmes SD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A human/mouse chimeric antibody heavy chain variable region was constructed (given in AAR70191) that contained the mouse anti-human IL-4 MAD 3B9 variable region including 3 CDRS (AAR70198-200) and a human antibody signal peptide (AAR70193). The construct was used for humanized antibody production. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heavy chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody, humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin B-mediated allergic reaction; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic dermatitis; atopic dermatitis; aropic dermatitis; and anaphylactic shock; rheumatoid arthritis; host-versus-graff disease; renal disease; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated and IgB-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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/note= "complementarity determining region"
120. 130
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/label= CDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               mediated allergic conditions.
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93US-00136783.
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
Mus sp.
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RESULT 21 AAY23770 ID AAY2

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Gaps

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Indels

; 0

2; Length 141;

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This sequence represents the light chain of the chimeric 3B9 antibody of the invention. The antibody is a chimeric or humanised interleukin-4 (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic dermattisis, atopic asthma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft versus host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody, interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease.
                                                                                                                                                                                                                                                                                                                                                                                                              Heavy chain sequence for humanised 3B9 antibody.
                                                                                                                                                                  Query Match 100.0%; Score 34; DB Best Local Similarity 100.0%; Pred. No. 42; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gross MS;
                                                                                                                                                                                                                                                                                                                         AAY18117 standard; protein; 141 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMITHKLINE BEECHAM PLC. SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 15; Fig 4; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93US-00117366.
93US-00136783.
94WO-US010308.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-00483636
                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Holmes SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-370482/31.
                                                                                                                                                                                                                                                      57
                                                                                                                                                                                                                          7
                                                                                                                                                                                                                           1 TSGMGVS
                                                                                                                                                                                                                                                      51 TSGMGVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAX79516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 141 AA;
                                                                                                                                         Sequence 141 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sylvester DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-SEP-1993;
14-OCT-1993;
07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                  11-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US5914110-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                      AAY18117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SMIK) (SMIK) 8
                                                                                                                                                                                                                                                                                               RESULT 24
                                                                                                                                                                                                                                                                                                             AAY18117
*555555555
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                                                                                                                                   The present sequence represents the heavy chain variable region of murine/human interleukin-4 (IL-4) chimeric antibody 3B9. The specification describes chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin E-mediated allergic reactions e.g. allergic thinitis, conjunctivitis, atopic astumia, anaphylactic shock, rheumatoid arthitis, host-versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endagenous IL-4 levels in humans. (Updated on 17-OCT-2003 to standardise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease.
                                                                    encoding recombinant antibodies useful for treating IL4
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant IL4 antibodies useful for tratment of allergic rhinitis,
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0
                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 34; DB 2; Length 141; 100.0%; Pred. No. 42; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              monoclonal antibody heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atopic ashthma and anaphylactic shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MS;
Gross MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY18125 standard; protein; 141 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gross
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                                                                                                            Example 3; Fig 3; 50pp; English
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94WO-US010308.
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Holmes SD, Sylvester DR,
                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
                                                                   molecules enc
ed conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-370482/31.
                          WPI; 1999-429500/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                 51 TSGMGVS 57
                                                                                                                                                                                                                                                                                                                                                                                                           1 TSGMGVS 7
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                                       N-PSDB; AAX85886
                                                                                                                                                                                                                                                                                                                           Sequence 141 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric 3B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-OCT-1993;
07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-AUG-1999
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                                                                                   -mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY18125;
                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                 DNA
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Matches
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This sequence represents the heavy chain of the humanised 389 antibody of the invention. The antibody is a chimeric or humanised interleukin-4 (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic demarkitis, atopic asthma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft versus host disease
Recombinant IL4 antibodies useful for tratment of allergic rhinitis,
                                                                         atopic ashthma and anaphylactic shock
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Length 141;

Score 34; DB 2;

100.08;

Query Match

Example 5; Fig 3; 50pp; English

3D6; heavy chain variable region; immunoglobulin; complementarity determining region; CDR; 10D5; variable framework region; neuroprotective; nootropic; gene therapy; amyloidogenic disease;

Alzheimer's disease

Mus musculus

Peptide Protein

1. .19 /label= signal peptide /label= mature protein

.142

WO2004080419-A2

23-SEP-2004.

cocation/Qualifiers

Murine 10D5 immunoglobulin heavy chain variable region SEQ ID NO:16.

(first entry)

16-DEC-2004

ADR88420 standard; protein; 142 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to new humanized immunoglobulin (Ig) light chain (LC) or heavy chain (HC) comprising variable region complementarity determining regions from 3D6/10D5 Ig LC or HC variable region sequence, and variable framework region from human acceptor Ig LC or HC sequence. The invention is useful for preventing or treating an amyloidogenic disease or Alzheimer's disease in a patient. The invention is also useful for in vivo imaging amyloid deposits in a patient. The present amino acid sequence represents a mouse 3D6/10D5 variable light (VL) chain or
                                                                                                                                                                                                                                                                          Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC; variable region complementarity determining region; 3D6; 10D5; variable framework region; amyloidogenic disease; Alzheimer's disease; amyloid deposit; variable light chain; VL; variable heavy chain; VH; nootropic; neuroprotective; inhibitor of beta amyloid accumulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel light/heavy chain of humanized immunoglobulin for treating amyloidogenic disease, has 3D6/10D5 variable region complementarity determining regions and variable framework region from human acceptor
                   Gaps
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                   Indels
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                 0; Mismatches
    Pred. No.
                                                                                                                                                      ABG76934 standard; protein; 142 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 142; Fig 10; 171pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yednock T;
   100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-DEC-2001; 2001WO-US046587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-DEC-2000; 2000US-0251892P
                                                                                                                                                                                                                  (first entry)
                 7; Conservative
                                                                                                                                                                                                                                                Mouse 10D5 VH protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saldanha J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NEUR-) NEURALAB LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-519658/55.
N-PSDB; ABS59429.
                                                                             57
Best Local Similarity
Matches 7; Conserv
                                                1 TSGMGVS 7
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Best Local Similarity
                                                                           51 TSGMGVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 142 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      WO200246237-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMHP ) WYETH.
                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus.
                                                                                                                                                                                                                  05-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-JUN-2002
                                                                                                                                                                                     ABG76934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Basi G,
                                                                                                                                                                                                                                                                                                                                                          Abeta.
                                                                                                                                     ABG7693
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New humanized antibodies that recognize beta amyloid peptides, useful for preventing or treating amyloidogenic diseases, such as Alzheimer's

Yednock T;

Saldanha JW,

Basi G,

2004-668880/65.

N-PSDB; ADR88419

disease.

(NEUR-) NEURALAB LTD. (AMHP ) WYETH.

12-MAR-2004; 2004WO-US007503 12-MAR-2003; 2003US-00388389

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The invention relates to a novel humanised immunoglobulin light or heavy chain. The humanised immunoglobulin light or heavy chain comprises:

variable region complementarity determining regions (CDR's) from the 3D6 immunoglobulin light chain variable region sequence of 132 amino acids fully defined in the specification (ADR88406), or heavy chain variable region sequence of 131 amino acids fully defined in the specification (ADR88408), or from the 10D5 immunoglobulin light chain variable region sequence of 131 amino acids given in the specification (ADR88418) or heavy chain variable region sequence of 142 amino acids fully defined in the specification (ADR88420); and a variable framework region from a human acceptor immunoglobulin light or heavy chain sequence, provided that a least one framework residue is a residue that confromed antigen directly, a residue adjacent to a CDR, a conceptor immunoglobulin light or heavy chain sequence, where the framework residue is a residue that confromation and incerly, a residue adjacent to a CDR, a CDR interacting residue or a residue participating in the VL-VH interface.

An antibody of the invention has neuroprotective and moctropic activity, a for and may have a use in gene therapy. The composition and methods are not a for a form a for a form of the for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for preventing or treating an amyloidogenic disease, such as Alzheimer's disease. The variable region sequence is useful in producing a three-dimensional image of a 356 or 1005 immunoglobulin, immunoglobulin chain, or its domain. The present sequence represents the murine 1005 immunoglobulin heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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100.0%; Pred. No. 43;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 85; SEQ ID NO 16; 176pp; English
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Matches 7; Conservative
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0; Mismatches

7; Conservative

Matches

50 TSGMGVS 56

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RESULT 26 ADR88420

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anti-idiotype antibody or fragment that specifically binds at least one
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to at least one isolated mammalian amyloid antibody comprising at least one variable region comprising at least one heavy chain and at least one light chain, of a fully defined sequence of SEQ ID NOS: 48, 49, 59, 60, 69, 70, 79 and 80, respectively. Also described are: (i) at least one isolated mammalian amyloid antibody that binds to the same region of an amyloid polypeptide as an antibody comprising at least one heavy chain or light chain complementarity determining region (CDR) having the amino acid sequence of at least one of SEQ ID NO: 73-78, (ii) thuman CDR, where the antibody specifically binds at least one epitope sequence of 42 amino acids (SEQ ID NO: 50), (iii) an isolated nucleic acid encoding at least one for any of the isolated mammalian amyloid antibodies mentioned and having at least one human CDR of a fully defined artibodies mentioned and having at least one human CDR of a fully defined antibodies mentioned and having at least one human CDR of a fully defined sequence of SEQ ID NO: 51, 52, 61, 62, 71, 72, 81 and 82, (iv) an isolated nucleic acid vector comprising an isolated nucleic acid encoding an amyloid antibody, (v) a prokaryotic or eukaryotic host cell comprising an isolated nucleic acid encoding an amyloid antibody, (v) a method of producing at least one amyloid antibody, (vi) a comprising at least one of any of the isolated mammalian amyloid antibodies at least one pharmaceutical carrier or diluent, (vii) an enchol of mentioned, and at least one pharmaceutical carrier or diluent, (viii) an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amyloid-associated disorders, such as Alzheimer's disease, cancer, allergies, autoimmune disease, Parkinson's disease, multiple sclerosis,
                                                                                                                                                                                                                                                                                                      Mammalian amyloid antibody, heavy chain variable region SEQ ID No:59.
                                                                                                                                                                                                                                                                                                                                               amyloid; antibody engineering; antibody production; amyloid-associated disorder; Alzheimers disease; cancer; allergy; autoimmune disease; Parkinsons disease; acquired immune deficiency syndrome; multiple sclerosis; migraine; dementia; infection; nootropic; neuroprotective; cytostatic; antiallergic; Immunosuppressive; antiparkinsonian; antimigraine; antimicrobial; anti-HIV; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated mammalian anti-amyloid antibodies useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; SEQ ID NO 59; 306pp; English.
                                                                                                                                                              ADZ08834 standard; peptide; 142 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-MAR-2003; 2003US-0458474P.
28-MAR-2003; 2003US-0458509P.
28-MAR-2003; 2003US-0458510P.
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                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mercken M, Benson JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CENZ ) CENTOCOR INC.
(MERC/) MERCKEN M.
(BENS/) BENSON J M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2005-242565/25.
                                         50 TSGMGVS 56
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                                                                                                                                                                                                            ADZ08834;
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treating an amyloid antibodies mentioned, (ix) a method of diagnosing or treating an amyloid related condition in a cell, tissue, organ or animal, comprising or administering a composition comprising or last least come of the antibodies mentioned, with, or to, the cell, tissue, organ or animal, (x) a medical device comprising at least one amyloid antibody an exticle of manufacture for human plaramentical and antibody, (xi) an article of manufacture for human plaramentical or diagnostic use, comprising packaging material and a container comprising a solution or a lyophilized form of at least one of the amyloid antibodies mentioned, and (xii) a method of producing at clast one of the isolated mammalian amyloid antibodies, comprising providing a host cell or transgenic animal or transgenic plant or plant compositions of the present invention are useful for cell capable of expressing the antibody in recoverable amounts. The producing therapeutic compositions and devices for treating amyloid associated disorders, such as Alzheimer's disease, cancer, allergies, allowing a host call or present invention are useful for present invention are useful for present and devices for treating amyloid associated disorders, such as Alzheimer's disease, cancer, allergies, allowing and antibody antibody and antibody and antibody and antibody antibody and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              migraine, dementia and infections. This sequence represents a heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polypeptide inhibiting binding of human interleukin-6 (IL-6) to its receptor - useful for treating auto:immune disease induced or aggravated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human interleukin-6 binding inhibitor; IL-6; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 34; DB 9; Length 142; ; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        variable region useful in the antibody of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hamuro J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     septic shock; multiple myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR58612 standard; protein; 246 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 18; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94EP-00102346.
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(first entry)
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Best Local Similarity 100...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shimamura T, Nakazawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AJIN ) AJINOMOTO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1994-295777/37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 142 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-FEB-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
28-APR-1995
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us-10-723-872-22.rag

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TSGMGVS
                                                                                                                                  Sequence 453 AA;
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Homo sapiens.
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31-MAR-2003
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                                                                                               os field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric.
                                                                                                                                                                    Query Match
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Peptide
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AC ABP58289
AC ABP5
AC ABB5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monoclonal antibody, 10D5, complementarity determining region, CDR, mouse; human; humanised antibody; antibody, Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New humanized 10D5 antibody, useful for the manufacture of a medicament for treating Down's syndrome, clinical or pre-clinical Alzheimer's disease or cerebral amyloid angiopathy.
                                                                                                                                  Gaps
rheumatoid arthritis, septic shock due to bacterial infection and multiple myeloma. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                  ö
                                                                                           Score 34; DB 2; Length 246; Pred. No. 73; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "light chain variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                        Humanised 10D5 antibody heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 10-12; 52pp; English.
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                                                                                                                                                                                                                                                                                                     ABP58287 standard; protein; 453
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31. .35
                                                                                           100.0%;
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/note= "CDR2"
100. .112
/note= "CDR3"
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                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                     Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .123
/note= "
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                                                                                                                                                                                                                                                                                                                                                                                   (revised)
                                                                                                                                                                                          |||||||
153 TSGMGVS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-183836/18.
                                                                                                                                                                      1 TSGMGVS 7
                                                       Sequence 246 AA;
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Homo sapiens.
Chimeric.
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31-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-NOV-2002
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Region
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                                                                                                                                                                                                                                                                   RESULT 29
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cells, and methods of using the humanised antibody to treat, prevent, alleviate, reverse or otherwise ameliorate symptoms and/or pathology associated with Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "light chain variable region, claimed in Claim 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New humanized 10D5 antibody, useful for the manufacture of a medicament for treating Down's syndrome, clinical or pre-clinical Alzheimer's disease or cerebral amyloid angiopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Mature_protein
/note= "the mature light chain is claimed in Claim 5"
                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                     Length 453;
                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                               100.0%; Score 34; DB 6; I
100.0%; Pred. No. 1.3e+02;
iive 0; Mismatches 0;
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/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanised 10D5 antibody heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP58289 standard; protein; 472 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71. .86
/note= "CDR2"
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/note= "CDR1"
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/note= "CDR3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-APR-2002; 2002WO-US011854.
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N-PSDB; ABZ24639, ABZ24641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note=
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                                                                                                                                                                                                                                                                                                                                                                                                                TSGMGVS 37
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                                                                                                                                                                                                                                                                           Local Similarity
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new blood vessel growth, angiogenesis, inhibition of which is an approach to limiting tumour growth, angiogenesis, inhibition of which is an approach therapeutics with a cytostatic activity as a collagen agonist or antagonist. The invention is useful for diagnosing and treating disorders associated with angiogenesis, tumour growth and/or cancer metastasis. The present sequence is the amino acid sequence of a mutant mouse anti-cryptic collagen site antibody HUI77 variable region heavy chain CBM which may be used during the creation of an antibody of the invention.

cryptic collagen epitope. The growth of all solid tumours requires

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the present sequence is the protein sequence of the heavy chain of a humanised antibody of the present invention. In the variable portion, the complementarity determining regions (CDRs) originate from murine monoclonal antibody 1005 and the framework region originates from human germline VH segment DP-28 and J segment JH4. Novel humanised antibodies of the invention have CDRs from 1005 and human framework sequences. These humanised antibodies have binding affinities (affinity and epitope location) approximately the same as those of the mouse 1005 antibody. The invention includes antibodies, single chain antibodies, and their invention includes antibodies, single chain antibodies, and their calls, and methods of using the humanised antibody to treat, prevent, alleviate, reverse or otherwise ameliorate symptoms and/or pathology associated with Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral amyloid anglopathy, and to inhibit formation or reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                heavy CDR; cryptic collagen epitope; solid tumour;
who blood vessel growth; anglogenesis; tumour growth; cytostatic;
collagen agonist; collagen antagonist; cancer metastasis;
anti-cryptic collagen; HUI77; variable region heavy chain; mouse; murine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse HUI77 antibody mutant heavy chain CDR amino acid sequence SeqID91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complementarity determining region; CDR; light CDR;
                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                            Length 472;
                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                           100.0%; Score 34; DB 6; I
100.0%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADD94206 standard; peptide; 12 AA.
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                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                          50 TSGMGVS 56
                                                                                                                                                                                                                                                                                                                                                                        1 TSGMGVS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 grafted antibody;
                                                                                                                                                                                                                                                                             Sequence 472 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
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                                                                                                                                                                                                                                               field)
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conter herbicide resistance activity. Crop plants, such as soybean, cotton, tobacco, sugarbeet, oilseed rape, canola, flax, sunflower, potato, tomato, alfalfa, lettuce, maize, wheat, sorghum, rye, bananas, barley, oat, turf grass, forage grass, sugar cane, pea, field bean, rice, pine, poplar, apple, grape, citrus or nut plants, transformed with a pine, poplar, apple, grape, citrus or nut plants, transformed with a cerbicide binding protein gene are resistant to the herbicide. Hence, weeds can be selectively controlled in a field of the transformed crops. The plants are substantially resistant or tolerant to herbicides, such as paraquat or diquat, that inhibit photosynthesis by accepting electrons from photosystem i thus generating free radicals which cause lipid proteins advantageously sequester the herbicide, e.g. at the cell surface or in the vacuoles of a treated plant. Sequestration at the cell surface prevents the entry of the herbicide into the cell so that the herbicide cannot reach its intracellular target and exert any significant cytotoxic effect. The herbicide binding protein inhibits the
                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Paraquat; antibody, light chain; herbicide; resistant; crop plant; weed control; tolerant; diquat; photosynthesis inhibitor; photosystem I; free radical; lipid peroxidation; electron transport; photosystem II; vacuole; cell surface; cytotoxic; sensitive.
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel herbicide binding protein which can
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                                                                                                                                                                                                 Length 12;
                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herbicide binding proteins and related polynucleotides
                                                                                                                                                                                                 7;
                                                                                                                                                                                             Score 31; DB 7
Pred. No. 15;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 43-44; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 AAY25396 standard; protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-GB003760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97GB-00026955
                                                                                                                                                                                                               Local Similarity 85.7
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9932630 Seq ID 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-405173/34.
                                                                                                                                                                                                                                                                                                TSGMGVA 12
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                                                                                                                                                                                                                                                                 1 TSGMGVS
                                                                                                                                                                Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998;
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                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                  RESULT 32
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This invention relates to a novel grafted antibody or its functional fragment comprising one or more complementarity determining regions (CDRs) of a defined light CDR and a heavy CDR with at least one amino acid (aa) substitution where the antibody has specific binding activity

determining regions, useful for diagnosing and treating disorders associated with angiogenesis, tumor growth and/or cancer metastasis.

Claim 24; SEQ ID NO 91; 232pp; English.

New cryptic collagen antibody with one or more complementarity

Brooks PC

Broek D,

Tang Y,

Huse WD,

Watking JD,

WPI; 2003-513649/48.

(CELL-) CELL MATRIX INC.

26-NOV-2002; 2002WO-US038147. 26-NOV-2001; 2001US-00995529. 06-DEC-2001; 2001US-00011250.

WO2003046204-A2.

05-JUN-2003

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New humanized immunoglobulin light or heavy chains comprising variable region complementary determining regions and variable framework regions, useful for preventing or treating e.g., Alzheimer's disease.
mobility of the herbicide from the application site to the whole plant preventing the herbicide reaching particularly sensitive organs. Additionally, tolerant plants can be produced against herbicides that have more than one target site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunoglobulin; Ig; neuroprotective; nootropic; gene therapy; vaccine; amyloidogenic disease; antibody.
                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                         Length 121;
                                                                                                                                                                 91.2%; Score 31; DB 2; Length 121
85.7%; Pred. No. 1.5e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse 12B4 antibody Vh mature peptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 5; Fig 2A-B; 122pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heavy chain mature peptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY42963 standard; protein; 123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-2003; 2003WO-US007715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Best Local Similarity 85.73
                                                                                                                                                                                                                      6; Conservative
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(AMHP ) WYETH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-779077/73.
                                                                                                                                                                                                                                                                                                             31 TSGMGVT 37
                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                1 TSGMGVS 7
                                                                                                                       Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003077858-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY42963;
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                                                                                                                                                                                                                                                                                                                                                                                          RESULT 33
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XX AAY4
XX AAX4
XX AA
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The invention relates to humanized immunoglobulin (Ig) light or heavy chains comprising variable region complementary determining regions (CDRs) from the 1284 Ig variable region sequence and variable framework regions from the 1284 Ig variable region sequence and variable framework regions from a human acceptor Ig light chain or heavy chain sequence. The humanized Ig light or heavy chain or its nucleic acid molecule is useful for preventing or treating an amyloidogenic disease in humans, associated with amyloid deposits of Abeta in the brain, e.g., Alzheimer's disease, Down's syndrome or mild cognitive impairment, all characterized by a three-dimensional image of a 1284 Ig, 1284 Ig chain or its domain. A humanized antibody is useful for reducing plaque or neuritic burden in a subject. The present sequence represents the humanised 1284VHV1 mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New humanized immunoglobulin light or heavy chains comprising variable region complementary determining regions and variable framework regions, useful for preventing or treating e.g., Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin; Ig; neuroprotective; nootropic; gene therapy; vaccine; amyloidogenic disease; antibody; 12B4v1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 1.5e+02;
1; Mismatches 0; Indels
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                                                                                                                                                         AAY42964 standard; protein; 123 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 49; Fig 2A-B; 122pp; English.
                                                                                                                                                                                                                                                                                                                Humanised 12B4VHv1 mature peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAR-2003; 2003WO-US007715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-MAR-2002; 2002US-0363751P.
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85.7%;
                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NEUR-) NEURALAB LTD
|:|||||
TNGMGVS 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-779077/73.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 123 AA;
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                                                                                                                                                                                                                                                                  12-FEB-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                               AAY42964;
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                                                                                                        RESULT 34
AAY42964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Query Match
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                                                                                                                                                                                                                                                                                                  The invention relates to humanized immunoglobulin (Ig) light or heavy chains comprising variable region complementary determining regions (CDRs) from the 12B4 Ig variable region sequence and variable framework regions from a human acceptor Ig light chain or heavy chain sequence. The humanized Ig light or heavy chain or its nucleic acid molecule is useful for preventing or treating an amyloidogenic disease in humans, associated with amyloid deposits of Abeta in the brain, e.g., Alzheimer's disease, Down's syndrome or mild cognitive impairment, e.g., Alzheimer's disease, Down's syndrome or mild cognitive impairment, all characterized by a three-dimensional image of a 12B4 Ig, 12B4 Ig chain or its domain. A humanized antibody is useful for reducing plaque or neuritic burden in a subject. The present sequence represents the humanised 12B4VHv1 sequence
                                                                                                                                                                                                                                     New humanized immunoglobulin light or heavy chains comprising variable region complementary determining regions and variable framework regions, useful for preventing or treating e.g., Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin, Ig; neuroprotective; nootropic; gene therapy; vaccine; amyloidogenic disease; antibody.
                   Immunoglobulin; Ig; neuroprotective; nootropic; gene therapy; vaccine;
amyloidogenic disease; antibody; 12B4v1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 31; DB 7; Length 142;
Pred. No. 1.8e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .20
/note= "leader peptide"
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/note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY42957 standard; protein; 142 AA.
                                                                                                                                                                                                                                                                                Example; Fig 4A-D; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse 12B4 antibody VH region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.2%;
                                                                                                              12-MAR-2003; 2003WO-US007715.
                                                                                                                                  12-MAR-2002; 2002US-0363751P.
Humanised 12B4VHv1 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                      (NEUR-) NEURALAB LTD
(AMHP ) WYETH.
                                                                                                                                                                                    Saldanha J;
                                                                                                                                                                                                         WPI; 2003-779077/73.
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50 TNGMGVS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                    N-PSDB; ACF58541.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 142 AA;
                                                                      WO2003077858-A2.
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                                                                                          25-SEP-2003
                                                   Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
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AAY42957
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The invention relates to humanized immunoglobulin (Ig) light or heavy chains comprising variable region complementary determining regions (CDRs) from the 1284 Ig variable region sequence and variable framework regions from the 1284 Ig variable regions sequence and variable framework regions from a human acceptor Ig light-chain or heavy chain sequence. The humanized Ig light or heavy chain or its nucleic acid molecule is useful for preventing or treating an amyloidogenic disease in humans, associated with amyloid deposits of Abeta in the brain, e.g., Alzheimer's disease, Down's syndrome or mild cognitive impairment, all characterized by a three-dimensional image of a 1284 Ig, 1284 Ig chain or its domain. A humanized antibody is useful for reducing plaque or neuritic burden in a subject. The present sequence represents a mouse 1284 antibody variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New humanized immunoglobulin light or heavy chains comprising variable region complementary determining regions and variable framework regions, useful for preventing or treating e.g., Alzheimer's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY42972 standard; protein; 142 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 63; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric 12B4VH region sequence.
71. .86
/note= "CDR 2"
                                                                 119. .131
/note= "CDR 3"
                                                                                                                                                                                                                                                                                                   12-MAR-2003; 2003WO-US007715.
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                                                                                                                                                                                                                                                                                                                                                                                                                                (NEUR-) NEURALAB LTD (AMHP ) WYETH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heavy chain sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-779077/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 TNGMGVS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric - Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ACF58516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 142 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003077858-A2.
                                                                                                                                                                      WO2003077858-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-SEP-2003
                                                                                                                                                                                                                                     25-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY42972;
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Gaps

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The invention relates to a novel enterohaemorragic Escherichia coli 0157:H7-specific nucleic acid molecule. A polynucleotide of the invention has anti-bacterial activity. The polypeptide can be used in detection and/or treatment of 057:H7 infection. The nucleotide sequence of the genome of Enterchaemorragic E coli 0157:H7 was determined. The present sequence represents an E. coli 0157:H7-specific polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel anti-human interleukin (IL)-18 rodent neutralizing monoclonal antibody having high affinity and useful for treating IL-18 mediated disorders such as multiple sclerosis, rheumatoid arthritis and psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mouse antibody 1369 heavy chain variable region. The antibody has high affinity for human interleukin-18 (IL-18) and is useful for treating and diagnosing IL-18-mediated disorders, e.g. autoimmune diseases such as "multiple sclerosis, rheumatoid arthritis, type I or insulin dependent diabetes, inflammatory bowel disease and psoriasis. Specific changes can be introduced into the nucleotide sequences encoding the complementarity determining regions (CDRs) or framework regions of the variable light chain and heavy chain peptides. The resulting modified or fusion nucleic acid sequences can then be introduced into a plasmid for expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is complementarity determining region (CDR) I of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse, antibody 13G9; antiarthritic; immunosuppressive; neuropro
antiinflammatory; antipsoriatic; interleukin-18; IL-18;
autoimmune disease; multiple sclerosis; rheumatoid arthritis;
type I diabetes; insulin dependent diabetes; IDDM; psoriasis;
inflammatory bowel disease; complementarity determining region;
                                                                                                                                                                                                                                                                                     Length 2793;
                                                                                                                                                                                                                                                                                Score 31; DB 7; Length 279
Pred. No. 3.4e+03;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse antibody 13G9 heavy chain variable region CDR I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ho YS, Holmes SD, Taylor AH, Abdel-Meguid SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB21368 standard; protein; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 4; 64pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                     91.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAR-2000; 2000WO-US007349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0125299P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           391 TAGMGVS 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-628249/60.
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                   Sequence 2793 AA;
                                                                                                                                                                                                                                                                                                                                                                                        1 TSGMGVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAA99647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200056771-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-2000.
                                                                                                                                                                                  invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB21368;
                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB21368
        ¥888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to humanized immunoglobulin (Ig) light or heavy chains comprising variable region complementary determining regions (CDRs) from the 12B4 Ig variable region sequence and variable framework regions from a human acceptor Ig light chain or heavy chain sequence. The humanized Ig light or heavy chain or its nucleic acid molecule is useful for preventing or treating an amyloidogenic disease in humans, associated with amyloid deposits of Abera in the brain, e.g., Alzheimer's disease, bown's syndrome or mild cognitive impairment, all characterized by cognitive impairment, all characterized by a three-dimensional image of a 12B4 Ig, 12B4 Ig chain or its domain. A humanized antibody is useful for reducing plaque or neuritic burden in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterohemorragic Escherichia coli 0157:H7-specific nucleic acid molecule and a polypeptide and its use, a polypeptide, a vector and a host cell.
                                                                                                                                                                                                                                                                                                     New humanized immunoglobulin light or heavy chains comprising variable region complementary determining regions and variable framework regions, useful for preventing or treating e.g., Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterohaemorragic E. coli 0157:H7-specific protein SEQ ID NO: 327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   subject. The present sequence represents a chimeric 12B4VH region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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. 1.8e+02;
.ches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADC00282 standard; protein; 2793 AA.
                                                                                                                                                                                                                                                                                                                                                                                                             Example; Fig 4A-D; 122pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enterohaemorragic; anti-bacterial
                                                  12-MAR-2002; 2002US-0363751P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.2%;
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12-MAR-2003; 2003WO-US007715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JAN-2002; 2002JP-00015959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli; 0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                  NEURALAB LTD
WYETH.
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                                                                                                                                                                             Saldanha J;
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                                                                                                                                                                                                                             WPI; 2003-779077/73
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50 TNGMGVS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TSGMGVS 7
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                                                                                                                                                                                                                                                             N-PSDB; ACF58540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 142 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JP2002355074-A.
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                                                                                                  (NEUR-)
                                                                                                                                                                             Basi G,
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#X#X##X##X##X###X###X
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(first entry)

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Mouse HUI77 light chain CDR1 partial amino acid sequence SeqID38.
                                                    ADD94153 standard; peptide; 12 AA.
                                                                                                      29-JAN-2004
                                                                            ADD94153;
                          RESULT 41
ADD94153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to a novel grafted antibody or its functional fragment comprising one or more complementarity determining regions (CDRs) of a defined light CDR and a heavy CDR with at least one amino acid (aa) substitution where the antibody has specific binding activity for a cryptic collagen epitope. The growth of all solid tumours requires new blood vessel growth, angiogenesis, inhibition of which is an approach to limiting tumour growth. The invention may allow development of therapeutics with a cytostatic activity as a collagen agonist or antagonist. The invention is useful for diagnosing and treating disorders associated with angiogenesis, tumour growth and/or cancer metastasis. The present sequence is the amino acid sequence of a mutant mouse anti-cryptic collagen site antibody HU177 variable region heavy chain CDR which may be used during the creation of an antibody of the invention.
                                                                                                                                                                                                                                               grafted antibody; complementarity determining region; CDR; light CDR; heavy CDR; cryptic collagen epitope; solid tumour; new blood vessel growth; angiogenesis; tumour growth; cytostatic; collagen agonist; collagen anti-cryptic collagen anti-cryptic wariable region heavy chain; mouse; murine;
                                                                                                                                                                                                                       Mouse HUI77 antibody mutant heavy chain CDR amino acid sequence SeqID89.
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New cryptic collagen antibody with one or more complementarity determining regions, useful for diagnosing and treating disorders associated with angiogenesis, tumor growth and/or cancer metastasis.
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25;
88.2%; Score 30; DB 3; Length 7; 71.4%; Pred. No. 2e+06; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang Y, Broek D, Brooks PC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.2%; Score 30; DB 100.0%; Pred. No. 25; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 24; SEQ ID NO 89; 232pp; English
                                                                                                                                          ADD94204 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                26-NOV-2002; 2002WO-US038147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-NOV-2001; 2001US-00995529.
06-DEC-2001; 2001US-00011250.
                                                                                                                                                                                              (first entry)
                            5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CELL-) CELL MATRIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Huse WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-513649/48.
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Best Local Similarity
Matches 6; Conserv
 Query Match
Best Local Similarity
                                                   1 TSGMGVS 7
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TSGMGIA 7
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                                                                                                                                                                                                                                                                                                               mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                      Mus musculus.
                                                                                                                                                                                              29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                       05-JUN-2003
                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                     ADD94204;
                         Matches
                                                                                                                  RESULT 40
                                                                                                                               ADD94204
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grafted antibody, complementarity determining region, CDR; light CDR; heavy CDR; cryptic collagen epitope; solid tumour; new blood vessel growth; angiogenesis; tumour growth; cytostatic; collagen agonist; cancer metastasis; anti-cryptic collagen; antiabody; HU177; variable region heavy chain; mouse; murine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New cryptic collagen antibody with one or more complementarity determining regions, useful for diagnosing and treating disorders associated with angiogenesis, tumor growth and/or cancer metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang Y, Broek D, Brooks PC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.2%; Score 30; DB 7;
100.0%; Pred. No. 25;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 25; SEQ ID NO 38; 232pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-NOV-2002; 2002WO-US038147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-NOV-2001; 2001US-00995529.
06-DEC-2001; 2001US-00011250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CELL-) CELL MATRIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Watking JD, Huse WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-513649/48.
N-PSDB; ADD94152.
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSGMGV 11
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                                                                                                                                                                                                                                                      Mus musculus.
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ADD94205
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Gaps

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0; Indels

6; Conservative

TSGMGV 11 1 TSGMGV 6

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Vezina C;

Qian X,

Varnum BC,

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Screening antibodies and other selective interleukin-1 IL-1 binding agents that bind to IL-1 receptor, by detecting binding of IL-1alpha/IL-1beta to IL-1R1 in presence of test agent and selecting agent that
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Fig 6B; 55pp; English.
                                                                                                                                                   09-NOV-2004; 2004US-00985299.
                                                                                                                                                                                       27-OCT-2000; 2000US-0244118P.
29-OCT-2001; 2001US-00011931.
heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                          decreases IL-1 activity.
                                                                                                                                                                                                                                                                                                                          WPI; 2005-313939/32
                                                                                                                                                                                                                                               (AMGE-) AMGEN INC.
                                                                           US2005084493-A1
                                       Homo sapiens.
                                                                                                               21-APR-2005,
                                                                                                                                                                                                                                                                                       Witte A,
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fragment comprising one or more complementarity determining regions cides of a defined light CDR and a heavy CDR with at least one amino acid (as) substitution where the antibody has specific binding activity for a cryptic collagen epitope. The growth of all solid tumours requires new blood vessel growth, angiogenesis, inhibition of which is an approach to limiting tumour growth. The invention may allow development of therapeutics with a cytostatic activity as a collagen agonist or antagonist. The invention is useful for diagnosing and treating disorders associated with angiogenesis, tumour growth and/or cancer metastasis. The present sequence is the amino acid sequence of a mutant mouse anti-cryptic collagen site antibody HU177 variable region heavy chain CDR which may be used during the creation of an antibody of the invention.
                                                                                     grafted antibody; complementarity determining region; CDR; light CDR; heavy CDR; cryptic collagen epitope; solid tumour; new blood vessel growth; angiogenesis; tumour growth; cytostatic; collagen agonist; collagen anti-cryptic collagen; HUI77; variable region heavy chain; mouse; murine;
                                                   Mouse HUI77 antibody mutant heavy chain CDR amino acid sequence SeqID90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drug screening, antibody identification; cell signaling; inflammation; antiinflammatory; antibody engineering; humanized antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New cryptic collagen antibody with one or more complementarity determining regions, useful for diagnosing and treating disorders associated with angiogenesis, tumor growth and/or cancer metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to a novel grafted antibody or its functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 7; Length 12; 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human germline heavy chain variable region VK-1 018/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Broek D, Brooks PC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.2%; Score 30; DB 100.0%; Pred. No. 25; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 24; SEQ ID NO 90; 232pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADZ47747 standard; protein; 100 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang Y,
                                                                                                                                                                                                                                                                                                                                                                                                26-NOV-2001; 2001US-00995529.
06-DEC-2001; 2001US-00011250.
                                                                                                                                                                                                                                                                                                                                                            26-NOV-2002; 2002WO-US038147
               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CELL-) CELL MATRIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huse WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-513649/48.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 TSGMGV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TSGMGV 6
                                                                                                                                                                                                                                                                                   WO2003046204-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12 AA;
                                                                                                                                                                                         mutant; mutein
                                                                                                                                                                                                                                               Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watking JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2005
               29-JAN-2004
                                                                                                                                                                                                                                                                                                                        05-JUN-2003
                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADZ47747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 43
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The invention relates to methods of screening for antibodies or other agents which selectively bind to the pro-inflammatory cytokine interleukin-1 [IL-1R form an antagonist complex which can still bind to IL-1R interpret in [IL-1R] but which cannot activate it. The agents identified using the methods act by blocking the recruitment of the IL-1 creeptor accessory protein (IL-1RAP) by the IL-1/IL-1R1 complex, consensing method of the invention involves detecting the binding of IL-18 pha or IL-19 and thereby reducing inflammatory responses. One screening method of the invention involves detecting the binding of IL-1RAP in the presence of a test agent, detecting IL-1R but which decreases IL-1 activity. A second method involves detecting the binding of IL-1RAP to IL-1R1 in the presence of involves detecting the binding of IL-1RAP to IL-1R1. In the presence of IL-18 pha or IL-18 pha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 framework regions derived from the human germline gamma heavy chain variable region 2-70 (ADS47747) and the human heavy chain joining region JH4 (ADS47749). The present sequence represents the human germline gamma VH 2-70 used in the design of the humanized MAB201 VH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30; DB 9; Lengtn 100, Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR66304 standard; protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSGMGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 44
AAR66304
ID AAR6
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ophthalmological; antiasthmatic; inflammatory response; autoimmune disease; idiopathic thrombocycopenic purpura; rheumatoid arthritis; systemic lupus erythematosus; autoimmune haemolytic anaemia; seleroderma; autoimmune haemolytic anaemia; seleroderma; vasculitis syndrome; systemic vasculitis; Goodpasture's syndrome; multiple sclerosis; speciatic arthritis; ankylosing spondylitis; Sjogren's syndrome; Reiter's syndrome; Kowasaki's disease; polymyositis; dermatomyositis; allergic asthma.
vasotropic; nephrotropic; neuroprotective; antipsoriatic; uropathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TSGMGV 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 118 AA;
                                                                                                                                                                                                                                                              WO2003101485-A1.
                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                              11-DEC-2003
                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                              sp.
                                                                                                                                                                                                              Mus
8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein sequences (AAR66295-51) are novel human immunoglobulin heavy chain sequences encoded by novel isolated genes. The genes (AAQ78939-7902) were isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21; Y6;Y24; 3-31; M84; M118 and M31, by PCR amplification using primers AAQ78917-38. The genes are subdivided into 5 families of Vh genes. The fragments cover a region of 800 kb. The DNA fragments were isolated from high molecular weight DNA from human placenta. The DNA was separated by gel elecrophoresis and 35-45 kb fractions were collected. The fragments were ligated with Clai-digested cosmid vector puBB1. The ligation products were in vitro packed and infected into E.coli 490A. The tragments were then subcloned by colony phybridisation. The Viragments were collected the DNA fragments were then subcloned by colony phybridisation. The Viragments were then subcloned by colony phybridisation. The Viragments encoding them are useful in producing human mammalian hosts. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anti-CD16A antibody; mouse; 3GB antibody; humanised anti-CD16A antibody; immune response; haemostatic; antirheumatic; antiarthritic; dermatological; immunosuppressive; antiinflammatory; antianaemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                  Primer, PCR, amplify, human, immunoglobulin, variable, heavy chain, cosmid; placenta, vector; pJB81; E.coli; mammalian.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA fragment comprising human immunoglobulin Vh genes - for the production of human immunoglobulin in mammalian hosts.
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0
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Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                   Human immunoglobulin variable heavy chain #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.2%; Scor.
100.0%; Pred. No. 4...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hu3G8VH-1 amino acid sequence SEQ ID NO:104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 19; Page 43-44; 130pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADF71905 standard; protein; 118 AA.
                                                                                                                                                                                                                                                                                              93WO-JP000603
                                                                                                                                                                                                                                                                                                                               93WO-JP000603.
                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                 (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                (revised)
                                                                                                                                                                                                                                                                                                                                                                                                      Honjo T, Matsuda F;
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-006791/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 111 AA;
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                                                                                                                                                                                                                         WO9426895-A1.
                                                                                                                                                                                                                                                                                            10-MAY-1993;
                                                                                                                                                                                                                                                                                                                               10-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-2004
                                                                                                                                                                                         Homo sapiens
                                               25-MAR-2003
02-AUG-1995
                                                                                                                                                                                                                                                            24-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADF71905;
              AAR66304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
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ID ADF7
AC ADF7
XX
XX
DY 26-1
XX
XX
XX
XX
XX
XX
XX
Antimut
XW dern
XW dern
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셤 ઠે

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The present invention describes an anti-CD16A antibody (I) comprising a VH domain comprising complementarity determining regions (CDRs) derived from the mouse 308 antibody value to an via derived from the mouse 308 antibody light chain or a humanised anti-CD16A antibody (II) that lacks effector function and comprises all six CDRs of antibody (II) that lacks effector function and comprises all six CDRs of antibody 3038. Also described is a method (MI) for reducting a deleterious immune response in a mammal in need of such reduction, which involves administering to the mammal a CD16A binding protein comprising a FC ceffector ligand (II) and (II) have haemostatic, antirheumatic, antiantanic, dermatological immunosuppressive, antiinflammatory, antiantanic, ophthalmological and antiasthmatic activities. (I) or (II) is useful for reducting a deleterious immune response in a mammal which involves administering to the mammal (I) or (II). The deleterious immune response in a mammal which involves administering to the mammal (I) or (II). The deleterious immune response in a nammal which involves administering to the mammal (I) or (II). The deleterious immune response in a mammal which involves administering to the mammal (I) or (II). The deleterious immune response in a mammal which involves administering to the mammal (I) or (II). The deleterious immune response in a mammal which including the presence caused by autoimmune disease such as idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA), celecroderma, autoantibody trigged utricaria, pemphydus, vasculitis syndrome, manned manned purpare consist (RS), poorlatic arthritis, syndrome, manned purpare consist of perfect arthritis, syndrome, manned purpare consisting and deleterious dele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel anti-CD16A antibody comprising complementarity determining regions derived from mouse 3G8 antibody and humanized anti-CD16A antibody that lacks effector function, useful for treating deleterious immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                             Tuaillon N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12; SEQ ID NO 104; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                             Li н,
29-MAY-2003; 2003WO-US017111.
                                                                                                         30-MAY-2002; 2002US-0384689P.
10-JAN-2003; 2003US-0439320P.
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Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                             (MACR-) MACROGENICS INC
                                                                                                                                                                                                                                                                                                                                                                                             Johnson LS, Huang L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-042985/04.
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Gaps

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Length 118;

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Hu3G8VH-5 amino acid sequence SEQ ID NO:109.
                                                                                                                                                                 Tuaillon N;
                                                                                                                                                                                                   Claim 12; SEQ ID NO 109; 103pp; English.
ADF71910 standard; protein; 118 AA.
                                                                                                                                  29-MAY-2003; 2003WO-US017111.
                                                                                                                                                                 Li H,
                                                                                                                                           30-MAY-2002; 2002US-0384689P
10-JAN-2003; 2003US-0439320P
                 (first entry)
                                                                                                                                                        (MACR-) MACROGENICS INC
                                                                                                                                                                 Johnson LS, Huang L,
                                                                                                                                                                          WPI; 2004-042985/04.
                                                                                                                 WO2003101485-A1.
                                                                                                    Mus sp.
Homo sapiens.
                 26-FEB-2004
                                                                                                                          11-DEC-2003
                                                                                               Synthetic.
       ADF71910;
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This is the amino acid sequence of the mature peptide from the murine anti-protein C monoclonal antibody HPC-4 heavy chain variable region. HPC-4 recognises the activation peptide region (AARSB106) of the heavy chain of protein C, a vitamin K-dependent plasma protein zymogen. Protein C is converted to activated protein C (APC) by cleavage between the Arg-Leu amino acid contained within the activation peptide sequence. HPC-4 prevents protein C activation to APC by binding to this region. The DNA sequences encoding the variable regions of the heavy and light chains of the antibody (AATO$299-302) were used to construct humanised antibodies using the PCR primers AATO$303-9. The humanised antibodies are useful as inhibitors of coagulation and can be used for the treatment of tumours by inhibiting the anticoagulant activity of APC by preventing conversion of
and also for treating diseases susceptible to treatment with intravenous immunoglobulin (IVIG) therapy e.g., allergic asthma. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Epitope, activation, heavy chain, protein C, vitamin K, plasma protein, zymogen, cleavage, mouse, humanised antibody, variable region, light chain, inhibition, anticoagulant, coagulation, tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Calcium-binding monoclonal antibody immunoreactive with Protein C - inhibits Protein C anticoagulant activation by thrombin-thrombomodulin,
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                                                                                                                                                                                            88.2%; Score 30; DB 8; L6
100.0%; Pred. No. 2.4e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR88109 standard; peptide; 120 AA.
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                                                                                                                                   Sequence 118 AA;
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                                                                                                                                                                                                                                                                                                                                         anti-CD16A antibody; mouse; 3G8 antibody; humanised anti-CD16A antibody; dermatological; laminosupressive; antiinflammatory; antianaemic; vasotropics; laminosupressive; antiinflammatory; antianaemic; vasotropic; nephrotropic; neuroprotective; antipsoriatic; uropathic; ophthalmological; antiasthmatic; inflammatory response; autoimmune disease; idiopathic thrombocytopenic purpura; rheumatoid arthritis; systemic lupus erythematosus; autoimmune haemolytic anaemia; scleroderma; autoimmune haemolytic anaemia; scleroderma; systemic autoimmune haemolytic anaemia; scleroderma; psystemic vasculitis; Goodpasture's syndrome; psoriatic arthritis; ankylosing spondylitis; Sjogren's syndrome; Reiter's syndrome; Kowasaki's disease; polymyositis; dermatomyositis; allergic asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel anti-CD16A antibody comprising complementarity determining regions derived from mouse 3G8 antibody and humanized anti-CD16A antibody that lacks effector function, useful for treating deleterious immune response.
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Gaps

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31 TSGMGV 36

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ABO10820

ABO10820 standard; protein; 120 AA. ABO10820; 

(first entry 21-AUG-2003

Human germline region variable region VH-2 2-70.

amyotrophic lateral sclerosis; Alzheimer's disease; cachexia; anorexia, asthma; pulmonary disease; atherosclerosis; autoimmune vasculitis; chronic fatigue syndrome; coronary condition; congestive heart failure; cancer; diabetes; endometriosis; fever; glomerulomephritis; ARDS; graft versus host disease; haemorrhagic shock; inflammatory condition; inflammatory bowel disease; osteoarchritis; rheumatori arthritis; ischammatory bowel disease; osteoarchritis; rheumatori arthritis; multiple sclerosis; pain; parkinson's disease; psoriasis; septic shock; reperfusion injury; aleep disturbance; uveitis; infection; antibody; MAB201; germline variable region. Human; interleukin-1; IL-1 alpha; IL-1 beta; acute pancreatitis; ALS;

Homo sapiens.

US2003026806-A1.

06-FEB-2003

29-OCT-2001; 2001US-00011931.

27-OCT-2000; 2000US-0244118P.

(AMGE-) AMGEN INC.

ΰ Vezina Qian X, Varnum BC, Witte A,

WPI; 2003-479525/45.

selective binding agent that binds to IL-lalpha or IL-lbeta, such that the complex binds to IL-1 receptor without activating the receptor. Treating interleukin-1 mediated disease, by administering an IL-1

Example 2; Fig 6B; 39pp; English.

The invention relates to treating interleukin-1 (IL-1)-mediated disease, or blocking IL-lalpha and IL-lbeta from binding to the IL-1 receptor, involving administering an IL-1 selective binding agent (e.g. a humanised mouse anti-IL-1 antibody) that is capable of binding to IL-1 alpha or IL-1 betain where the selective binding agent-II-1 complex is capable of binding to IL-1 alpha or IL-1 chocking formation of IL-lbeta/IL-1 receptor/IL-1RacP complex were of mouse, chimaeric and humanised monoclonal antibody (MAD) 201 in chocking formation of IL-lbeta/IL-1 receptor/IL-1RacP complex were studied. The results showed that anti-IL-lbeta antibody MAD201 is the const effective inhibitor of IL-lbeta antibody MAD201 is the most effective inhibitor of IL-lbeta signalling. The method is useful for treating IL-1-mediated disease e.g. acute pancreatitis, amyotrophic lateral sclerosis (ALS), Alzheimer's disease, cachexia, anorexia, asthma, pulmonary diseases, atherosclerosis, autoimmune vasculitis, chronic farigue syndrome, Clostridium associated illness, coronary conditions (e.g. congestive heart failure, coronary restenosis, myocardial candometriosis, fever, ibromyalgia, hyperalgesia, cancers, diabetes, endometriosis, fever, ibromyalgia, hyperalgesia, cancers, diabetes, endometriosis, fever, ibromyalgia, hyperalgesia, conformatic arthritis and rheumatory conditions (e.g. congeriatic arthritis and rheumatory conditions (alsease) (arthritis), inflammatory physis springer, learning impairment, lung diseases (adult respiratory equisease, cancerm labour, conditions (ARDS)), multiple sclerosis, myopathies, neurocoxicity, osteoporosis, panin, Parkinson s disease, periodontal disease, preterm labour, periodon injury, septic shock, side effects from radiation

ö therapy, temporal mandibular joint disease, sleep disturbance, uveitis and inflammatory conditions resulting from strain, sprain, cartilage damage, trauma, orthopaedic surgery and infection. The present sequence is a human gremline variable region used to determine which residues or CDRs required to be changed in mouse anti-IL-1 monoclonal antibody MAB201 in order to humanise it or make it into a chimaeric molecule with human CDR (complementarity determining region) sequences Mouse, interleukin-1; IL-1 alpha; IL-1 beta; acute pancreatitis; ALS; amyotrophic lateral sclerosis; Alzheimer's disease; cachaxia; anorexia; asthma; pulmonary disease; atherosclerosis; autoimmune vasculitis; chronic fatigue syndrome; coronary condition; congestive heart failure; cancer; diabetes; endometriosis; fever; glomerulonephritis; ARDS; graft versus host disease; haemorrhagic shock; inflammatory condition; inflammatory bowel disease; osteoarthritis; rheumatoid arthritis; inflammatory bowel disease; osteoarthritis; theumatoid arthritis; schaemia; stroke; lung disease; adult respiratory distress syndrome; multiple sclerosis; pain; Parkinson's disease; psoriasis; septic shock; reperfusion injury; sleep disturbance; uveitis; infection; antibody; Gaps ö Length 120; 0; Indels 88.2%; Score 30; DB 6; Le 100.0%; Pred. No. 2.4e+02; ive 0; Mismatches 0; Mouse monoclonal antibody heavy chain V region. ပဲ Vezina ABO10813 standard; protein; 120 AA. Qian X, 29-OCT-2001; 2001US-00011931. 27-OCT-2000; 2000US-0244118P 21-AUG-2003 (first entry) 6; Conservative Witte A, Varnum BC, WPI; 2003-479525/45. Query Match Best Local Similarity Matches 6; Conserv 31 TSGMGV 36 1 TSGMGV 6 (AMGE-) AMGEN INC Sequence 120 AA; US2003026806-A1. 06-FEB-2003 ABO10813; MAB201. Wив вр. 88888888 유 ð

The invention relates to treating interleukin-1 (IL-1)-mediated disease, or blocking IL-1alpha and IL-1beta from binding to the IL-1 receptor, involving administering an IL-1 selective binding agent (e.g. a humanised mouse anti-IL-1 antibody) that is capable of binding to IL-1 alpha or IL-bleta, where the selective binding agent. IL-1 complex is capable of binding to IL-1 receptor without activating the receptor. The activities of mouse, chimaeric and humanised monoclonal antibody (MAD) 201 in blocking formation of IL-1beta/IL-1 receptor/IL-1RacP complex were studied. The results showed that anti-IL-1beta antibody MAB201 is the most effective inhibitor of IL-1beta signalling. The method is useful for that Treating interleukin-1 mediated disease, by administering an IL-1 selective binding agent that binds to IL-lalpha or IL-1beta, such the the complex binds to IL-1 receptor without activating the receptor. Example 2; Page 19; 39pp; English.

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treating IL-1-mediated disease e.g. acute pancreatitis, amyotrophic lateral sclerosis (ALS), Alzheimer's disease, cachexia, anorexia, asthma, pulmonary diseases, arberosclerosis, autoimmune vasculitis, chronic fatigue syndrome, Clostridium associated illness, coronary conditions (e.g. congestive heart failure, coronary restenosis, myocardial coronary artery bypass graft), cancers, diabetes, endometriosis, fever, fibromyalgia, hyperalgesia, conflammatory bowel disease; inflammatory bowel disease; inflammatory bowel disease; conflammatory bowel disease, inflammatory conflammatory experients, inflammatory conditions (e.g. osteoarthritis, conflammatory bowel disease, inflammatory bowel disease, lastning impairment, lung diseases (adult respiratory distress syndrome (AROS)), multiple sclerosis, myopathies, neurotoxicity, osteoporosis, candin, Parkinson's disease, periodontal disease, preterm labour, corpain, Parkinson's disease, periodontal disease, preterm labour, corpainsis, reperfusion injury, septic shock, side effects from radiation therapy, temporal mandibular joint disease, sleep disturbance, uveitis and inflammatory conditions resulting from strain, sprain, cartilage candiation injury, surgery and infection. The present sequence is a heavy, light or kappa chain of the mouse anti-IL-I monoclonal antibody MAB201 which was humanised or made into a chimaeric molecule cy, with human CDR (complementarity determining region) sequences
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Gaps ö 88.2%; Score 30; DB 6; Length 120; 100.0%; Pred. No. 2.4e+02; ive 0; Mismatches 0; Indels 6; Conservative Query Match Best Local Similarity Matches

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ADQ09629 standard; protein; 120 AA. CCCX8X4445XBX8X6X6X6X6X6X6X6X6X6X6X6X6X6X6X6

ADQ09629;

(first entry) 07-OCT-2004

Variable heavy chain protein of murine anti-human GPR64-16 antibody ID15. murine; mouse; antibody; GPR64; cytotoxic; ovarian cancer;
uterine cancer; Ewing's sarcoma; cell death; cytostatic; gene therapy;
immunotherapy; cellular proliferation.

Мив вр

WO2004058171-A2

15-JUL-2004

19-DEC-2003; 2003WO-US040820

(PROT-) PROTEIN DESIGN LABS INC. 20-DEC-2002; 2002US-0435618P

Bhaskar V; Dubridge R, Wang Q, Law D,

WPI; 2004-525780/50. N-PSDB; ADQ09619. New antibody that inhibits binding of a GPR64 polypeptide to an antibody comprising GPR64-18, GPR64-81, GPR64-93 or GPR64-101, useful in preparing a composition for diagnosing or treating ovarian cancer. Example 2; SEQ ID NO 15; 75pp; English. This invention relates to novel antibodies that bind to the G protein coupled receptor protein identified as GPR64, namely GPR64-1, GPR64-16, GPR64-18, GPR64-20 and GPR64-48. Specifically, it refers to the use of

expressing tumour cells such as those associated with ovarian cancer, uterine cancer and Bwing's sarcoma. The present invention describes epitope mapping of those antibodies that show high affinity binding to GPR64 through competitive binding analyses, such that the antibodies can be assessed for GPR64 dependent cell death in vitro. Accordingly, they can be used to develop cytostatic compositions for gene therapy or immunotherapy that inhibit cellular proliferation of an ovarian cancerous cell and furthermore can diagnose and inhibit growth of tumour cells. This polypeptide is encoded by a heavy chain variable region DNA sequence of a murine anti-human GPR64 antibody of the invention. these anti-GPR64 antibodies as selective cytotoxic agents against GPR64 

Sequence 120 AA;

Gaps ö 88.2%; Score 30; DB 8; Length 120; 85.7%; Pred. No. 2.4e+02; ive 1; Mismatches 0; Indels 6; Conservative Best Local Similarity Query Match Matches

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C,Accession: 873091
R,Sensen, C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, S. Mol. Microbiol. 22, 175-191, 1996
A,Title: Organizational characteristics and information content of an archaeal genome: 1 A,Reference number: 873076; MUID:97055432; PMID:8899719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteoglycan core protein, cartilage - bovine (fragments)
N;Alternate names: aggrecan; aggregating cartilage proteoglycan
N;Alternate names: aggrecan; aggregating cartilage proteoglycan
C;Species Bos primigentus taunas (cattle)
C;Date: 20-Mar-1992 #sequence revision 23-Mar-1995 #text change 09-Jul-2004
C;Accession: A34234; A27752; A39808; A27751; E29164; B27751; C27751; D27751; E27751; F27
R;Antonsson, P; Heinegard, D; Oldberg, A.
J; Biol. Chem. 264, 16170-16173, 1989
A;Title: The Keratan sulfate-enriched region of bovine cartilage proteoglycan consists c
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: nRNA
A; Molecule type: nRNA
A; Molecule type: 136-621 <ann.
A; Molecule type: 136-621 <ann.
A; Cross-references: UNIPROT: P13608; UNIPARC: UPI0000177421; GB:J05028
R; Oldberg, A.; Antonsson, P.; Heinegard, D.
R; Oldberg, A.; Antonsson, P.; Heinegard, D.
A; Title: The partial amino acid sequence of bovine cartilage proteoglycan, deduced from a A; Reference number: A27752; MUID:87270630; PMID:3111460
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J. Biol. Chem. 266, 8108-8205, 1991
A;Title: Analysis of the catabolism of aggrecan in cartilage explants by quantitation of
A;Reference number: A39808; MUID:91217051; PMID:2022637
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A;Molecule type: protein
A;Molecule type: protein
A;Kesidues: 1-28;59-82;131-137,'QSET',142-149;196-207;226-249;1137-1143;1252-1267;1274-1
A;Cross-references: UNIPARC:UPI0000177422, UNIPARC:UPI0000177423; UNIPARC:UPI0000177424,,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-1068 <SEN>
A;Cross-references: UNIPROT:P95871; UNIPARC:UPI00001373B1; EMBL:Y08256; NID:g1707679; P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Experimental source: strain P2
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1996
C;Superfamily: tricorn protease
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C;Species: Sulfolobus solfataricus
C;Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
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                      DB 2; Length 143;
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Pred. No. 1.5e+02;
1; Mismatches 0; Indels
                                                                     Indels
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                                                                  Mismatches
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A;Modecule type: mRNA
A;Residues: 622-1340 <0LD>
A;Cross-references: UNIPARC:UPI0000087C64
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                   100.0%;
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                   Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 31-0-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996
C;Accession: PT0174
R;Perfetti, V.; Borden, P.; Tao, M.H.; Morrison, S.L.; Kabat, B.A.
Mol. Immunol. 28, 505-515, 1991
A;Title: Specificity and variable region cDNA sequence of an isogeneic monoclonal antiid
A;Reference number: PT0174; MUID:91287738; PMID:1712074
A;Reference number: PT0174; MUID:91287738; PMID:1712074
A;Rolecule type: mRNA
A;Refunces: UNIPARC:UP10000176976
A;Experimental source: strain BALB/c
C;Comment: IdB5.7 is an antibody to anti-alpha (1-6) dextran.
C;Comment: IdB5.7 is an antibody to anti-alpha (1-6) dextran.
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heteroterramer; immunoglobulin
F;34-118/Domain: immunoglobulin homology <IMM>
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19 heavy chain precursor V-D-J region - mouse (fragment)

() Species: Mus musculus (house mouse)

() Species: Mus musculus (house mouse)

() Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

() Accession: $11740

R. Hyman, R.; Hardy, R.R.

R. Hardy, R.R.

R. Hardy, R.R.

A) Bescription: Natural autoantibodies to thymocytes: Origin, VH genes, fine specificitie

A) Reference number: $11740

A) Residues: 1-122 < EMB>
A) Residues: 1-122 < EMB>
A) Residues: UNIPARC:UPI000011100BS; EMBL:X53097; NID:G52368; PIDN:CAA37261.1; PID

C) Superfamily: immunoglobulin V region; immunoglobulin homology

C) Reywords: heterotetramer; immunoglobulin

F; 22-106/Domain: immunoglobulin homology < IMM>
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100.0%; Pred. No. 3.5;
ive 0; Mismatches 0;
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                                          F90923
T49450
B85772
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JC4796
D84985
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E86700
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AC2051
WZBE58
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C64922
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Matches 7; Conservative
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A; Deceute Fyor: DNA
A; Residues: 1-2793 <HAY>
A; Residues: 1-2793 <HAY>
A; Residues: 1-2793 <HAY>
A; Residues: 1-2793 <HAY>
A; Cross-references: UNIPROT: Q8X2Q2; UNIPARC: UPI0000D2A88; GB: BA000007; PIDN: BAB34665.1
A; Experimental source: strain O157:H7, substrain RIMD 0509952
C; Genetics:
A; Gene: EC81242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein Z1495 [imported] - Escherichia coli (strain O157:H7, substrain EDL. C;Species: Escherichia coli (c)Species: Escherichia coli (c)Species: Escherichia coli (c)Species: Escherichia coli (c)Accession: D85644 (c)Accession: D85644 (c)Accession: D85644 (c)Accession: D8564 (c)Accession: D8664 (c)Accession: D8664
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A;Residues: 1-2806 csTO->
A;Cross-references: UNIPROT:Q8X470; UNIPARC:UPI000009BB7E; GB:AE005174; NID:g12514354; A
A;Experimental source: strain O157:H7, substrain EDL933
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A;Residues: 1-113 *KAV>
A;Cross-references: UNIPARC:UP10000115F69; EMBL:X59115; NID:g51928; PIDN:CAA41841.1; PII
C;Superfamaily: immunoglobulin V region; immunoglobulin homology
C;Keywords: hererotetramer; immunoglobulin
F;6-90/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Accession: S26465
R;Kavaler, J.
Submitted to the EMBL Data Library, April 1991
A;Reference number: S26455
A;Accession: S26465
A;Status: preliminary
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Pred. No. 3.9e+02;
1; Mismatches 0; Indels
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85.7%; Pred. No. s...
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Best Local Similarity 85.7.
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Best Local Similarity 85.7%
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Matches 6; Conservative
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   A; Accession: B90784
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C;Species: Bos primigenius taurus (cattle)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T4250
A;Hering, T.M.; Kollar, J.; Huynh, T.D.
submitted to the EMBL Data Library, September 1996
A;Bescription: Complete coding sequence of bovine aggrecan: comparative structural analy A;Reference number: Z22182
A;Accession: T4250
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-237 *HER>
A;Cross-references: UNIPPRC;PI3608; UNIPARC;UPI00002B0E1; EMBL:U76615; NID:g1730259; PI
A;Experimental source: articular chondrocytes
C;Superfamily: aggreean; C-type lectin homology; complement factor H repeat homology; ECC;Keywords: cartilage; chondroitin sulfate proteoglycan; extracellular matrix; glycoprot
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C'Species: 18-011-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C'Accession: B90784
R'Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
R;Hayashi, T.; Makinoga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genc
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                          FEBS Lett. 206, 73-77, 1986
A;Title: Structural relationship between link proteins and proteoglycan monomers.
A;Reference number: A27751; MUID:87005253; PMID:3530809
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85.7%; Pred. No. 1.8e+02;
ive 1; Mismatches 0; Indels
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85.7%; Pred. No. 3.3e+02;
.ive 1; Mismatches 0; Indels
R; Perin, J.P.; Bonnet, F.; Jolles, P.
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                               A;Accession: A27751
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A, Experimental source: strain 972h-; cosmid c56F8
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2748 TEGMGVS 2754
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A;Gene: CESP:Y47D3B.5
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Cibate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
CiAccession: H75057
Rianonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Bescription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Reference number: A75001
A;Accession: H75057
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-188 «KAW>
A;Residues: 1-188 «KAW>
A;Cross-references: UNIPROT:Q9UYQ5; UNIPARC:UPI000063447; GB:AJ248287; GB:AL096836; NIC
A;Experimental source: strain Orsay
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
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C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38913
R;Pearson, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
R;Pearson, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
A;Reference number: Z21817
A;Reference number: Z31817
A;Accession: T38913
A;Accession: T38913
A;Accession: Dreliminary; translated from GB/EMBL/DDBJ
A;Residues: preliminary;
A;Residues: 1-1079 < PERA
A;Cross-references: UNIPROT:Q10251; UNIPARC:UPI000012D2C8; EMBL;Z69728; PIDN:CAA93574.1;
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                                                         hypothetical protein PAB0965 - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 30; DB 2
Pred. No. 40;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     88.2%;
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Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 85.7
Matches 6; Conservative
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A)Reference number: 219407
A;Reference number: 219407
A;Reference number: 219407
A;Accession: T21328
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3147 <MIL>
A;Residues: UNIPROT:QSXV66; UNIPARC:UPI0000164296; EMBL:Z81512; PIDN:CAB04172.1;
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A;Introns: 32/2; 57/2; 73/3; 113/3; 157/3; 366/1; 456/1; 509/1; 638/1; 773/2; 848/1; 902
/3; 2510/2; 2737/3; 2827/1; 2902/3; 3093/3; 3121/1
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A;Introns: 35/2; 95/3; 132/3; 175/2; 206/2; 266/1; 312/2; 386/1; 433/3; 508/3; 531/2; 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA*
*Residues: 1-113 < WILD.
A;Cross-references: UNIPROT:09XX01; UNIPARC:UPI000016411B; EMBL:AL031635; PIDN:CAA21041.
A;Experimental source: clone Y47D3B
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26953
R;Matthews, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
C;Accession: T21328
R;Matthews, L.
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C;Genetics;
A;Gene: SPDB:SPAC56F8.03
A;Map position: 1
F;485-612/Domain: translation elongation factor Tu homology <ETU>
                                                                                                                            Length 1079;
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                                                                                                                         Query Match 88.2%; Score 30; DB 2; Length 107 Best Local Similarity 85.7%; Pred. No. 2.4e+02; Matches 6; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein Y47D3B.5 - Caenorhabditis elegans
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Pred. No. 2.5e+02;
0; Mismatches 1;
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Pred. No. 7.3e+02;
0; Mismatches 1;
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Best Local Similarity 85.7-
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Best Local Similarity 85.7
Matches 6; Conservative
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A;Cross-references: UNIPARC:UPI0000035C93; EMBL:U33761; NID:g995825; PIDN:AAC50242.1; P)
C;Genetics:
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A;Molecule type: mRNA
A;Residues: 1-719 <HE2>
A;Cross-references: UNIPROT:Q61281; UNIPARC:UPI0000039DD1; EMBL:X80478; NID:g607131; PIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pyruvate, water dikinase (EC 2.7.9.2) - Salmonella enterica subsp. enterica serovar Typh C; Species: Salmonella enterica subsp. enterica serovar Typhi C; Species: Salmonella enterica serovar Typhi C; Species: Salmonella enterica serovar Typhi C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C; Accession: AB0704 G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connexton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001 A; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K., A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serova, A; Reference number: AB0502; MUID:21534947; PMID:11677608
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A;Cross-references: UNIPARC:UP1000059DD6; GB:AL513382; PIDN:CAD02003.1; PID:g16502841;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Mus musculus (house mouse)
C;Species: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: $60227; $51739
R;He, G.P.; Mutse, A.; Li, A.W.; Ro, H.S.
Nature 378, 92-96, 1995
A;Title: A eukaryotic transcriptional repressor with carboxypeptidase activity. A;Reference number: $60227; MUID:96061010; PMID:7477299
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                                                                                                                                                                  85.3%; Score 29; DB 2; Length 435;
100.0%; Pred. No. 1.6e+02;
iive 0; Mismatches 0; Indels
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83.3%; Pred. No. 2.6e+02;
ive 1; Mismatches 0; Indels
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100.0%; Pred. No. 2.9e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        transcription repressor AEBP1 - mouse
                                                                                           A;Gene: Skp2
C;Keywords: cell cycle control
                                                                                                                                                                                                                   6; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 100.
Matches 6; [Conservative
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TSGMGI 427
                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                            SGMGVS 51
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                                                                                                                                                                                                                                                                   2 SGMGVS 7
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A; Molecule type: mRNA
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A;Status: preliminary
A;Molecule type: DNA
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RESULT 15
AG0585
citrate utilization protein B [imported] - Salmonella enterica subsp. enterica subsp. citrate utilization protein B [imported] - Salmonella enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AG0585
R;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D.; Wain, J; Churcher, th, T.; Connerton, P.; Cronnin, A.; Davis, P.; Davies, R.M.; Dowd, L.; Waite, N.; Farrar, S.; Moule, S; O'Gacra, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Acteus: preliminary
A;Molecule type: DNA
A;References: UNIPARC:UPI00005A149; GB:AL513382; PIDN:CAD05153.1; PID:g16501926;
C;Genetics:
Citt protein - Salmonella typhimurium (fragment)
C.Species: Salmonella typhimurium
C.Species: Salmonella typhimurium
C.Species: Salmonella typhimurium
C.Species: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C.Accession: PQ0098
R.Shimamoto, T.; Izawa, H.; Daimon, H.; Ishiguro, N.; Shinagawa, M.; Sakano, Y.; Tsuda, J. Biochem. 110, 22-28, 1991
A.Title: Cloning and nucleotide sequence of the gene (citA) encoding a citrate carrier f A; Reference number: JQ076; MUID:92041761; PMID:1718953
A.Accession: PQ0008
A.Accession: PQ0008
A.Accession: PQ0008
A.Accession: PQ0008
A.Accession: PABL>
A.Accession: Cita carrier f A; Residues: 1-S8 <ALI>
A.Accession: PQ0008
A.Accession: PQ0008
A.Accession: PQ0008
A.Accession: PQ0008
A.Accession: PABL>
A.Accession
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Cyclin A/CDK2-associated p45 - human
Cyspecies: Homo sapiens (man)
Cybate: 23-Reb-1996 #sequence_revision 23-Reb-1996 #text_change 21-Jul-2000
Cyaccession: 139171
R;Zhang, H.; Kobayashi, R.; Galaktionov, K.; Beach, D.
Cell 82, 915-925, 1995
A;Title: p195kp1 and p455kp2 are essential elements of the cyclin A-CDK2 S phase kinase.
A;Reference number: 139170; MUID:96016087; PMID:7553852
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C, Superfamily: Escherichia coli plasmid pWR60 hypothetical 42K protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 83.3%; Score 29; DB 2; Length 58, Similarity 83.3%; Pred. No. 19; 5; Conservative 1; Mismatches 0; Indels
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TSGMGI 9
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Matches

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Query Match Best Loc Matches

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Best Local Similarity 100.
Matches 6; Conservative
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SGMGVS 44
A;Molecule type: DNA
A;Residues: 1-792 <NIE>
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C; Function:
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                                       phosphoenolpyruvate synthase [imported] - Escherichia coli (strain O157:H7, substrain ED C; Species: Escherichia coli
C; Species: Escherichia coli
C; Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
R; Perna, N.T.; Plunket III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409; 529-531, 2001
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Reference number: B8577B
A; Reference number: B8577B
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Reference number: B8577B
A; Reference strain 0157:H7, substrain EDL933
C; Gentices
A; Gentice: Recherichia coli pyruvate, water dikinase: phosphotransferase avarem envem
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pyruvate, water dikinase (EC 2.7.9.2) ppsA [validated] - Escherichia coli (strain K-12) pyruvate, water dikinase (EC 2.7.9.2) ppsA [validated] - Escherichia coli (strain K-12) N;Alternate names: phosphoenolpyruvate synthase
C;Species: Bscherichia coli
A;Variety: strain K12
C;Date: 16-56p-1992 #sequence revision 16-5ep-1992 #text_change 09-Jul-2004
C;Accession: S20554; F64928; $14838
C;Accession: S20554; F64928; $14838
NN:Nerabach, M; Kreusaler, F; Geerse, R.H.; Postma, P.W.; Hirsch, H.J.
Mol. Genet. 231, 332-336, 1992
A;Title: Cloning and nucleotide sequence of the Escherichia coli K-12 ppsA gene, encodin A;Reference number: S20554; MUID:92140374; PMID:1310524
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K.; Apodaca,
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Matches 6; Conservative
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A. Receives 1.723 (1812)
A. Receives 1.723 (1812)
A. Receives 1.723 (1812)
A. Receive 1.724 (1812)
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A;Genome: chloroplast
C;Superfamily: H(+)-transporting ATP synthase; H+-transporting ATP synthase alpha chain
C;Keywords: ATP biosynthesis; chloroplast; hydrolase; membrane-associated complex; thyl-
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C; Species: chloroplast Solanum tuberosum (potato)
C; Date: 1D-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 31-Dec-2004
C; Accession: PQ0792
R; Kawagoe, Y.; Kikuta, Y.
R; Kawagoe, Y.; Kikuta, Y.
A; Theor. Appl. Genet. 81, 13-20, 1991
A; Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.).
A; Reference number: JQ2306
A; Accession: PQ0792
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C;Superfamily: H(+)-transporting ATP synthase; H+-transporting ATP synthase alpha chain
C;Keywords: ATP biosynthesis; chloroplast; hydrolase; thylakoid
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                                                                                                                                                                                                                                                                                                                       H-transporting two-sector ATPase (EC 3.6.3.14) beta chain - tomato chloroplast N;Alternate names: ATPase beta chain C;Species: chloroplast Lycopersicon esculentum (tomato) C;Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 31-Dec-2004
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R;Kawagoe, Y.; Kikuta, Y.
Theor. Appl. Genet. 81, 13-20, 1991
A;Title: Chloroplast DNA evolution in potato (Solanum tuberosum A;Reference number: JQ2306
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   Indels
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A,Residues: 1-122 <KAW>
A,Cross-references: UNIPROT:09SCBS; UNIPARC:UPI0000175E6D
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A;Residues: 1-122 «KAW»
AZCross-references: UNIPROT:Q7M2HO; UNIPARC:UPI0000175E7D
C;Genetics:
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Pred. No. 69;
0; Mismatches
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Pred. No. 69;
0; Mismatches
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Best Local Similarity 85...
6; Conservative
6; Conservative
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Best Local Similarity
Matches 6; Conserv
                                                                      1 TSGMGVS
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Matches
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               A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Molecule type: Train 168
A:Experimental source: strain 168
A:Experimental source: strain 168
C:Genetics:
A:Genetics:
A:Genet
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Gispecies: Mus musculus (house mouse)
Giscossion: A99442

Ristura, E.A.; Stanfield, R.L.; Fieser, G.G.; Silver, S.; Roguska, M.; Hincapie, L.M.; Sproteins 14, 499-508, 1992

Arfitle: Crystallization, sequence, and preliminary crystallographic data for an antiper A; Reference number: A49442; MUID:93066166; PMID:1438187

A; Reference number: A49442

A; Reference number: DNA
A; Residues: preliminary; not compared with conceptual translation
A; Residues: 1-107 < STU>
A; Cross-references: UNIPARC:UPI00001768FD
G; Superfamily: immunoglobulin tomology
C; Superfamily: immunoglobulin homology < IMM>
F; 7-91/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein E01G6.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20406
A;Riloyd, C.
submitted to the EMBL Data Library, February 1996
A;Accession: T20406
A;Accession: T20406
A;Accession: T20406
A;Accession: T20406
A;Accession: T20406
A;Residues: 1-1391 *WILb-
A;Residues: 1-1391 *WILb-
A;Cross-references: UNIPROT;Q19021; UNIPARC:UP1000007DCE8; EMBL:Z69717; PIDN:CAA93531.1;
A;Residues: 1-1391 *WILb-
A;Cross-references: Uniproc: clone E01G6
C;Genetics:
A;Gene: CESP:E01G6.1
A;Map position: X
A;Introns: 44/1; 84/3; 175/1; 389/2; 423/1; 501/1; 1358/1
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Pred. No. 60;
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R;Ryseck, R.P.; Macdonald-Bravo, H.; Mattei, M.G.; Bravo, R.
cell Growth Differ. 2, 252-23, 1991
A;Title: Structure, mapping, and expression of fisp-12, a growth factor-inducible gene e A;Reference number: A53228, MUID:91363290; PMID:1888698
A;Accession: A53228
A;Accession: A53228
A;Accession: A53228
A;Accession: A53228
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-160, K',162-348 <RYS>
A;Residues: 1-160, K',162-348 <RYS>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A40551; S44205
C;Accession: A40551; S44205
R;Bradham, D.M.; Igarashi, A.; Potter, R.L.; Grotendorst, G.R.
C, Call Bahol. 114, 1285-1294, 1991
A;Title: Connective tissue growth factor: a cysteine-rich mitogen secreted by human vasc. A;Reference number: A40551; MUID:91373462; PMID:1654338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: UNIPROT: P29279; UNIPARC: UPI000003FD13; GB:M92934; GB:M36965; GB:S562 R; Cemar, B.S.; Werner, A.; Yang, Z.; Garnier, J.M.; Gentz, R.; Luescher, T.F. submitted to the EMBL Data Library, April 1994
A; Description: Differential cloning and expression of human connective tissue growth fac A; Reference number: S44205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dranched-chain-amino-acid transaminase (EC 2.6.1.42) BAT2, cytosolic - yeast (Saccharomy N.Alternate names: protein 12209; protein YJR148w; TWT2 protein C.Species Eaccharomyces cerevisiae C.Species Baccharomyces cerevisiae C.Date: 23-Aug-1995 #sequence_revision 08-Sep-1995 #text_change 05-Oct-2004 C.Accession: S57177; 861565
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A;Residues: 1-376 <SCA>
A;Residues: 1-376 <SCA>
A;Cross-references: UnIPARC: UPI0000052E2B; EMBL: Z49648; NID:gl015896; PI
R;Kisola: G: Lill, R:; Neupert, N.
Submitted to the EMBL Data Library, April 1995
A;Reference number: S61565
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*Kesidues: 1-34 «CEM»
A;Cross-references: UNIPARC:UP1000003FD13; EMBL:X78947; NID:g474933; PID:g474934
C;Superfamily: IGFBP-related protein, CNN type
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Bubmitted to the Protein Sequence Database, September 1995
A;Reference number: S57169
A;Accession: S57177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.4%; Score 28; DB 2; 71.4%; Pred. No. 2e+02;
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Pred. No. 2e+02;
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C,Superfamily: IGFBP-related protein, CNN type
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Best Local Similarity 71.4
Matches 5; Conservative
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Best Local Similarity
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A; Residues: 1-349 < BRA>
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A;Status: preliminary
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Theor. Appl. Genet. 81, 13-20, 1991

A;Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.).
A;Reference number: J02306
A;Accession: PQ0793
A;Molecule type: DNA
A;Residues: 1-122 <RNA
A;Residues: UNIPROT:Q7MZH1; UNIPARC:UPI0000175E7C
A;Experimental source: cv. W553-4
A;Molecule type: DNA
A;Residues: 1-122 <RNA>
A;Gene: cf. Cobbler
C;Genetics:
A;Experimental source: cv. I. Cobbler
C;Genetics:
A;Gene: atpB
A;Gene: Afp
A;Residues: Afp
A;
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C;Species: Staphylococcus aureus (Strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: F89929
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
Ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramateu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: F89929
A;Status: preliminary
A;Molecule type: DMA
A;Residues: 1-251 ckUR
A;Residues: 1-251 ckUR
A;Cross-references: UNIPROT:Q99TZ1; UNIPARC:UPI00000CA987; GB:BA000018; PID:g13701301; F
A;Genetics:
A;Genetics:
A;Genetics:
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beta IG-M2 protein precursor - mouse
beta IG-M2 protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Mar-1992 #sequence_revision 06-Mar-1992 #text_change 31-Dec-2004
B;Brunner, A; Chinn, J; Neubauer, M.; Purchio, A.F.
DNA Cell Biol. 10, 293-300, 1991
A;Title: Identification of a gene family regulated by transforming growth factor-beta.
A;Reference number: A40578
A;Reference number: A40578
A;Accession: A40578
A;Accession: A40578
A;Accession: A40578
A;Molecule type: mRNA
A;Residues: 1-348 - RBU>
A;Cross-references: UNIPROT:P29268; UNIPARC:UPI0000028AEF; GB:M80263; NID:g201945; PIDN:
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Pred. No. 1.4e+02;
2; Mismatches 0; Indels
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Pred. No. 69;
0; Mismatches
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Best Local Similarity 85.,
6, Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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TSGSGVS 13
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A;Residues: 1-498 (-SHI>
A;Cross-references: UNIPROT:P00826; UNIPARC:UPI000012648D; EMBL:K00507; NID:g343480; PID
A;Experimental source: variety BY4
R;Avni, A.; Anderson, J.D.; Rochhaix, J.D.; Edelman, M.
submitted to the EMBL Data Library, July 1991
A;Description: The receptor site for tentoxin sensitivity in chloroplasts.
A;Reference number: S15722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPARC:UP1000012648D; EMBL:X61319; NID:g11788; PIDN:CAA43612.1; PIC R;Avni, A.; Anderson, J.D.; Holland, N.; Rochaix, J.D.; Gromet-Elhanan, Z.; Edelman, M. Science 257, 1245-1247, 1992
A;Title: Tentoxin sensitivity of chloroplasts determined by codon 83 of beta subunit of A;Reference number: A43264; MUID:92390714; PMID:1387730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: H(+)-transporting ATP synthase; H+-transporting ATP synthase alpha chain C;Keywords: ATP biosynthesis; chloroplast; hydrolase; membrane-associated complex; nucle F;172-179/Region: nucleotide-binding motif A (P-loop)
F;198-374/Domain: H+-transporting ATP synthase alpha chain homology <ATP>
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A;Residues: 1-498 <ANN>
A;Cross-references: UNIPROT:P26531; UNIPARC:UPI0000126468; EMBL:X61317; NID:g11765; PIDN
C;Genetics:
A;Gene: atpB
                                                                                                                                                                                                          H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain - common tobacco chloroplast N;Alternate names: CF1-beta; coupling factor-1 beta; proton-ATPase beta subunit C;Species: chloroplast Wicctiana tabacum (common tobacco)
C;Date: 03-Aug-1984 #sequence revision 03-Aug-1984 #text_change 31-bec-2004
C;Accession: A01027; S15726; Ā42264
R;Shinozaki, K.; Deno, H.; Kato, A.; Sugiura, M.
R;Shinozaki, K.; Deno, H.; Kato, A.; Sugiura, M.
A;Title: Overlap and cotranscription of the genes for the beta and epsilon subunits of the A;Reference number: A91502; MUID:84059075; PMID:6227526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Experimental source: var. Xanthi, tentoxin-resistant
A;Note: sequence extracted from NCBI backbone (NCBIP:112485)
A;Note: variants of Nicotiana sp. and engineered sequences with Glu-83 showed tentoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: nucleic acid sequence not shown; not compared with conceptual translation
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C; Species: al-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 31-Dec-2004
C; Accession: 315725
R; Avni, A.; Anderson, J.D.; Rochhaix, J.D.; Edelman, M.
Submitted to the EMBL Data Library, July 1991
A; Pescription: The receptor site for tentoxin sensitivity in chloroplasts.
A; Reference number: $15722
A; Accession: $15725
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Pred. No. 2.9e+02;
0; Mismatches 1; Indels
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Cross-references: UNIPARC:UP10000172E12
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211 TSGLGVA 217
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Best Local Similarity
Matches 6; Conserv
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A, Molecule type: DNA
A, Residues: 1-498 <AVN>
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PWNTB9
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C;Species: Acinetobacter calcoaceticus
C;Species: Acinetobacter calcoaceticus
C;Species: Acinetobacter calcoaceticus
C;Accession: F3225; T01635; T01636
R;Goosen, N.; Horsman, H.P.A.; Huinen, R.G.M.; van de Putte, P.
J. Bacteriol. 177, 447-455, 1989
A;Title: Acinetobacter calcoaceticus genes involved in biosynthesis of the coenzyme pyrr
A;Accession: F32252
A;Accession: F32252
A;Accession: P32252
A;Accession: P32252
A;Status: preliminary; not compared with conceptual translation
A;Accession: L384 <GOO>
A;Cross-references: UNIPROT:P07782; UNIPARC:UPI0000132133; GB:X06452; NID:G38740; PIDN:C
C;Punction:
A;Description: involved in synthesis of coenzyme pyrrolo-quinoline-quinone (PQQ)
A;Accession: S61565
A;Molecule type: mRNA
A;Residues: 'NSARV',2-147,'MA',150-169,'LWVLIT',176,'LDLRRSDWKPLIMPOELAQEAV',199-206,'V
A;Cross-references: UNIPARC:UPI0000168EA4; EMBL:X86568; NID:g1107862; PIDN:CAA60376.1;
C;Genetics: SGD:BAT2; TWT2
A;Gene: SGD:BAT2; TWT2
A;Cross-references: MIPS:YJR148w; SGD:S0003909
A;Map position: 10R
C;Superfamily: branched-chain amino acid aminotransferase, BCAT1 type
C;Keywords: aminotransferase; cytosol
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Pred. No. 2.2e+02;
2; Mismatches 0; Indels
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Pred. No. 2.6e+02;
2; Mismatches 0; Indels
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Best Local Similarity 71.4%; Pred. No. 2.2e
Matches 5; Conservative 2; Mismatches
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Best Local Similarity 71.4
Matches 5; Conservative
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151 TAGLGVS 157
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Gaps

A;Genome: chloroplast

6; Conservative

Matches

Query Match Best Local Similarity

TSGSGVS 13

1 TSGMGVS 7

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C;Superfamily: H(+)-transporting ATP synthase; H+-transporting ATP synthase alpha chain C;Superfamily: blosynthesis; chloroplast; hydxolase; membrane-associated complex; nucle F;172-179/Region: nucleotide-binding motif A (F-loop) F;198-374/Domain: H+transporting ATP synthase alpha chain homology <ATP>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-498 <AVN>
A;Cross-references: UNIPROT:P26530; UNIPARC:UPI0000126467; EMBL:X61318; NID:g11763; PIDN
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R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Doddon, R.; Gwin, M.; Nelsen, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
                                                                                                                                                                                            H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain - Aztec tobacco chloroplast
C;Species: chloroplast Nicotiana rustica (Aztec tobacco)
C;Date: 31-Mar-1992 #text_change 31-Dec-2004
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C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                            C;Accession: S15724
R;Avni, A.; Anderson, J.D.; Rochhaix, J.D.; Edelman, M.
Bubmitted to the EMBL Data Library, July 1991
A;Description: The receptor site for tentoxin sensitivity in chloroplasts.
A;Reference number: S15722
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A;Cross-references: UNIPROT:049714; UNIPARC:UPI0000A0E02; EMBL:AL021890
A;Experimental source: cultivar Columbia; BAC clone T805
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A;Note: T805.120
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Pred. No. 3e+02;
1; Mismatches
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Best Local Similarity 85.7
Lag 6; Conservative
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nes 5; Conserv
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SGMGIS 81
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TSGSGVS 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: S15724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Genetics:
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A; Reference number: $15722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P26529; UNIPARC:UPI0000126466; EMBL:X61316; NID:g11745; PIDN
C;Genetics:
A;Gene: atpB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Genome: Chloroplast
C;Superfamily: H(+)-transporting ATP synthase; H+-transporting ATP synthase alpha chain
C;Superfamily: H(+)-transporting ATP synthase; hydrolase; membrane-associated complex; nucle
F;172-179/Region: nucleotide-binding motif A (P-loop)
F;198-374/Domain: H+-transporting ATP synthase alpha chain homology <ATP>
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A;Residues: 1-498 <AVN>
A;Cross-references: UNIPROT:P26529; UNIPARC:UP10000126466; EMBL:X61320; NID:g11756; PIDN
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                           C;Superfamily: H(+)-transporting ATP synthase; H+-transporting ATP synthase alpha chain Keywords. ATP biosynthesis, Chloropbast; hydrolase; membrane-associated complex; nucle F:172-179/Region: nucleotide-binding motif A (P-loop)
F:198-374/Domain: H+-transporting ATP synthase alpha chain homology <ATP>
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                                                                                                                                                                                            82.4%; Score 28; DB 1; Length 498;
85.7%; Pred. No. 2.9e+02;
ive 0; Mismatches 1; Indels
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Pred. No. 2.9e+02;
0; Mismatches 1; Indels
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85.7%; Pred. No. 2.9e+02;
ive 0; Mismatches 1;
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82.4%;

A; Accession: S15722 A; Molecule type: DNA A; Residues: 1-498 <AVN>

6; Conservative

Similarity

Query Match Best Local S

Matches

TSGSGVS 13

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RESULT 37

TSGMGVS 7

Conservative

1 TSGMGVS 7

Query Match Best Local Similarity Matches 6; Conserv

A; Genome: chloroplast

Gaps

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Collagen alpha 1(XVII) chain - human (fragment)
N;Alternate names: bullous pemphigoid 180K autoantigen BPAG2; bullous pemphigoid antiger C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: 156325; 155345; A61262
R;Giudice, G.J.; Emery, D.J.; Diaz, L.A.
A;Giudice, G.J.; Emery, D.J.; Diaz, L.A.
A;Title: Cloning and primary structural analysis of the Bullous pemphigoid autoantigen, A;Reference number: 156325; MUD: 92381323; PMID: 1324962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-1532 <RES>
A; Residues: 1-1532 <RES>
A; Cross-references: UNIPROT: Q9UMD9; UNIPARC: UP1000006F673; GB: M91669; NID: 9179516; PIDN A; Cross-references: UNIPROT: Q9UMD9; UNIPARC: UP100006F673; GB: M91669; NID: 91701. Chu, M.L.; Gawamura, D.; Giudice, G.J.; Diaz, L.A.; Mattei, M.G.; Chu, M.L.; Uitto, J. J. Biol. Chem. 266, 24064-24069; 1991
A; Title: Genomic organization of collagenous domains and chromosomal assignment of humar A; Reference number: 155345; MUID: 92084712; PMID: 1748679
A; Accession: 155345
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 543-890,'P' <RE2>
A;Cross-references: UNIPARC:UP1000006F72A; GB:M63730; NID:g179520; PIDN:AAA51839.1; PID
R;Giudice, G.J.; Squiquera, H.L.; Elias, P.M.; Diaz, L.A.
J. Clin. Invest: 87, 734-738, 1991
A;Title: Identification of two collagen domains within the bullous pemphigoid autoantigr A;Reference number: A61262; MUID:91123476; PMID:1846881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cition-independent mannose-6-phosphate receptor - chicken (Species: Gallus gallus (chicken) (Species: Gallus gallus (chicken) (Chate: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004 (Chacession: 150726 (Chacession: 150726 (Chacession: 150726 (Chacession: 150726 (Chacession: 150726) (Chacession: Chicken (Chicken (Ch
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Mealecule type: TAHO
A;Cross-references: UNIPROT:Q90681; UNIPARC:UPI00000FB0C6; EMBL:U35037; NID:g1019118; PI
C;Superfamily: mannose 6-phosphate receptor, cation-independent; fibronectin type II rep
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                                                                        Length 706;
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Pred. No. 9.4e+02;
0; Mismatches 1;
                                                                        Score 28; DB 2; I
Pred. No. 4.2e+02;
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A;Molecule type: mRNA
                                                                                                                                                         1; Mismatches
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A;Cross-references: GDB:131396; OMIM:113811
A;Map position: 10q24.3-10q24.3
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A;Residues: 543-890,'P' <GIU>
A;Cross-references: UNIPARC:UP1000006F72A
                                                                        82.4%;
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                                                                   Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                 297 SGMGIS 302
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: D2-P5-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01351
R;Ryan, E.; Edwards, J.; Pape, K.
A;Reference number: Z14297
A;Reference number: Z14297
A;Reference number: Z14297
A;Reference number: Z14297
A;Residues: L-706 <RYA>
A;Residues: L-706 <RYA
A;Residues: L-707/3; 330/2; 418/2; 454/3; 526/1
A;Residues: L-707/3; 330/2; 418/2; 454/3; 526/1
A,Reference number: A81500; MUID:20150255; PMID:10684935
A,Accession: B81711
A,Actatus: preliminary
A,Molecule type: DNA
A,Residues: 1-558 <-TET>
A,COSE-references: UNIPROT:QPRV6; UNIPARC:UPI00000578C2; GB:AE002303; GB:AE002160; NID
C,Genetics:
A,Gene: TC0355
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Pred. No. 3.3e+02;
2; Mismatches 0; Indels
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416 TAGLGVS 422
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Best Local Similarity
Matches 5; Conserv
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A.Title: Physical structure and genetic organisation of the genome of maize streak virus A,Reference number: A93538; MUID:85037917; PMID:6493977 A,Accession: A04172
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A;Residues: 1-244 <HOW>
A;Cross-references: UNIPROT:P03569; UNIPARC:UP10000127D6A; GB:X01089; NID:g59364; PIDN:C
C;Superfamily: maize streak virus coat protein
C;Keywords: coat protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RiLazarowitz, S.G.
Nucleic Acids Res. 16, 229-249, 1988
A;Title: Infectivity and complete nucleotide sequence of the genome of a South African i
A;Recence number: S04804; WUID:88124198; PMID:2829117
A;Accession: S04805
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A;Molecule type: DNA
A;Residues: 1-244 <LAZ>
A;Cross-references: UNIPROT:P14986; UNIPARC:UPI0000127D6B; EMBL:Y00514; NID:g59365; PIDN
C;Superfamily: maize streak virus coat protein
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(Species: maize streak virus

(Species: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

(Species: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

(Species: 10-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

(Species: 10-Jul-1999 #sequence 09-Jul-2004

(Species: 10-Jul-1999 #sequence 09-Jul-2004

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(Species: 10-Jul-1999 #sequence 09-Jul-1999

(Species: 10-Jul-1999 #sequence 09-Ju
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A;Cross-references: UNIPROT:073473; UNIPARC:UPI00000F721F; EMBL:AJ225008; NID:g2980718;
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 09-Jul-2004 C;Accession: A04172 R;Howell, S.H. Nucleic Acids Res. 12, 7359-7375, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: maize streak virus
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S04805
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Pred. No. 2.3e+02;
1; Mismatches 0;
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C;Superfamily: maize streak virus coat protein
C;Keywords: capsid protein
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Best Local Similarity 83.3%;
Matches 5; Conservative
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191 TSGLGV 196
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S04805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein Rv2272 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Suleton, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D7030
A;Accession: D7030
A;Residues: 1-122 <COL>
A;Residues: 1-122 <COL>
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A;Residues: 1-244 <MUL.
A;Cross-treferences: UNIPROT:P06448; UNIPARC:UPI00000039D; GB:X01633; GB:K02026; NID:g59
C;Superfamily: maize streak virus coat protein
C;Keywords: coat protein
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A,Experimental source: strain H37Rv
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C;Species: maize streak virus
C;Species: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
R;Mullineaux, P.M.; Donson, J.; Morris-Krsinich, B.A.M.; Boulton, M.I.; Davies, J.W.
EMBO J. 3, 3063-3068, 1984
A;Title: The nucleotide sequence of maize streak virus DNA.
A;Reference number: A90997; MUID:85126910; PMID:6526009
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                                                                                             82.4%; Score 28; DB 2; Length 2470;
85.7%; Pred. No. 1.5e+03;
ive 0; Mismatches 1; Indels
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                    F;1882-1921/Domain: fibronectin type II repeat homology <2F1>
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C;Species: maize streak virus
A;Note: host Zea mays (maize)
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Best Local Similarity 83.3
Matches 5; Conservative
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191 TSGLGV 196
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70 TSGMGL 75
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A;Gene: Rv2272
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RESULT 50
H90130
60s ribosomal protein L1 [imported] - Guillardia theta nucleomorph
C;Species: nucleomorph Guillardia theta
C;Species: nucleomorph Guillardia theta
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Uul-2004
C;Accession: H90130
R;Douglas, S; Zauner, S; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
Nature 410, 1091-1096, 2001
A;Tille: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671
A;Retaus: preliminary
A;Molecule type: DNA
A;Retaus: preliminary
A;Molecule type: DNA
A;Retaus: preliminary
A;Molecule type: DNA
A;Retaus: preliminary
A;Genetics:
A;Cross-references: UNIPROT:Q98S44; UNIPARC:UP100009423E; GB:AF083031; NID:g13794362; F
C;Genetics:
A;Genetics:
A;Gene : rpl.
A;Map position: 3
A;Gene : mucleomorph
C;Superfamily: rat ribosomal protein L4
C;Keywords: nucleomorph
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79.4%; Score 27; DB 2; Length 255;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels
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191 TSGLGV 196
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Search completed: February 23, 2006, 09:51:34 Job time: 23.9077 secs

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OGAGET2 leifBonia x OG7856 aquifex aeo Q4t137 tetrandon n Q8trz uncultured Q6sfa3 uncultured Q6z4t5 oryza sativ Q54x56 dictyosteli Q4t919 tetrandon n O10551 schizosacch	Q9xx01 concreabdi Q61bn8 caenorhabdi Q61bn8 caenorhabdi Q7474 geobacter s Q6550 crimean-con Q51yx7 magnaporthe Q7jkt8 caenorhabdi Q9xv6 caenorhabdi	Q841m9 clostridium Q82619 plasmodium Q89k76 xanthomonas Q61015 picrophilus Q8379 pseudomonas Q83302 yellow feve Q44aff pseudomonas Q41ue5 burkholderi Q7wef2 bordecella	xenol xenol borde salmc salmc salmc ralst	Q7mr64 wolinella s Q58hz9 gallus gall Q13309 homo sapien Q92023 mus musculu Q56929 mus musculu	Q52m59 gallus gall Q519e5 bacteroides Q64pm9 bacteroides Q7muv7 porphyromon Q89pH3 bradyrhizob Q61281 mus musculu Q5nci9 mus musculu Q5nci9 ms musculu Q5nci9 ms musculu Q5nci9 ms musculu	(Vature representation of the control of the contro	070kj4 bacillus am 070kj4 bacillus am 019021 caenorhabdi 05crg7 cryptospori 06c9f6 oryza sativ 09udl6 homo sapien 07m2h0 solanum tub 07m2h0 solanum tub 07m2h0 solanum tub 07m2h0 oryza sativ 0691x0 oryza sativ 0691x1 debaryomyce 05bax7 ehrlichia r 055ax7 ehrlichia r
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to sp|P13856 Saccharomyces cerevisiae YGR152c RSR1 GTP-binding
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R Matter 430.35-44(2044).

R GO; GO:000525; F:GTP binding; IEA.

R GO; GO:0005264; P:small GTPase mediated signal transduction; IEA.

R GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.

R InterPro; IPR00357; GTPase Rab.

R InterPro; IPR00357; GTPase Rab.

R InterPro; IPR00357; GTPase Rab.

R InterPro; IPR003578; GTPase Rab.

R InterPro; IPR00449; Ras trnsfrang.

R Pfan; PF00071; Ras; 1.

R PRINTS; PR00449; RASTRNSFRANG.

R SMART; SM00175; RAB; 1.
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OrderedlocusNames=YALIOF231779;
Yarrowia lipolytica (Candida lipolytica).
Sukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
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Prust C., Hoffmeister M., Liesegang H., Wiezer A., Fricke W.F.,
Ehrenreich A., Gottschalk G., Deppenmeier U.;
"Complete genome sequence of the acetic acid bacterium Gluconobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chloroplast.
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Araceae, Aroideae, Thomsonieae, Amorphophallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Acetobacteraceae; Gluconobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
SWART; SM00173; RAS; 1.
SWART; SM00174; RHO; 1.
TIGRFAMS; TIGR00231; small_GTP; 1.
Cell cycle; Cell division; Complete proteome; GTP-binding;
Nucleotide-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 15;
                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chiang T.Y., Feng C.I.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ224958; CAB39368.1; -; Genomic_DNA.
GO; GO:0009507; C:chloroplast; IEA.
                                                                                                                    254 AA; 28209 MW; AEAED29C136EAC27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chioroplast.
NON TER 15 15
SEQÜENCE 15 AA; 1547 MW; 8875F4EE641DED5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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Last annotation update)
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Gluconobacter oxydans (Gluconobacter suboxydans)
                                                                                                                                                                  ..
7
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Pred. No. 16;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           15 AA
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                                                                                                                                                               100.0%; Score 34; DB
100.0%; Pred. No. 53;
tive 0; Mismatches
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illarity 85.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-JUN-2003 (TrEMBLrel. 24, AtpB protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
                                                                                                                                                                                                                                                                                                                                                                                                                    QOWTA3 9ARAE PRELIMINARY;
QOWTA3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QSHXS1 GLUOX PRELIMINARY;
QSHXS1;
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Matches 7; Conservative
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RATAIN-ENT.

RAY Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,

RA Arachchi H.M., Barna N., Calvo S.B., Camarata J., Chang J.,

ROUKBalter B., Butler J., Calvo S.B., Camarata J., Chang J.,

ROUGED IY., Collymore A., Cooke P., Corum B., DeArellano K.,

RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,

RA Erickson J., Faro S., Faretira P., FitzGerald M., Gage D., Galagan J.,

RA Angopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,

RA Angopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,

RA Angobian D., Hagos R., Jones C., Kamal M., Kamat A., Karatas A.,

RA Malls C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,

RA Mathews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,

RA Michsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,

RA Michsen C.B., Norbu C., O'Connor T., O'Donnell S.,

RA Roman J., Schauer S., Schupback R., Searer R., Severy P., Smirnov S.,

RA Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,

RA Roman J., Tesfaye S., Theedore J., Topham K., Travers M.,

RA Vassillev H., Venkataraman V.S., Viel R., Zembek L., Zimmer A., Zody M.,

RA Lander E.,

RA 
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UCLEOTIDE SEQUENCE.
STRAIN-MASSACHUSTOR.
STRAIN-MASSACHUSTOR.
STRAIN-MESSACHUSTOR.
STRAIN-MESSACHUSTOR.
STRAIN-MESSACHUSTOR.
Brueggemann H., Baeumer S., Fricke W.F., Wiezer A., Liesegang H.,
Brueggemann H., Baeumer S., Fricke W.F., Weizer A., Liesegang H.,
Gottschalk G.,
"The genome sequence of Clostridium tetani, the causative agent of tetanus disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Rusarium graminearum genome sequence.";
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clostridium tetani.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
NCBI_TaxID=1513;
                                                                                                  Gibberella zeae PH-1.
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Hypocreomycetidae, Hypocreales, Nectriaceae, Gibberella.
NCBI_TaxID=229533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.2%; Score 31; DB 2; Length 285; 85.7%; Pred. No. 2.7e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
SEQUENCE 285 AA; 31434 MW; 779697211DB4C67C CRC64;
                                   (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Putative sialidase (EC 3.2.1.18).
             Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AACM01000196; EAA75749.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
          31,
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          13-SEP-2005 (TrEMBLrel.
                                                           Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preliminary data.
                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                    ORFNames=FG04790.1;
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TSGMGLS 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                   STRAIN=PH-1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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(08984) CLG
(08984) CLG
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DT (01-J)
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          DDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDD
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                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PATHWAY: Respiratory chain; terminal step.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Acanthocephala, Archiacanthocephala,
Oligacanthorhynchida, Oligacanthorhynchidae, Oligacanthorhynchus.
NCBI_TaxID=84287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO1165; CYCOXIDASBI.
PROSTIRS, PSGOBSS; COX1, 1.
COPDEr; Electron transport; Heme; Inner membrane; Membrane;
Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                       Score 31; DB 2; Length 197; Pred. No. 1.9e+02; 1; Mismatches 0; Indels
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EMBL; CP000004; AAM59682.1; -; Genomic_DNA.
Complete proteome; Plasmid.
SEQUENCE 197 AA; 20780 MW; A6471EEC023EFF91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219
23629 MW; DF9DA0E5262F833E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Cytochrome oxidase subunit I (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                     219 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligacanthorhynchus tortuosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.2%;
85.7%;
                                                                                                             91.2%;
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                                                                                                                                                                                                                                                                                                                                                                     9 9BILA
Q4R029 9BILA PRELIMINARY;
Q4R029;
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Q4IDB8_GIBZE PRELIMINARY;
Q4IDB8;
                                                                                                  Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                             |||:|||
136 TSGLGVS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1
219 2
219 AA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                               1 TSGMGVS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TSGMGVS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrion.
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NON TER
SEQUENCE
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Q4IDB8 GII
ID Q4IDI
AC Q4IDI
DT 13-SI
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NUCLEOTIDE SEQUENCE
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R GO; GO:0005507; C:Chloroplast; IEA.

R GO; GO:0016205; C:Mydrogen-translocating F-type ATPase complex; IEA.

R GO; GO:0016205; C:Membrane; IEA.

R GO; GO:0016529; C:thylakoid; IEA.

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0006553; F:Mydrogen-exporting ATPase activity, phospho. .; IEA.

R GO; GO:0016787; F:Mydrogen-transporting ATPase activity, rota. .; IEA.

R GO; GO:0016787; F:Mydrogen-transporting ATPase activity, rota. .; IEA.

R GO; GO:0016787; F:Mydrogen-transporting ATPase activity, IEA.

R GO; GO:0016787; F:Mydrogen-transporting ATPase activity; IEA.

R GO; GO:0016787; F:Mydrogen-transporting ATPase activity; IEA.

R GO; GO:0016787; F:Mydrogen-transporting ATPase.

R GO; GO:0016991; F:Mydrogen-transporting ATPase.

R GO; GO:0015986; P:MTP synthesis coupled proton transport; IEA.

R GO; GO:0015986; P:MTP synthesis coupled proton transport; IEA.

R GO; GO:0015992; P:Proton transport; IEA.

R InterPro; IPR003593; AAA_ATPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IEA.
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IEA.
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SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five subunits: alpha(3), bash), gamma(1), delta(1), epsilon(1). CF(0) has three main subunites a, b and c (By similarity).

SUBCELLULAR LOCATION: Chloroplast thylakoid membrane (By
                                                                                                                                                                                                                                                   Gaps
Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).

EMBL, AE015937; AA035087.1; -; Genomic_DNA.

GO; GO:0004308; F:exo-alpha-sialidase activity; IEA.

GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.

GO; GO:0005975; P:carbohydrate metabolism; IEA.

Complete proteome; Glycosidase; Hydrolase.

SEQUENCE 292 AA; 33689 MW; EF27726FDCE6ADEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
PubMed=15084683; DOI=10.1093/molbev/msh147;
Goremykin V., Hirsch-Erns K.I., Wolfl S., Hellwig F.H.;
"The chloroplast genome of Nymphaea alba: whole-genome analyses and the problem of identifying the most basal angiosperm.";
Mol. Biol. Evol. 21:1445-1454(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Produces ATP from ADP in the presence of a proton gradient across the membrane. The beta chain is the catalytic subunit (By similarity).

CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; basal Magnoliophyta; Nymphaeales;
Nymphaeaceae; Nymphaea.
Nym_TraxID=34301;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
-!- SIMILARITY: Belongs to the ATPase alpha/beta chains family.
EMBL; AJ627251; CAF28600.1; -; Genomic_DNA.
SMR; Q6EW72; 19-485.
                                                                                                                                                                                              Score 31; DB 2; Length 292;
Pred. No. 2.8e+02;
1; Mismatches 0; Indels
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Goremykin V.;
Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      498 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                   91.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                     Query Match
Best Local Similarity 85./",
Best Gonservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              QGEW72 NYMAL PRELIMINARY;
QGEW72;
                                                                                                                                                                                                                                                                                                                         36 TSGLGVS 42
                                                                                                                                                                                                                                                                                             1 TSGMGVS 7
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C STRAIN-C57BL/61 TISSUB-Olfactory brain;

KATAIN-C57BL/61 TISSUB-Olfactory brain;

KATAIN-C57BL/61 TISSUB-Olfactory brain;

KATAIN-C57BL/61 TISSUB-OLFACTORY brain;

KATAIN-C57BL/61 TISSUB-OLFACTORY STATE TO MAN I THAN I Y.,

A Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Raito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakanoto N.,

Sasaki H., Sato K., Schoenbach C., Saya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Wumbhaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Wannahaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male olfactory brain cDNA, RIKEN full-length
enriched library, clone:6430539K2l product:hypothetical Zinc finger,
CZH2 type/KRAB box containing protein, full insert sequence.
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ATP synthesis; ATP-binding; CF(1); Chloroplast;

Atyrogen ion transport; Hydrolase; Ion transport; Membrane;

Nucleotide-binding; Thylakoid; Transport.

SEQUENCE 498 AA; 53678 WW; AE984F2728341879 CRC64;
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Pred. No. 4.6e+02;
1; Mismatches 0; Indels
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InterPro; IPR005722; ATP synthF1 beta. InterPro; IPR00793; ATPase_a/b_C. InterPro; IPR000110; ATPase_a/b_N. InterPro; IPR00194; ATPase_a/b_N. Ffam; PF00006; ATP-synt_ab; 1. Pfam; PF00306; ATP-synt_ab, 1. Pfam; PF02874; ATP-synt_ab_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00382; AAA; 1. TIGRFAMB; TIGR01039; atpD; 1.
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QBBVHO;
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Matches 6; Conservative
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NUCLEOTIDE SEQUENCE.
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                                                                                                                         QBGH2 PIG PRELIMINARY;
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TSGLGVS 549
                                                 486 TSGLGVS 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (Pig)
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Putuda S., Puruno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hirandco K., Hiracka T., Hirozane T.,
Hayashida K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Katch H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohaato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku. Akahira S., Takeda Y., Tanaka
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
Submitted (ApR-2002) to the EMBL/GenBank/DDBJ databases.
R. EMBL; AK078250; BAC37193.1; -; mRNA.
                                The PANTOM Consortium, the Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; Manlysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUB=Olfactory brain; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., Muramatsu M., Hayashizaki Y., proparatization and subbraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-C57BL/60; TISSUE-Olfactory brain;
MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Niahi K., Kitsunai T., Taahiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
"RIKEN integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:00046872; F:netal:10n binding; IEA.
GO; GO:0003576; F:nucleic acid binding; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:000825; P:regulation of transcription, DNA-dependent; IEA.
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    STRAIN=C57BL/6J; TISSUE=Olfactory brain;
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PS00028; ZINC_FINGER_C2H2_1; 7.
PS50157; ZINC_FINGER_C2H2_2; 7.
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InterPro; IPR003655; KRAB related.
InterPro; IPR007087; Znf_C2H2.
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SMART; SM00349; KRAB; 1.
SMART; SM00355; Znf_C2H2; 8.
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STRAIN=C57BL/6J; TISSUE-Cerebellum;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ol-Mak-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:B930095306 product:hypothetical Zinc finger,
CZHZ type/KRAB box containing protein, full insert sequence.
                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
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MEDLINE=C1085660; PubMed=11217851; DOI=10.1038/35055500;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakwai T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasuwa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J
Schriml L.M., Staubii F., Suzuki R., Tomita M., Wagner L., Washio I
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
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                                                                                                                                                                                                                                                                                 Grimm D.R., Westling-Fredericks J., Colter M.B., Sandy S.D.; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF314814; AAK01170.1; -; mRNA.
InterPro; IPR001000; Glyco hydro 10.
PROSITE; PS00591; GLYCOSYL_HYDROL_F10; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.2%; Score 31; DB 2; Length 616; 85.7%; Pred. No. 5.7e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   616 AA; 59816 MW; 85C40EF3A27A45E0 CRC64;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       643 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                             Aggrecan CS2 domain (Fragment).
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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STRAIN=ATCC 35092 / DSM 1617 / P2;
STRAIN=ATCC 35092 / DSM 1617 / P2;
STRAIN=97065432; PubMed=8899719;
Sensen C.W., Klenk H.-P., Singh R.K., Allard G., Chan C.C.-Y.,
Liu Q.Y., Penny S.L., Young F., Schenk M.E., Gaasterland T.,
Doollttle W.F., Ragan M.A., Charlebois R.L.;
"Organizational characteristics and information content of an archaeal genome: 156 kb of sequence from Sulfolobus solfataricus P2.";
Mol. Microbiol. 22:175-191(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Pletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Charlebols R.L., Doolittle W.F., Duguet M., Gaasterland T.,
Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.,
"The complete genome of the crenarchaeon sulfolobus solfataricus P2.";
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
-- FUNCTION: Degrades oligopeptides in a sequential manner (By
                                                                                                                                                                                                                                                                                                                              Gaps
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Archaea, Crenarchaeota, Thermoprotei, Sulfolobales, Sulfolobaceae,
Sulfolobus.
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16-OCT-2001 (Rel. 40, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Tricorn protease homolog (EC 3.4.21..).
Name=tri; OrderedLocusNames=SSO2098; ORFNames=C06024, C06_007;
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STRAIN=ATCC 35092 / DSM 16.7 / P2;
STRAIN=ATCC 35092 / DSM 16.7 / P2;
MEDLINE=21332296; PubMed=11427726; DOI=10.1073/pnas.141222098;
MEDLINE=21332296; PubMed=11427726; DOI=10.1073/pnas.141222098;
                                                                                                                                                                                                                                                        Length 643;
                                                                                                                                                                                                           91.2%; Score 31; DB 2; Length 643
85.7%; Pred. No. 5.9e+02;
wicmmatches 0; Indels
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-1. SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-1. SIMILARITY: Belongs to the peptidase S41 family.
                                                                                                                                            Hypothetical protein. – – SEQUENCE 643 AA; 71479 MW; 4B8471333DCD2522 CRC64;
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EMBL, AE066B16; AAK42276.1; -; Genomic_DNA.
PIR, S73091; S73091.
HSSP; P96086; 1K32.
PROSITE; PS50805; KRAB, 1.
PROSITE; PS50806; KRAB, RELATED; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 7.
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InterPro; IPR012393; Pept S41 tricorn.
InterPro; IPR005151; PeptIdase_S41.
Pfam; PF07676; PD40; 2.
Pfam; PF03572; Peptidase_S41; 1.
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Best Local Similarity
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RA NUCLEOTIDE SEQUENCE.

RA SUDMITTED (JAN-2003) to the EMBL/GenBank/DDBJ databases.

Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

REMBL; AV2268615 AAP44492.11; JOINED; Genomic_DNA.

EMBL; AV2268660 AAP44492.11; JOINED; Genomic_DNA.

EMBL; AV2268661 AAP44492.11; JOINED; Genomic_DNA.

EMBL; AV226863 AAP44492.11; JOINED; Genomic_DNA.

EMBL; AV226867 AAP44492.11; JOINED; Genomic_DNA.

EMBL; AV226867 AAP44492.11; JOINED; Genomic_DNA.

EMBL; AV226871 AAP44492.11; JOINED; Genomic_DNA.

EMBL; AV226872 AAP44492.11; JOINED; Genomic_DNA.

EMBL; AV226872 AAP44492.11; JOINED; Genomic_DNA.

EMBL; AV226864 AAP44492.11; JOINED; Genomic_DNA.

EMBL; AV226866 AAP44492.11; JOINED; Genomic_DNA.

EMBL; AV226866 AAP44492.11; JOINED; Genomic_DNA.

EMBL; AV226866; AAP44492.11; JOINED; Genomic_DNA.

EMBL; AV226861; AAP44492.11; JOINED; Genomic_DNA.

EMBL; AV226861; AAP4492.11; JOINED; Genomic_DNA.

EMBL; AV22686; AAP4492.11; JOINED; Genomic_DNA.

EMB
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
              PROSITE; PS50963; LINK 2; 4.
SEQUENCE 2149 AA; 220968 MW; 11FFBAAB15196EE6 CRC64;
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SWART; SM00032; CCP; 1.
SWART; SM00409; GG; 1.
SWART; SM00409; IG; 1.
SWART; SM00406; IGV; 1.
SWART; SM00445; LINK; 4.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS0051; G_TYPE_LECTIN_2; 1.
PROSITE; PS00591; G_TYPE_LECTIN_2; 1.
PROSITE; PS00591; G_LKE; 1.
PROSITE; PS01241; LINK; 1.
PROSITE; PS01241; LINK_1; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                               Query Match 91.2%; Score 31; DB 2; I Best Local Similarity 85.7%; Pred. No. 1.9e+03; Matches 6; Conservative 1; Mismatches 0.
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QEXLEG;
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A Cavanagh J.A.L., Tammen I., Nicholas F.W., Gill C.A., Raadsma H.W.;

L. Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AV226869; AAP44493.1; -; Genomic_DNA.

REMBL, AV226869; AAP44493.1; JOINED; Genomic_DNA.

REMBL, AV226860; AAP44493.1; JOINED; Genomic_DNA.

REMBL, AV226861; AAP44493.1; JOINED; Genomic_DNA.

REMBL, AV226864; AAP44493.1; JOINED; Genomic_DNA.

REMBL, AV226867; AAP44493.1; JOINED; Genomic_DNA.

REMBL, AV226867; AAP44493.1; JOINED; Genomic_DNA.

REMBL, AV226867; AAP44493.1; JOINED; Genomic_DNA.

REMBL, AV226861; AAPA4493.1; JOINED; Genomic_DNA.
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                                                                                                                                                                                                                                                                                              similarity).
C-1 (By similarity).
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C-2 (By similarity).
Charge relay system (By similarity).
Substrate specificity switch (By
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Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
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Seven-bladed beta propeller (By
similarity).
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Pred. No. 9.6e+02;
1; Mismatches 0; Indels
PIRSF; PIRSP036421; Tricorn_protease; 1.
SMART; SM00245; TSPc; 1.
Complete proteome; Hydrolase; Protease; Serine protease.
REGION 61 326 Six-bladed beta propeller (By
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InterProj IPR001209; EGF_like.

InterProj IPR001209; IGF_like.

InterProj IPR0013599; IG.

InterProj IPR0013599; IG.

InterProj IPR0013599; IG.

InterProj IPR001310; Ig-like.

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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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85.7%;
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Best Local Similarity
Matches 6; Conserv
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P13608; P79317; Q28159;
01-JAN-1990 (Rel. 13, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Aggredan core protein precursor (Cartilage-specific proteoglycan core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLECTIDE SEQUENCE OF 563-1056.

MEDLINE=89380219; PubMed=2528543;

Antoneson P., Heinegaard D., Oldberg A.;

"The keratan sulfate-enriched region of bovine cartilage proteoglycan consists of a consecutively repeated hexapeptide motif.";
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MEDLINE=87005253; PubMed=3530809; DOI=10.1016/0014-5793(86)81343-6;
Perin J.P., Bonnet F., Jolles P.;
"Structural relationship between link proteins and proteoglycan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE OF 1609-2113 AND 2151-2364.
MEDLINE=87270630; PubMed=3111460;
Oldberg A., Antonseon P., Heinegaard D.;
"The partial amino acid sequence of bovine cartilage proteoglycan, deduced from a cDNA clone, contains numerous Ser-Gly sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUB=Cartilage;
PUBDLINE=93352525;
PUBDLINE=93352525;
PUBLOSP C., Walcz E., Valyon M., Glant T.T.;
Pustospio of alternatively spliced epidermal growth factor-like "Expression of alternatively spliced epidermal growth factor-like domains in aggrecans of different species. Evidence for a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
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                                                      91.2%; Score 31; DB 2; Length 2327; 85.7%; Pred. No. 2e+03;
                                                                                                 0; Indels
                2327 AA; 242481 MW; 5C048060466806B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hering T.M., Kollar J., Huynh T.D.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem. 268:17377-17383(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arranged in homologous repeats.";
Biochem. J. 243:255-259(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovidae; Bovinae; Bos
PROSITE; PS50923; SUSHI; 1.
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                                                                         Local Similarity 85.7
nes 6; Conservative
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                                                                                                                                       1 TSGMGVS 7
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                SEQUENCE
                                                        Query Match
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PGCA_BOVIN
                                                                                              Matches
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Table 1 18013=P13608-2; Sequence=VSP 003072;

-1- DOWAIN: Two globular domains, Gl and G2, comprise the N-terminus of the proteoglycan, while another globular region, G3, makes up the C-terminus. Gl contains Link domains and thus consists of the chee disulfide-bonded loop structures designated as the A, B, B' motifs. G2 is similar to Gl. The Keratan sulfate (KS) and the chondroitin sulfate (CS) attachment domains lie between G2 and G3.

--- PTM: Contains mostly chondroitin sulfate, but also N-linked and O-linked (about 40) oligosaccharides.

--- PTM: The keratan sulfate considerably between adult and fetal bovine proteoglycans.

--- STMILARITY: Belongs to the aggrecan/versican proteoglycan family.

--- SIMILARITY: Contains 1 C-type lectin domain.

--- SIMILARITY: Contains 1 IG-like V-type (immunoglobulin-like)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                  -1- SIMILARITY: Contains 4 Link domains.
                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=P13608-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U76615; AAB38524.1; -; mRNA.
EMBL; L07053; -; NOT_ANNOTATED_CDS; mRNA.
PIR; A34334; A39808.
PIR; T42630; T42630.
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PROSITE; PS00010; ASX HYDROXYL; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PSS0041; C_TYPE_LECTIN_2; 1.
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PS50026; EGF 3; 1.
PS01187; EGF CA; 1.
PS50835; IG LIKE; 1.
PS00290; IG WHC; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMR; P13608; 2154-2277.
InterPro; IPR002353; AntifreezeII.
InterPro; IPR000152; Ask hydroxyl_S.
InterPro; IPR000742; EGF_2.
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InterPro; IPR000436; Sushi_SCR_CCP.
MEDLINE=91217051; PubMed=2022637;
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InterPro; IPR006209; EGP_like.
InterPro; IPR007110; IG-like.
InterPro; IPR003006; IG_MHC.
InterPro; IPR001304; id_ctin_C.
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Pfam; PF00193; Xlink; 4.
PRINTS; PR00356; ANTIFREEZEII.
PRINTS; PR01265; LINKMODULE.
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                                                                                                                                                                                                                                                                                                                               similarity).
-!- ALTERNATIVE PRODUCTS;
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Pfam; PF00059; Lectin_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P01132; 1GK5.
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Aggrecan.

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Luurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                           PRT; 2365 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002353; Antifreezell; InterPro; IPR00152; Asx hydroxyl S. InterPro; IPR00152; Asx hydroxyl S. InterPro; IPR001615; Asx hydroxyl S. InterPro; IPR00181; EGF Ca bd. InterPro; IPR00181; EGF Ca bd. InterPro; IPR001000; GlyCo hydro—10. InterPro; IPR001000; GlyCo hydro—10. InterPro; IPR0013599; IG InterPro; IPR0013599; IG InterPro; IPR001359; IG InterPro; IPR000389; Ig V. InterPro; IPR000389; Ig V. InterPro; IPR000389; InterPro; IPR000038; Edetin C. InterPro; IPR000436; Sushi_SCR_CCP. Pfam; PF00008; EGF; I. Pfam; PF000084; Sushi_SCR_CCP. Pfam; PF000084; Sushi_SCR_CCP. Pfam; PF000084; Sushi_I. SWART; SW00032; CCP; I. SWART; SW00032; CCP; I. SWART; SW00018; EGF; I. SWART; SW00019; EGF; I. SWART; SW000406; IGV; I. SWART; SW00406; IGV; I. SWART; SW00406; IGV; I. SWART; SW00406; IGV; I. SWART; SW00406; IGV; I. SWART; SW00416; LINK; 4. PROSITE; PS00001; ASX HYDROXYL; I. PROSITE; PS00011; C_TYPE_LECTIN—2; I.
                                                                                                                   RESULT 15

GGXL67_BOVIN PRELIMINARY;
AC GGXL67_BOVIN PRELIMINARY;
AC GGXL67_BOVIN PRELIMINARY;
AC GGXL67_BOVIN PRELIMINARY;
AC GGXL67_BOVIN PRELIMINARY;
DT 05-JUL-2004 (TrEMBLrel. 27,
DT 05-JUL-2004 (TrEMBLrel. 27,
DT 05-JUL-2004 (TrEMBLrel. 27,
DE GENEL, 2004 (TrEMBLrel. 27,
DE GS-JUL-2004 (TREMBLRel. 27,
DE GS-JUL-2004)
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DE GS-JUL-2004)
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22.
EGF-like, calcium-binding (Potential)
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PROSITE; PS01241; LINK 1; 4.
PROSITE; PS5063; LINK 2; 4.
PROSITE; PS50923; SUSHI; 1.
Alternative splicing; Calcium; Direct protein sequencing; EGF-like domain; Glycoprotein; Immunoglobulin domain; Lectin; Proteoglycan; Repeat; Signal; Sushi.
SIGNAL 1 16
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Pred. No. 2.1e+03;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 X 6 AA tandem repeats of [PL]-[FSI]-[PAT]-[STPL].
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6FF83763420C3D4C CRC64;
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N-linked (GlCNAc...) 
                                                                                                                                                                                                                                          Aggrecan core protein.
Ig-like V-type.
Link 1.
Link 2.
Link 3.
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2364 AA; 246362 MW;
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Best Local Similarity 85.7
Matches 6; Conservative
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Sato T., Shimizu T., Watarai M., Kobayashi M., Kano S., Hamabata T.,
Takeda Y., Yamasaki S.; anovel Shiga toxin 1 (Stx1)-converting phage
Which is closely related to Stx2-converting phages but not to other
Stx1-converting phages.";
J. Bacceriol. 185:396-3971(2003).
EMBL; AP005154; BAC78032.1; -; Genomic_DNA.
InterPro; IPR060225; Pept M Zn BS.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
8xz converting bacteriophage II.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae; Lambda-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=83334;
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                                                                                                                                                                                                               91.2%; Score 31; DB 2; Length 2365;
85.7%; Pred. No. 2.1e+03;
ive 1; Mismatches 0; Indels
                                                                                                                                                                      2365 AA; 246477 MW; 39D84712B8F9391E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2576 AA; 284255 MW; 23E34828764E016C CRC64;
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QBX2Q2_01
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Hypothetical protein ECS1242.
OrderedLocusNames=ECS1242;
E; PS00022; EGF_1; UNKNOWN_1.
E; PS01026; EGF_3; 1.
E; PS01187; EGF_CA; 1.
E; PS00591; GLYGCSYL, HYDROL_F10; UNKNOWN_1.
E; PS50835; IG LIKE; 1.
E; PS50243; LINK 2; 4.
E; PS50923; SUSHI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1] -
NUCLEOTIDE SEQUENCE.
STRAIN=0157:H7 / Sakai / RIMD 0509952 / EHEC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 2576 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Stx2 phage-II;
MEDLINE=22697399; PubMed=12813092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q7Y2T1_9CAUD PRELIMINARY;
                                                                                                                                                                                                                                   Local Similarity 85.7 les 6; Conservative
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1977 TSGLGVS 1983
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404 TAGMGVS 410
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Best Local Similarity
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                     PROSITE;
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Q7Y2T1_9CAUD
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MEDLINE=21156231; PubMed=11258796; Hayabih T., Makino K., Ohilshi M., Kurokawa K., Ishii T., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H., Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEULINESTEZ Pidage-I;
STRIN-SEKZ Pidage-I;
MEDLINE-22612959; PubMed=12727356; DOI=10.1016/S0378-1119(03)00487-6;
Sato T., Shimizu T., Watarai M., Kobayashi M., Kano S., Hamabata T.,
Takeda Y., Yamasaki S.;
"Distinctiveness of the genomic sequence of Shiga toxin 2-converting
phage isolated from Escherichia coli 0157:H7 Okayama strain as
compared to other Shiga toxin 2-converting phages.";
Gene 309:35-48(2003).
EMBL; AP004402; BAB87898.1; -; Genomic_DNA.
InterPro; IRN06025; Pept M Zn BS.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_I.
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01-007-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
8txl converting bacteriophage.
Viruses; debnia viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda-like viruses.
NCBI_TAXID=194948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Stx2 converting bacteriophage I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2793;
                                                                                                                                                                                                                           DNA Res. 8:11-22(2001).

EMBL; BA000007; BAB34665.1; -; Genomic_DNA.

PIR; B90784; B90784.

Interpro; IPRO06025; Pept_M_Zn_BS.

PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.

Hypothetical protein.

SEQUENCE 2793 AA; 308319 MW; 94C9EE314922BBE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.2%; Score 31; DB 2; Length 279
85.7%; Pred. No. 2.4e+03;
ative 1; Mismatches 0; Indels
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Best Local Similarity 85.70,
6; Conservative
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Q7x392;
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Matches 6; Conservative
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Makino K., Yokoyan K., Kubota Y., Yutsudo C.H., Kimura S.,
Kurokawa K., Ishiin K., Hattori M., Tatsuno I., Abe H., Iida T.,
Yamamoto K., Ohnishi M., Hayashi T., Yasunaga T., Honda T.,
Sasakawa C., Shinagawa H.,
"Complete nucleotide sequence of the prophage VT2-Sakai carrying the
verotoxin 2 genes of the enterohemorrhagic Escherichia coli O157:H7
Genes Genet. Syst. 74:227-239(1999).
EMBL; APONO42; BAA94178.1; -; Genomic_DNA.
InterPro; IPR006025; Pept M. Zn. BS.
PROSTIE; PSO142; ZINC_PROTEASE; UNKNOWN_1.
                                  NUCLEOTIDE SEQUENCE.
MEDITIRE-9913898, PubMed=10074068;
MEDITIRE-9913898, PubMed=10074068;

"Sequence of Shiga toxin 2 phage 933W from Escherichia coli 0157:H7:
Shiga toxin as a phage late-gene product.";

(2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
MEDLINE=20198780; PubMed=10734605; DOI=10.1266/998.74.227;
                                                                                                                                                                                     Plunkett G. III.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF125520; AAD25477.1; -; Genomic_DNA.
InterPro; IPR006025; Pept M Zn BS.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                   2806 AA; 309701 MW; 5CFAD8824F83B373 CRC64;
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Last sequence update)
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Last sequence update)
Last annotation update)
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85.7%; Pred. No. 2.4e+03;
tive 1; Mismatches 0;
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Enterobacteriaceae, Escherichia
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Q8X470;
Q1-MAR-2002 (TrEMBLrel. 20, C
01-MAR-2002 (TrEMBLrel. 20, L
01-MAR-2004 (TrEMBLrel. 26, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2004 (TrEMBLrel. 26, Hypothetical protein H0150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9KXA6_ECO57 PRELIMINARY;
Q9KXA6;
                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
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                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
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Matches 6; Conserv
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NCBI_TaxID=10730;
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Q9KXA6_ECC
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08X470 E
1D 08X
AC 08X
DT 01-
DT 01-
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Miyamoto H., Nakai W., Yajima N., Fujibayashi A., Higuchi T., Sato K.,
Matsushiro A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                               DDI=10.1128/JB.155.759; FubMed=12013;
Sato T., Shimizu T., Watarai M., Kobayashi M., Kano S., Hamabata T., Takeda Y., Yamasaki S.;
Which is closely related to Stx2-converting phages but not to other Stx1-converting phages.";
J. Bacterion phages.";
EMBL; AP005153; BAC77866.1; -; Genomic_DNA.
InterPro; PR006052; Pept M Zn BS.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
Hypotherical protein.
Bacteriophage VT2-Sa.
Viruses, dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence analysis of Stx2-converting phage VT2-Sa shows a great divergence in early regulation and replication regions.";

DNA Res. 6:235-240(1999)

EMBL, AP000363; BAA84354-11; -; Genomic_DNA.

ENEL, AP000363; PROFOTEASE; UNKNOWN.1.

PROSITE; PS000425; ZINC_PROTEASE; UNKNOWN.1.

Hypothetical protein.

SEQUENCE 2806 AA; 309690 MW; 0335F50D6E4EA9A9 CRC64;
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Pred. No. 2.4e+03;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                 Length 2806;
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Pred. No. 2.4e+03;
1; Mismatches 0; Indels
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Last annotation update)
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                                  STRAIN=Stx1 phage;
MEDLINE=22697399; PubMed=12813092
                                                                                                                                                                                                                                                                                                                 91.2%;
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01-NOV-1999 (TrEMBLrel. 12,
01-MAR-2004 (TrEMBLrel. 26,
Hypothetical protein L0134.
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Q9XJM1;
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                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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404 TAGMGVS 410
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                                                                                                                                                                                                                                                                              SEQUENCE
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20%/JM1 BP933
AC 09/XJM1 Bl
AC 09/XJM1 Bl
DT 01-NOV-1:
DT 01-NOV-1:
DT 01-NOV-1:
DT NOMBELOI
CN NAMBELOI
CN NAMBELOI
CN BACKERIO
CO Lambda-1
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MEDLINE=22511545; PubMed=12622808;
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ID 082YY2_ENTFA PRELIMINARY;
AC 082YY2;
AC 082YY2;
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QOUYQS;
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                                                 6; Conservative
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Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                              1 TSGMGV 6
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                                                                                                                                                    NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=0157:H7 / EDL933 / ATCC 700927 / EHEC;

WEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;

WEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;

WEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Davis N.W., Lim A., Shao Y., Miller L.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Melch R.A., Blattner F.R.;

"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";

IT Nature 409:529-533(2001).

REMBL; AB005174; AA655616.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Anti-human Fc gamma receptor III 3G8 gamma heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Bukaryota, Wetazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Euarchontoglires; Glires; Rodentia, Sciurognathi;
Muridae, Murines, Mus.
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PubMed=15059139; DOI=10.1111/j.1365-2141.2004.04893.x;
Bruenke J., Fischer B., Barbin K., Schreiter K., Machter Y., Mahr K.,
Titgemeyer F., Niederweis M., Peipp M., Zunino S.J., Repp R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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"A recombinant bispecific single-chain Fv antibody against HLA class
II and FcgammaRIII (CD16) triggers effective lysis of lymphoma
                                          Bscherichia coli 0157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.2%; Score 31; DB 2; Length 2806; 85.7%; Pred. No. 2.4e+03; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro, IPR006025, Pept M Zn BS.
PROSITE, PS00142, ZINC PROTEASE, UNKNOWN 1.
Complete proteome; Hypothetical protein.
SEQUENCE 2806 AA, 309701 MW; 5CFAD8824F83B373 CRC64;
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EMBL; AY173025; AA018227.1; -; mRNA.
HSSP; P01820; 1A7N.

ENR; Q811U5; 1-118.

Ensembl; ENSWUSG0000057010; Mus musculus.

G0; G0:0004872; F:receptor activity; IEA.

InterPro; IPR003596; Ig-1ike.
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                                                                                    Enterobacteriaceae; Escherichia.
NCBI_TaxID=83334;
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Q#11U5 MOUSE PRELIMINARY;
Q#11U5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 85.,
6; Conservative
                      OrderedLocusNames=z1495;
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081105 MOU
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Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O., Porden G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O., Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O., Van der Cost J., Weissenbach J., Zivanovic Y., Forterre P., Carden Pyrococus abyssi. "An integrated analysis of the genome of the hyperthermophilic archaeon Pyrococus abyssi.";

Mol. Microbiol. 47:1495-1512(2003).

EMBL, AJ248287, CAS50357.1; -, Genomic_DNA.

PIR, H75057, H75057, Gonomic_DNA.

GO; GO:0003557, F:DWA binding; IEA.

GO; GO:0003557, P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR007501; DUF531.
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Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,

Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,

Tettelin H., Dodson R.J., Umayam L.A., Nolonay J.F., Madupu R.J.,

Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,

Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,

Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
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Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI_TaxID=1351;
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        Length 118;
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                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JOCT-2003 (TrEMBLrel. 25, Last annotation update)
ATPase, ParA family.
OrderedLocusNames=EF3299;
88.2%; Score 30; DB 2; Le
100.0%; Pred. No. 1.9e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
OrderedLocusNames=PYRAB14520; ORFNames=PAB0965;
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85.7%; Pred. No. 3e+02;
iive 0; Mismatches
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Pred. No. 5.3e+02;

85.78;

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Best Local Similarity
Matches 6; Conserv
                                                                                                                  1 TSGMGVS
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MBDLINE=Z260306; PubMed=12692562; DOI=10.1038/hbt820;
Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.;
"Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:526-531(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                             GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0042242; F:Cobyrinic acid a,c-diamide synthase activity; IEA.
GO; GO:0016491; F:Cobyrinic acid a,c-diamide synthase activity; IEA.
GO; GO:0009236; F:Cobalamin biosynthesis; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR002586; CbiA P synth.
InterPro; IPR00392; NitrogenaseII.
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STRAIN=MA-4680 / ATCC 31267 / NCIME 12804 / NRRL 8165;

K MEDLINE-2147403; PubMed=11572948; DOI=10.1073/pnas.211433198;

MEDLINE-2147403; PubMed=11572948; DOI=10.1073/pnas.211433198;

A Cmurza S., Ikeda H., Iehikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi C., Sakaki Y., Hattori M.;

"Genome sequence of an industrial microorganism Streptomyces T avermitilis: deducing the ability of producing secondary metabolites.";

Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).

R GO: GO:0016301; F:kinase activity; IEA.

GO: GO:000614; P:D-ribose metabolism; IEA.

InterPro: IPR001161; PfKB region.

InterPro: IPR001161; PfKB region.

InterPro: IPR001161; PfKB region.
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Fraser C.M.; "Role of mobile DNA in the evolution of vancomycin-resistant
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 AA; 27879 MW; ED483365A4BB0A46 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            345 AA
                                                                                                                             EMBL; AE016957; AA082964.1; -; Genomic_DNA.
HSSP; Q8U311; 1G3Q.
TIGR; EF3299; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00091; NITROGNASEII.
                                                                  Enterococcus faecalis.";
Science 299:2071-2074(2003).
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082MA4 STRAW PRELIMINARY;
082MA4;
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Best Local Similarity
Matches 6; Conserv
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DB 2; Length 345;

88.2%; Score 30;

Query Match

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Maucali E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Maucali E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Maucali E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Micaud S., Jaffe D., Fisher S., Iuffalla G., Dossat C., Segurens B.,
Dasilva C., Salancoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Mandrourd C., Duprat S., Brottier P., Coutancau J.P., Gouzy J.,
Rallis M., Volff JN., Gugple C., McKernan K.J., McEwan P., Bosak S.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
III Nature 431:946-957(2004).
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
1; Indels
                                                                                                                                                                                                                                                                                               13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 11 SCAF14979, whole genome shotgun sequence.
ORFNames=GSTENG00027276001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preliminary data.
., CAAE01014979; CAG06782.1; -; Genomic_DNA.
JENCE 404 AA; 44505 MW; 03EC303B66BD448B CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypotheitcal protein Bl008E06.28.
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  Mismatches
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Q4RXVO;
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6; Conservative
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NUCLEOTIDE SEQUENCE.
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1 TSGMGV 6
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SEQUENCE 472 AA
                                                                                                                 Query Match
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Q6AER2 LEI
ID Q6AER
                                                                                                                                                              Matches
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EMBL, ACIS9703, AAX80013.1; -; Genomic_DNA.
SEQUENCE 434 AA, 48547 MW; 69F02D5053C7BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trypanosoma brucei.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5691;
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                                          Sasaki T., Maľsumoto T., Katayose Y.; "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 9, BAC
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
GLP 561 3816 2467.
Glardia lamblia ATCC 50803.
Eukaryota, Diplomonadida, Hexamitidae, Glardiinae, Giardia.
                                                                                                                                                                                                                                                 88.2%; Score 30; DB 2; Length 417; 100.0%; Pred. No. 6.4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.2%; Score 30; DB 2; Length 434; 85.7%; Pred. No. 6.7e+02;
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"Draft sequence of the Giardia lamblia genome.";
Submitted (MAR-202) to the EMBL/GenBank/DDBJ databases.
-- CAUTION: The sequence shown here is derived from an
                                                                                                               Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005829; BAD26267.1; -; Genomic_DNA.
                                                                                                                                                                              Hypothetical protein.
SEQUENCE 417 AA; 45227 MM; 63C6C528E407D56C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypothetical protein.
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Q57TW1;
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OTOUW4;
                                                                                                                                                                                                                                                 Query Match 88.2
Best Local Similarity 100.
Matches 6; Conservative
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(1)
NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                       291 TSGMGV 296
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                                                                                                                                                           Gramene; Q6H4T2; -
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                                                                                                                                                                                                                                                                                                                                             1 TSGMGV 6
                                                                                       clone: B1008E06."
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EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Micrococcineae, Microbacteriaceae; Leifeonia.
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                                                                                                                                                                                                                   Length 449;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 24, Last annotation update)
01-AUG-1999 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein ag 2082.
OrderediocusNames=AQ_2082;
Aquifex acolicus.
Bacteria; Aquificee; Aquificales; Aquificaceae; Aquifex.
                                    preliminary data.
EMBL; AACBO1000089; EAA38817.1; -; Genomic DNA.
SEQUENCE 449 Aa; 52112 MW; 6A24348FD40F814B CRC64;
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MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
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Last annotation update)
                                                                                                                                                                                                              Score 30; DB 2; Le
Pred. No. 6.9e+02;
                                                                                                                                                                              88.2%; Scor.
100.0%; Pred. No. v.
0; Mismatches
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
OrderedLocusNames=Lxx12950;
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ID O67856 AQUAE PRELIMINARY;
AC O67856;
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                                                                                                                                                                                                                                                       Local Similarity 100
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Best Local Similarity
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Pred. No.

71.48;

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Best Local Similarity
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                                                                                                                                                                                                    요
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Smead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olsen G.J., Swanson R.V., Fort T.M., The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tetraodon nigroviridis (Green puffer).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF10731, whole genome shotgun sequence.
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-!- CAUTION: The sequence shown here is derived from an EMBI/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 88.2%; Score 30; DB 2; Length 537; Similarity 100.0%; Pred. No. 8.2e+02; 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                               InterPro; IPR007816; ResB.
Pfam, PF05140; ResB; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 537 AA; 61601 MW; 8F73489AAA7676C3 CRC64;
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-!- SIMILARITY: Contains 4 PDZ (DHR) domains.
BMBL; CARABO1010/731; CAF93395.1; -; Genomic_DNA.
InterPro; IPR001478; PDZ.
Pfam; PP00595; PDZ; 4.
SMART; SM00228; PDZ; 4.
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                                                                                                                                                                                            Nature 392:353-358(1998).
EMBL; AE000711; AAC07820.1; -; Genomic_DNA.
PIR; D70478; D70478.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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Q4T137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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10 AC 047131
AC 047131
BD 113-SE
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DB 2; Length 580;

88.2%; Score 30;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 415:630-633(2002).

Reful, AECOBO19; ALT/6414.1; -; Genomic_DNA.

GO; GO:0005737; C:cytoplasm; IEA.

GO; GO:0004047; F:aminomethyltransferase activity; IEA.

GO; GO:001491; F:cxidoreductase activity; IEA.

GO; GO:0006118; P:electron transport; IEA.

GO; GO:0006518; P:electron transport; IEA.

RiterPro; IPRO06076; Fad oxred.

RiterPro; IPRO06076; Fad oxred.

RiterPro; IPRO06025; GCV-T.

RiterPro; IPRO06056; NaD_BS.
                                        Indels
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glycine cleavage system T protein, putative.
8.8e+02;
0;
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                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; environmental samples
                                                                                                                                                                                                            814 AA.
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                                      2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL_2004 (TrEMBLrel. 27, 05-JUL_2004 (TrEMBLrel. 27, 05-JUL_2004 (TrEMBLrel. 27, Oxidoreductase, FAD-binding.
                                                                                                                                                                                                                                                                                                                           Name=gcvT;
uncultured proteobacterium.
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                                                                                                                                                                                                            QBRTR2_9PROT PRELIMINARY;
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                                      5; Conservative
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353 TSGLGIS 359
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                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=153809;
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                                                                            1 TSGMGVS
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RESULT 38
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0624T5.
0624T5.
06-4T15.
06-4T15.
06-4T15.
06-4T15.
06-4T16.
06-4T16.
06-4T16.
06-4T16.
01-FEB-2004 (TrEMBLrel. 27, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
01-FEB-2005 (TrEMBLrel. Synonyms=001134_B10.8-1;
00-yoza sativa (japonica cultivar-group).
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R Gramene; 022475; ...

R GO; GO:0005622; C:intracellular; IEA.

GO; GO:0003677; F:DNA binding; IEA.

GO; GO:0003877; F:DNA binding; IEA.

R GO; GO:0005877; F:DNA directed DNA polymerase activity; IEA.

R GO; GO:000520; P:DNA replication; IEA.

R InterPro; IPR002262; 3 S exonuclease.

R InterPro; IPR002299; DNA_pol.

R Pfam; PF01612; 3 S exonuc;

R Pfam; PF01612; 3 S exonuc;

R Pfam; PR01612; 4 S exon
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"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, BAC clone:OJ1134 B10.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AP003164; BAD05554.1; -; Genomic_DNA.
HSSP; P19821; 1JXE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saeaki T., Matgumoto T., Katayose Y.; "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, BAC clone:OSJNBa0054L03.";
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
GO; GO:0004047; F:aminomethyltransferase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
GO; GO:0006464; P:glycine catabolism; IEA.
InterPro; IPR006076; Pad oxred.
InterPro; IPR006022; GCV_T.
InterPro; IPR006025; NAD_BS.
Pfam; PF01266; DAO;
Pfam; PF01266; DAO;
Pfam; PF01271; GCV_T; 1.
SEQUENCE 814 AA; 90235 MW; 0D4F9717D6A9F963 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
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100.0%; Pred. No. 1.2e+03;
iive 0; Mismatches 0;
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Best Local Similarity 85...
Free 6; Conservative
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Best Local Similarity
Local 6; Conserve
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                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
01-FBB-2005 (TrEMBLrel. 29, Last sequence update)
01-FBB-2005 (TrEMBLrel. 29, Last annotation update)
01-FBB-2005 (TrEMBLrel. 29, Last annotation update)
01-FBB-2005 (TrEMBLrel. 29, Last sequence
01-FBB-2005 (TrEMBLrel. 201134_B10.10;
01-FBB-2005 (TremBLrel. 201134_B10.10;
01-FBB-2005 (TremBLrel. 201134_B10.10;
01-FBB-2005 (TremBLrel. 201134_B10.10;
01-FBB-2005 (TremBLrel. 201124, TremBLrel. 201124
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Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
Sucgang R., Berriman M., Song J., Oleen R., Szafranski K., Xu Q.,
Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
Bankler A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
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"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, BAC clone:OJ1134 B10.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005164; BAD05556.1; -; Genomic_DNA.
EMBL; AP03882; BAD05229.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sasaki T., Mateumoto T., Katayose Y.; "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, BAC clone:OSJNBa0054L03.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0008408; F:3'-5' exonuclease activity; IEA.
GO; GO:000387; F:DNA binding; IEA.
GO; GO:000387; F:DNA directed DNA polymerase activity; IEA.
GO; GO:0006260; P:DNA replication; IEA.
InterPro; IPR002298; DNA pol.
InterPro; IPR001998; DNA pol.
InterPro; IPR001998; DNA pol.
InterPro; IPR001298; DNA pol.
Pfam; PF00476; DNA pol A; 1.
PRINTS; PR00868; DNAPOLI.
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85.7%; Pred. No. 1.5e+03;
tive 1; Mismatches 0; Indels
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein.
ORFNames=DDB0206214;
Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetcozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
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QEZ4T3 ORYSA PRELIMINARY;
QEZ4T3;
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Best Local Similarity 85...
6; Conservative
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ID OS4XP6_DICDI PRELIMINARY;
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SMART; SMO0482; POLAC;
SEQUENCE 1035 AA; 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=39947;
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Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
Parbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
Wardroper A., Pelder M., Thangavelu M., Johnson D., Knights A.,
Loulseged H., Mungall K., Oilver K., Price C., Quail M.A.,
Wurshihara H., Hernandez J., Rabbinowitsch E., Steffen D., Sanders M.,
M. J., Kohara Y., Sharp S., Simmonds M., Splegler S., Tivey A.,
Sugano S., White B., Walker D., Woodward J., Winckker T., Tanaka Y.,
Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
"The genome of the social amoeba Dictyostelium discoideum.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Butaryota; Metazoa; Chordata; Craniata; Vertebrata; Neoteleostei;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAR7518, whole genome shotgun sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preliminary data.
L; AAF101000053; EAL68009.1; -; Genomic_DNA.
G0:0005255; F:GTP binding; IEA.
G0:0005743; F:translation initiation factor activity; IEA.
G0:0006412; P:protein biosynthesis; IEA.
G0:0006413; P:translational initiation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88.2%; Score 30; DB 2; Length 1045; 85.7%; Pred. No. 1.6e+03; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1045 AA; 115835 MW; D6F82472E3DE3683 CRC64;
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Interpro; IPR001795; ProteSyn GTPbind.
Interpro; IPR005225; Small GTP.
Pfam; PF00009; GTP EFTU; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q4T9N9_TETNG PRELIMINARY;
Q4T9N9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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REC STRAINS=972;

MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;

RED WEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;

RA WOOD V. Gailliam R., Rajandream M.A., Lyne M.H., Lyne R.S. Stewart A., Ray Gourcos J.G., Peat N., Hayles J., Baker S.G., Basham D., Bowman S., RA Squurcos J.G., Peat N., Hayles D., Baker S.G., Hidalon D., Bowman S., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Rodlins M., Connor R., Cronin A., Davis D., Hidalon J., Hodgeon G., Holroyd S., Hornesby T., Howarth S., Huckle B.J., Hunt S., Jagels K., James K.D., Jones M., Leather S., McDenal J., Hodgeon G., Admes K., O'Neil S., Mangall K.L., Murphy L.D., Niblett D., Odell C., RA Monory P., Moule S., Mangall K.L., Murphy L.D., Niblett D., Odell C., RA Retherford K.M., Rutter S., Saunders D., Seeger K., Sharp S., Raylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J.R., Volckaert G., Aert R., Robben J., Grymonprez B., Moodward J.R., Volckaert G., Aert R., Robben J., Grymonprez B., Meltjens I., Vanstreels E., Rieger M., Schaefer M., Meller E., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedler H., Wannbutt R., Purnelle B., Rodfeau A., Cadieu E., Dreano S., Gloux S., Lehrach H., Reinhardt R., Lowes S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., A. Daga R.R., Cruzado L., Jimenz J., Sanchez M., Garzon A., Thode G., Rudon M., Goffeau J., Sanchez M., Rabaga R.R., Cruzado L., Jimenz J., Sanchez M., Garzon A., Thode G., Rudon M., Mosery D., Barrell B.G., Nurse P., Rayler M., Rudon M., Potsburg P., R., Rudon M., Rudon M., Potsburg P., R., Rudon M., Rudon M., Rudon M., Rudon M., Rudon M., Potsburg P., R., Rudon M., Markelle M., Baller M., Galler M., Garzon M., Thode G., Rudon M., Rudon M., Baller M., Baller M., Baller M., Baller M., Galler M., Garzon M., Thode G., Rudon M., Baller M., Galler M., Baller M., Galler M., Baller M., Bal
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SIMILARITY: Belongs to the IF-2 family.
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Bukaryotic translation initiation factor 5B (eIF-5B) (Translation initiation factor IF-2).
ORFNames=SPAC56F8.03;
                                                                                                                                     -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                         Score 30; DB 2; Length 1050;
Pred. No. 1.6e+03;
1; Mismatches 0; Indels
                                                                                         Whitehead Institute Centre for Genome Research, (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                               1050 AA; 114803 MW; A400D1E0E728A2E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                         CAAE01007518; CAF90393.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1079 AA
the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                         h 88.2%;
Similarity 85.7%;
6; Conservative
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                                                                                                                                                                                                                                                          1050
                                                                                                                                                                                      preliminary data.
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SEQUENCE
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FIRESTOUCHTES
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EMBL; Z69728; CAA93574.1; -; Genomic_DNA.

PRR; T38913; T38913.

RISSP; O26359; 1G75.

RIGEPPO; IPRO04161; EFTU_D2.

RIGEPPO; IPRO00196; EFTU_D2.

RIGEPPO; IPRO00795; ProtSyn

RIGEPPO; IPRO00795; Small_GTP_bd.

RIGEPPO; IPRO00795; Small_GTP_bd.

RIGEPPO; IPRO00196; GTP_EFTU_D2.

REAT; PF003144; GTP_EFTU_D2.

REAT; PF003145; ELONGATNFCT.

PRODM; PD186100; IF2; 1.

ROSUTE; PS01176; IF2; 1.

ROSUTE; PS01176; IF2; FALSE NEG.

Complete proteome; GTP-binding; Initiation factor; Nucleotide-binding;
This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein twk-31.
Name=twk-31; ORRName14703B.5, Y47D3B.5a;
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditodea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Bristol N2;
MDDLINE=99069613; PubMed=9851916;
The C. elegans sequencing consortium;
"Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                               88.2%; Score 30; DB 1; Length 1079;
85.7%; Pred. No. 1.6e+03;
iive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                           491 498 GTP (By similarity).
1079 AA; 119931 MW; 73A01CE933C1F6AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            investigating biology.", Science 282:2012-2018 (1998).
BMBL, AL0131635, CA21041.2; -; Genomic_DNA.
PIR, 72693; 72693.
HSSP, O54397; 1BL6.
Ensembl; Y47D3B.5; Caenorhabditis elegans.
WormBase, WBGene00006683; Y47D3B.5.
WormPep; Y47D3B.5a; CB31838.
GO; GO:0016020; Cincentragral to membrane; IEA.
GO; GO:0016020; Cincentragral to membrane; IEA.
GO; GO:0016216; Fion channel activity; IEA.
GO; GO:006811; Pion transport; IEA.
GO; GO:006811; Pion transport; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003280; K+channel_2pore.
InterPro; IPR001622; K+channel_pore.
PRINTS; PR01333; 2POREKCHANEL.
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Q9XX01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                               Protein biosynthesis.
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829 TSGIGVS 835
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SEQUENCE
                                                                   removed.
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Matches
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Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR01333; 2POREXCHANBL. —
Hypothetical protein; Ion transport; Ionic channel; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                         The C.briggsae Sequencing Consortium, Submitted (SEP-2003) to the EMBL/Genbank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry which is
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NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=Bristol N2;
MEDLINE=99069613; PubWed=9851916;
The C. elegans sequencing consortium;
"Genome sequence of the nematode C. elegans: a platform for
              Length 1088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1100 AA; 124435 MW; 292B4110B011A843 CRC64;
                                                                                                                                                                                                 25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein CBG11286 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypotherical protein twk-31.
Name=twk-31; ORFNames=Y47D3B.5, Y47D3B.5B;
                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; CARCO1000063; CAB67712.1; -; Genomic DNA. GO; GO:0016021; C:integral to membrane; IEA. GO; GO:0016020; C:immbrane; IEA. GO; GO:0005216; F:ion channel activity; IEA. GO; GO:0006811; F:ion channel activity; IEA. GO; GO:0006811; F:ion transport; IEA. InterPro; IPR003280; K-channel_2pore.
              Score 30; DB 2; 1
Pred. No. 1.6e+03;
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                                                                                                                                                                        PRT; 1100 AA.
                                         0; Mismatches
              88.2%;
Ouery Match
Best Local Similarity 85.,
6; Conservative
                                                                                                                                                                     QGIBNB_CAEBR PRELIMINARY;
QGIBNB;
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                                                                                                                                                                                                                                                                      Caenorhabditis briggsae.
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                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary data.
                                                                                                 956 TSGMGTS 962
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NUCLEOTIDE SEQUENCE.
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                                                                     1 TSGMGVS
                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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QEEUTB CAE
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Birren B., Nusbann C., Abebe A., Abouelleil A., Adekoya E.,
Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
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Bayul T., Blitshsteyn B., Bloom T., Blye J., Boguslavskiy L.,
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                                                                                                                                                                                                                                                                                                                                                                    PubMed=14976418; DOI=10.1023/B:VIRU.0000016857.94136.89;
Seregin S.V., Samokhvalov E.I., Petrova I.D., Vyshemirskii O.I.,
Samokhvalova E.G., Lvov D.K., Gutcrov V.V., Tyunnikov G.I.,
Shchelkunov S.N., Netesov S.V., Petrov V.S.;
"Genetic characterization of the m RNA segment of crimean-congo
hemorrhagic Fever virus strains isolated in Russia and tajikistan.";
Wirus Genes 28:187-193 (2004).
EMBL; AXI19962; AAG52016.1; -; Genomic_RNA.
GO; GO:0019031; C:viral envelope; IRA.
InterPro; IPR001865; Ribosomal_S2.
InterPro; IPR001087; Znf_C2H2.
                                                                                                                                                        Envelope glycoprotein.

Crimean-Congo hemorrhagic fever virus.

Viruses; ssRNA negative-strand viruses; Bunyaviridae; Nairovirus.
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Bukaryota, Pungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetes incertae sedis, Magnaporthaceae, Magnaporthe.
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Pred. No. 2.5e+03;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1689 AA; 187110 MW; SDBSF609DCD33B02 CRC64;
                                                                               (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00962; RIBOSOMAL S2 1; UNKNOWN 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN 1.
Envelope protein.
SEQUENCE 1689 AA; 187110 MW: KDRKFCOOLDING.
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                 PRT; 1689 AA
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                 Q6Y5E0 9VIRU PRELIMINARY;
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
ORFNames=MG07408.4;
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                                                                               05-JUL-2004
                                                                                                                                                 05-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome; Hypothetical protein; Ion transport; Ionic channel; Transmembrane; Transport. SEQUENCE 1136 AA; 127586 MW; 3C9BSOBIDEEC1047 CRC64;
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Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
Geobacteraceae; Geobacter.
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Pred. No. 1.7e+03;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 88.2%; Score 30; DB 2; Length 1136; Similarity 85.7%; Pred. No. 1.7e+03; 6; Conservative 0; Mismatches 1; Indels
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                                                                                                                        Wormbase, WBGene00006683; Y4703B.5.
Wormpage, Y4703B.5b; CE19178.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016020; C:integral to membrane; IEA.
GO; GO:0005216; F:ion channel activity; IEA.
GO; GO:0005217; F:potassium channel activity; IEA.
GO; GO:0006813; P:potassium ion transport; IEA.
X GO; GO:006813; P:potassium ion transport; IEA.
X InterPro; IPR003280; K+channel_zpore.
X InterPro; IPR001622; X+channel_zpore.
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PROSITE; PS06583; PPKB KINASES 1; UNKNOWN 1.
Complete protecome; Hypôthetical protein.
SEQUENCE 1175 AA; 123298 WW; 3133E9AB71D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1175 AA
investigating biology.";
Science 282:2012-2018(1998).
EMBL; AL031635; CAH04762.1; -; Genomic_DNA.
Ensembl; Y47D3B.5; Caenorhabditis_elegans.
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EMBL; AE017180; AAR36522.1; -; Genomic_DNA.
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Best Local Similarity 71.4%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OrderedLocusNames=GSU3131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 GEOSL
Q747Y4 GEOSL PRELIMINARY;
Q747Y4;
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TSGMGIA 74
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Length 3175;

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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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PubMad=15480790; DOI=10.1007/800438-004-1056-y;

Pubmad=15480790; DOI=10.1007/800438-004-1056-y;

Ruchersava N., Steinborn G., Franke P., Grammel N., Zwintscher A., Leendcar P., Hitzeroth G., Vater J., Geneddra P., Hitzeroth G., Vater J., Geneddra P., Grammel N., Zwintscher A., Genetic analysis of the biosynthesis of non-ribosomal peptide- and polyketide-like antibiotics, iron uptake and biofilm formation by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The C. elegans sequencing consortium;
"Genome sequence of the nematode C. elegans: a platform for investigating biology.";
Science 282:2012-2018(1998).
ENEL; 281512; CAB04172.2; -; Genomic_DNA.
PIR; T21328; T21328.
Ensembl; F2568.3; Caenorhabditis elegans.
Wormbease; WaGene00009105; F2568.3.
Wormbep; F2568.3; Caenorhabditis elegans.
Complete proteome; Hypothetical protein.
SEQUENCE 3184 AA; 358109 MW; F296F176A3AFD120 CRC64;
         WormBase; WBGene00009105; F25C8.3.
WormPep; F25C8.3b; CE35507.
Complete proteome; Hypothetical protein.
SEQUENCE 3175 AA; 357150 MW; 2349FAF5914D10AE CRC64;
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85.7%; Pred. No. 4.6e+03;
tive 0; Mismatches 1; Indels
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein F5C6.3a.
ORFNames=F25C8.3, F25C8.3a;
Caenorhabditis elegans.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
SrfAC surfactin synthetase (Fragment).
                                                                                                                                                                  Score 30; DB 2; L
Pred. No. 4.5e+03;
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                                                                                                                                                                                                                              0; Mismatches
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MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                     88.2%;
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Query Match
Best Local Similarity 85.70,
6, Conservative
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Q9XV66;
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NUCLEOTIDE SEQUENCE.
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Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Mlenga V., Moru K., Mozes J., Mulrain L., Munson G., Naylor J., Newes C., Nguyen C., Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizari M., Norbu C., Norbu N., O'donnell P., Okoawo O., O'leary S., Camctosho B., O'neill K., Osman S., Parker S., Perrin D., Phunkhang P., Piqani B., Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C., Retra R., Richardson S., Rise C., Rodriguez J., Rogor D., Retta R., Richardson S., Rasen C., Settipalli S., Sharpe T., Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C., Sperson K., Stone C., Stone S., Stubbe M., Talamas J., Tchninga P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K., Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K., Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K., Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K., Temana V., Vinson J., Wo A., Wade C., Wang S., Wangchuk T., Wang S., Yang X., Yeager S., Yee B., Young G., Zainoun J., Zembeck L., Xang S., Zaimer A., Zody M., Lander B., Young G., Zainoun J., Zembeck L., The genome sequence of Magnaporthe grisea.";

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"The genome sequence of Magnaporthe grisea.";
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhu H., Blackmon B.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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EMBL; AACU01000890; EAA53131.1; -; Genomic_DNA.

Interpro; IPR001440; TPR.

Interpro; IRR011990; TPR-like_helical.

SMART; SM00028; TPR; 3.

PROSITE; PS50029; TPR EGION; 1.

Hypothetical protein; Repeat; TPR repeat.

SEQUENCE 2125 AA; 232813 MW; B1F5A282D4A861C9 CRC64;
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Dean R., Mitchell T., Brown D., Pan H., Thon M.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
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05-UTL-2004 (TrEMBLrel. 27, Last sequence update)
05-UTL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein F25C8.3b.
ORFNames=F25C8.3, F25C8.3B.
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MEDLINE=99069613; PubMed=9851916;
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A Hofemeister J.W., Adler B.C., Conrad B., Hofemeister B.H., Stein T.,
AT "Lipoperide antibiotic, siderophore and polyketide gene activities of R Baciluse subtilis A1/3: Gene tagging and mutation studies.";
BLE Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
BLE SUBMIL; AF520864; AA008791.1; -; Genomic DNA.
GO, GO:00081824; F:catalytic activity; IEA.
BC GO:0008182; F:metabolism; IEA.
BC GO:0008182; F:metabolism; IEA.
BC GO:0008182; P:metabolism; I
Bacillus subtilis Al/3.";
Mol. Genet. Genomics 272:363-378(2004).
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NUCLEOTIDE SEQUENCE.
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0; Gaps Query Match

85.3%; Score 29; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels q ઠે

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Search completed: February 23, 2006, 09:51:20 Job time : 89.3077 secs

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3B9 was positive. cDNA clones of the 3B9 light and heavy chains were cloned into pGEM7f+ and transformed into E. coli DH5-alpha. A heavy chain cDNA clone was sequenced (AAQ83491) that encoded the protein given in AAR70190. 3 CDRs (AAR70198-200) were identified. (Updated on 25-MAR-2003 to correct PN field.)

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Gaps

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Indels

100.0%; Score 95; DB 2; Length 16; 100.0%; Pred. No. 5.6e-08;

Mismatches

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Query Match 100. Best Local Similarity 100. Matches 16; Conservative

Sequence 16 AA;

8888888

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Murine-ex
Murine-ex
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Human ant
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Murine-ex
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Adx652388
Adx652388
Adx66603
Adx66603
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                                                                                                 AAE38325
ADP03935
ADP03868
ADP03876
ADS16556
AAG00027
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AAU81276
AAX56713
ADX98263
ADX98259
ADZ57713
AAX24373
ADX52388
ADX52388
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ADP03870
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ADX98417
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ADG30499
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ADG96435
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93US-00136783.
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WO9507301-A1.
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20-SEP-1995
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  AAR70199;
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New DNA molecules encoding recombinant antibodies useful for treating IL4 -mediated conditions.
                                                                                                                                                                                                                                         Heavy chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin E-mediated allergic reaction; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a complementarity determining region (CDR) of the heavy chain variable region of murine interleukin-4 (IL-4) antibody 319. The specification describes chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic rhinitis, rheumatoid arthritis, host-versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans
                                                                                                                                                                                                            CDR of the heavy chain variable region of antibody 3B9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Col 47-48; 50pp; English.
                                                                                                                                                                                                                                                                                                                              complementarity determining region.
                                                                                                             AAY23776 standard; peptide; 16 AA
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93US-00136783.
94WO-US010308.
               1 HIYWDDDKRYNPSLKS 16
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1 HIYWDDDKRYNPSLKS 16
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                                                                                                                                                                               13-SEP-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                             US5928904-A.
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                                                                                                                                             AAY23776;
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                                                                              RESULT 2
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Spleen cells from mice immunized with human IL-4 were used to prepare hybridomas, which were screened for anti-IL-4 MAD secretion. Only clone

Disclosure; Page 57; 97pp; English.

Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated and IgE-mediated allergic conditions.

Gross MS, Sylvester DR,

Holmes S,

WPI; 1995-123387/16.

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New polynucleotide encoding a complementarity- or framework-determining region of an anti-idiotypic antibody that binds to human or primate antihuman immunodeficiency virus (HIV) antibodies, for use in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention relates to coding sequences of the murine 1F7 anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            idiotypic antibody complementarity-determining region (CDR) or framework-determining region (FR). The antibody binds to human or prinate antihuman immunodeficiency virus (HIV) antibodies and can be used in the treatment of HIV infection. The present sequence is a region of the IF7
                                                                                                               Mouse; 1P7; antibody; immune modulator; anti-HIV antibody; CDR; complementarity determining region; framework-determining region; PR; heavy chain; light chain; HIV infection.
                                                                                       Murine Mab 1F7 heavy chain CDR2 region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 21; 27pp; English.
   AAO18532 standard; peptide; 16
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                                                                                                                                                                                                                                                                                             11-JAN-2001; 2001US-00759112.
                                                                                                                                                                                                                                                                                                                          (IMMP-) IMMPHERON INC
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-590668/63.
N-PSDB; AAL48656.
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                                 AA018532;
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                                                                                                                                                                                                                                                                        Antibody; interleukin-4; II4; immunoglobulin E; IgE mediated disease; allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease; complementarity determining region; CDR.
                               Gaps
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100.0%; Score 95; DB 2; Length 16; 100.0%; Pred. No. 5.6e-08;
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100.0%; Pred. No. 5.6e-08;
ive 0; Mismatches 0;
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                              Mismatches
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Best Local Similarity 100.0%; P
Matches 16; Conservative 0;
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93US-00136783.
94WO-US010308.
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                                                                                                                                                                                                                     (first entry)
               Best Local Similarity 100.
Matches 16; Conservative
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   Query Match
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                                                                                                                                                                                                                   Monoclonal antibody; 10D5; complementarity determining region; CDR; mouse; humanised antibody; antibody; Alzheimer's disease; Down's syndrome; cerebral amyloid anglopathy; neuroprotective; nootropic.
                         Gaps
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0
 Length 16;
                      Indels
                                                                                                                                                                                                Murine monoclonal antibody 10D5 heavy chain CDR2.
100.0%; Score 95; DB 5; 100.0%; Pred. No. 5.6e-08;
                       Mismatches
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                                                                                                                            ABP58280 standard; peptide; 16
                                               16
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                                                          1 HIYWDDDKRYNPSLKS
                                                                                                                                                                         (first entry)
                                              1 HIYWDDDKRYNPSLKS
                      Conservative
                                                                                                                                                                                                                                                                                        WO200288307-A2
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                                                                                                                                                                                                                                                                  Mus sp.
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AAO18532

New isolated mammalian anti-amyloid antibodies useful for treating amyloid-associated disorders, such as Alzheimer's disease, cancer, allergies, autoimmune disease, Parkinson's disease, multiple sclerosis,

Benson JM;

Mercken M,

MERCKEN M. BENSON J M.

(MERC/) (BENS/)

WPI; 2005-242565/25.

Claim 6; SEQ ID NO 54; 306pp; English.

migraine and dementia.

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                                                                                                                                                                                              The present sequence is that of complementarity determining region (CDR) 2 of the heavy chain of murine monoclonal antibody 10D5. Novel humanised antibodies of the invention have CDRs from 10D5 and human framework sequences. These humanised antibodies have binding affinities (affinity and epitope location) approximately the same as those of the mouse 10D5 antibody. The invention includes antibodies, single chain antibodies, and their fragments, as well as nucleotide sequences, vectors, transformed host cells, and methods of using the humanised antibody to treat, prevent, alleviate, reverse or otherwise ameliorate symptoms and/or pathology associated with Down's syndrome, (pre-)clinical crebral amyloid angiopathy, and to inhibit
                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amyloid, antibody engineering; antibody production; allergy; anayloid-associated disorder; Alzheimers disease; cancer; allergy; autoimmune disease; Parkinsons disease; acquired immune deficiency syndrome; multiple sclerosis; migraine; dementia; infection; nootropic; neuroprotective; cytostatic; antiallergic; Immunosuppressive; antiparkinsonian; antimingraine; antimicrobial; anti-HIV; heavy chain; complementarity determining region.
                                                                                                                           New humanized 10D5 antibody, useful for the manufacture of a medicament for treating Down's syndrome, clinical or pre-clinical Alzheimer's disease or cerebral amyloid angiopathy.
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 95; DB 6; Length 16; 100.0%; Pred. No. 5.6e-08; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalian amyloid antibody, heavy chain CDR SEQ ID No:54.
                                                                                                                                                                                                                                                                                                                                   formation or reduce Abeta plaque in the brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADZ08829 standard; peptide; 16 AA
                                                                                                                                                                         Claim 2; Page 29; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-WAR-2003; 2003US-0458469P.
28-WAR-2003; 2003US-0458474P.
8-MAR-2003; 2003US-0458599P.
28-WAR-2003; 2003US-0458510P.
                                 30-APR-2001; 2001US-0287653P.
                                                                                                                                                                                                                                                                                                                                                                                                                               16
         26-APR-2002; 2002WO-US011854
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 HIYWDDDKRYNPSLKS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAR-2004; 2004WO-US009522
                                                                                                                                                                                                                                                                                                                                                                                                                            1 HIYWDDDKRYNPSLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                        (ELIL ) LILLY & CO ELI
                                                                                Hinton PR, Vasquez M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CENZ ) CENTOCOR INC
                                                                                                      WPI; 2003-183836/18.
                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2005028511-A2.
                                                                                                                                                                                                                                                                                                                                                          Sequence 16 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2005.
                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADZ08829;
                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia
                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
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The invention relates to at least one isolated mammalian amyloid antibody one comprising at least one variable region comprising at least one light Chain, of a fully defined sequence of SEO 10 (8):48, 58, 60, 56 70, 79 and 80, respectively. Also described are: (1) at least one isolated mammalian amyloid antibody that binds to the came relation of comprising at least one isolated mammalian amyloid antibody that binds to the batch of the comprising to the came relation of comprising at least one and sequence of SEO 100 (8):48, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134-3, 134
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This invention relates to novel antibodies that bind to the G protein coupled receptor protein identified as GRR64, namely GRR64-1, GRR64-16, GRR64-18, GRR64-18, GRR64-10, and GRR64-18. Specifically, it refers to the use of these anti-GRR64 antibodies as selective cytotoxic agents against GRR64 expressing tumour cells such as those associated with ovarian cancer, uterine cancer and Ewing's sarcoma. The present invention describes epitope mapping of those antibodies that show high affinity binding to GRR64 through competitive binding analyses, such that the antibodies can be assessed for GRR64 dependent cell death in vitro. Accordingly, they can be used to develop cytostatic compositions for gene therapy or immunotherapy that inhibit cellular proliferation of an ovarian cancerous cell and furthermore can diagnose and inhibit growth of tumour cells. This polypeptide is encoded by a heavy chain variable region DNA sequence of a murine anti-human GRR64 antibody of the invention.
                                                                                                                                                                                           New antibody that inhibits binding of a GPR64 polypeptide to an antibody comprising GPR64-18, GPR64-81, GPR64-93 or GPR64-101, useful in preparing a composition for diagnosing or treating ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Light chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin E-mediated allergic reaction; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy; IS NEW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 95; DB 8; Length 120; 100.0%; Pred. No. 5e-07; ive 0; Mismatches 0; Indels
                                                                                         Bhaskar V;
                                                                                                                                                                                                                                                                                Example 2; SEQ ID NO 15; 75pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heavy chain variable region of 1g NEW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY23780 standard; protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.08; Fr.
                                            (PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SMIK ) SMITHKLINE BEBCHAM CORP. (SMIK ) SMITHKLINE BEBCHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93US-00136783.
94WO-US010308.
    20-DEC-2002; 2002US-0435618P.
                                                                                         Dubridge R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-00483632.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIYWDDDKRYNPSLKS
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nes 16; Conservative
                                                                                                                                 WPI; 2004-525780/50.
                                                                                                                                                     N-PSDB; ADQ09619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 120 AA;
                                                                                         Wang Q,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-SEP-1993;
14-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JUL-1999
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                                                                                         Law D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes the variable heavy and light chain regions (I) of murine monoclonal antibody (mAB) 1F7. AAY91014 to AAY91016 represent specifically claimed amino acid sequences of the variable light chain, and AAY91017 to AAY91019 represent specifically claimed amino acid sequence of the variable heavy chain. The antibodies are used for treatment of HIV (human immunodeficiency virus) infection and AIDS (acquired immunodeficiency syndrome). They are also used for detecting HIV in serum and for stimulating HIV antigen related and committed B cells to produce broadly reactive and neutralising antibodies by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Variable heavy and light chain regions of murine monoclonal antibody 1F7, useful for treating HIV infection and AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Variable heavy chain protein of murine anti-human GPR64-16 antibody ID15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        murine; mouse; antibody; GPR64; cytotoxic; ovarian cancer;
uterine cancer; Ewing's sarcoma; cell death; cytostatic; gene therapy;
immunotherapy; cellular proliferation.
                                                                                  1F7 antibody; murine; monoclonal antibody; diagnosis; HIV; infection; AIDS; anti-HIV; human immunodeficiency virus; detection; acquired immunodeficiency syndrome.
                                        1F7 antibody variable heavy chain H2 amino acid sequence SEQ ID NO:9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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(first entry)
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nes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      (IMMP-) IMMPHERON INC
                                                                                                                                                                                                                                                                                                                                                                                                                            Muller S, Kohler H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-338622/29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 41 AA;
                                                                                                                                                                                                                                                                                                                                              30-NOV-1994;
                                                                                                                                                                                                                                                                                                  03-DEC-1997;
  05-SEP-2000
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                                                                                                                                                                                                               US6057421-A.
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Best Loca Matches

ADQ09629 RESULT

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Gaps

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This sequence represents the heavy chain of the humanised 3B9 antibody of the invention. The antibody is a chimeric or humanised interleukin-4 (IL4) monoclonal antibody for the treatment of immunoglobulin B (IgE) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhimitis, conjunctivitis, atopic demarkitis, atopic asthma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft versus host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotide encoding a complementarity- or framework-determining region of an anti-idiotypic antibody that binds to human or primate antihuman immunodeficiency virus (HIV) antibodies, for use in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to coding sequences of the murine 1F7 anti-
idiotypic antibody complementarity-determining region (CDR) or framework-
determining region (FR). The antibody binds to human or primate anti-
human immunodeficiency virus (HIV) antibodies and can be used in the
treatment of HIV infection. The present sequence is the 1F7 heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR; complementarity determining region; framework-determining region; FR; heavy chain; light chain; HIV infection.
                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                      100.0%; Score 95; DB 2; Length 121; 100.0%; Pred. No. 5e-07; tive 0; Mismatches 0; Indel8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Page 18-19; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAO18528 standard; protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JAN-2002; 2002WO-US000927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JAN-2001; 2001US-00759112.
                                                                                                                                                                                                                                                                                                                         1 HIYWDDDKRYNPSLKS 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine Mab 1F7 heavy chain.
                                                                                                                                                                                                                                                                                                                                                 HIYWDDDKRYNPSLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 HIYWDDDKRYNPSLKS
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nes 16; Conservative
                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMMP-) IMMPHERON INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muller S, Kohler H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-590668/63.
                                                                                                                                                                                                                                                         Local Similarity
nes 16; Conserv
                                                                                                                                                                                              Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAL48652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200255668-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    against HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-0CT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA018528;
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                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                             antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin armaceutical compositions e.g. allergic rhinitis, conjunctivitis, atopic asthma, anaphylactic shock, rheumacoid arthritis, host-versus-graft disease and renal disease. They are also asthmitis, host-versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans. The present sequence represents the heavy chain variable region of Ig NEW, and is used in the course of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                         molecules encoding recombinant antibodies useful for treating IL4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allargic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant IL4 antibodies useful for tratment of allergic rhinitis, atopic ashthma and anaphylactic shock.
                                                                                                                                                                                                                specification describes chimeric and humanised IL-4 monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 95; DB 2; Length 121; 100.0%; Pred. No. 5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heavy chain sequence for humanised 389 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                        Disclosure; Col 65-66; 50pp; English.
    Gross MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gross MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Col 65-66; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY18122 standard; protein; 121 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95US-00483636.
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94WO-US010308.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 HIYWDDDKRYNPSLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 HIYWDDDKRYNPSLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
    Holmes SD, Sylvester DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-370482/31.
N-PSDB; AAX79527.
                                                                                                                               -mediated conditions
                                           WPI; 1999-429500/36.
N-PSDB; AAX85929.
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Les 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 121 AA;
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07-SEP-1994;
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                                                                                                           New DNA
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This invention relates to novel antibodies that bind to the G protein coupled receptor protein identified as GPR64, namely GPR64-1, GPR64-16, GPR64-18, GPR64-19, GPR64-10, GPR6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antibody that inhibits binding of a GPR64 polypeptide to an antibody comprising GPR64-18, GPR64-81, GPR64-93 or GPR64-101, useful in preparing a composition for diagnosing or treating ovarian cancer.
                                                                                                                  Variable heavy chain protein of murine anti-human GPR64-18 antibody ID17.
                                                                                                                                                                       murine; mouse; antibody; GPR64; cytotoxic; ovarian cancer;
uterine cancer; Ewing's sarcoma; cell death; cytostatic; gene therapy;
immunotherapy; cellular proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Law D, Wang Q, Dubridge R, Bhaskar V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; SEQ. ID NO 17; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PROT-) PROTEIN DESIGN LABS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-DEC-2002; 2002US-0435618P.
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                                                          (first entry)
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31-MAR-2003 (first en
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                                                                                                                                                                                                                                                                                                                                                       WO2004058171-A2
                                                          07-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-2004.
   ADQ09631;
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                                                                                                                                                                                                                                                                                               Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes an isolated antibody that binds specifically to a stalk of CD30 of a cell, or to an epitope destroyed upon cleavage of soluble CD30 (sCD30) from intact CD30. Also described:

(1) a composition comprising the antibody conjugated or fused to a therapeutic part; (2) a nucleic acid encoding an antibody that binds specifically to a stalk of CD30 of a cell, or to an epitope destroyed upon cleavage of sCD30 from intact CD30; (3) an expression vector comprising the nucleic acid operably linked to a promoter; (4) inhibiting growth of a CD30+ cancer cell; (5) detecting the presence of a CD30+ cell or a biological sample; (6) a host cell expressing the isolated nucleic acid encoding the antibody having variable heavy and variable light chains; and (7) a kit for detecting the presence of a CD30+ cancer cell a biological sample comprising a container and an anti-CD30 antibody has cytostatic activity, and can be used in gene therapy. The anti-CD30 antibody that binds specifically to a stalk of therapy. The anti-CD30 antibody that binds specifically to a stalk of intact CD30 is useful for the manufacture of a medicament for inhibiting the growth of a CD30+ cancer cell. The present sequence is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antibody that binds specifically to a stalk of CD30 of a cell, or to an epitope destroyed upon cleavage of soluble CD30 (sCD30) from intact CD30, useful for inhibiting the growth of a CD30+ cancer cell.
                                                                                                                                                                                                                                                                                                                                        antibody; CD30; anti-CD30 antibody; cytostatic; gene therapy; cancer.
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                                                                                                                                                                                                                                                                                      Anti-CD30 monoclonal antibody VH variable region T105 SEQ ID NO:14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Numata Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                            ADG25814 standard; protein; 121 AA.
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16-SEP-2002; 2002US-0411032P
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Sinha A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                       ADG25814;
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                                                         Gaps
                                                      ö
100.0%; Score 95; DB 8; Length 122; 100.0%; Pred. No. 5e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Humanised 10D5 antibody heavy chain variable region.
                                                                                                                                                                                                                                                                                                ABP58285 standard; protein; 123 AA.
                                                                                                        1 HIYWDDDKRYNPSLKS 16
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                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                         HIYWDDDKRYNPSLKS
                                                      16; Conservative
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ADQ09631 standard; protein; 122 AA.

RESULT 13 ADQ09631 ID ADQ

Matches

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Spleen cells from mice immunized with human IL-4 were used to prepare hybridomas, which were screened for anti-IL-4 MAD secretion. Only clone 189 was positive. cDNA clones of the 189 light and heavy chains were cloned into pGEM7f+ and transformed into E. coli DH5-alpha. The clones were sequenced (AAQ89490-91), and used for antibody engineering. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heavy chain variable region; interleukin-4; IL-4; antibody 389; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin E-mediated allergic reaction; allergic rhinitis; conjunctivitis; atopic dermattis; atopic asthma; anaphylactic shock; rhenmatoid arthritis; host-versus-graft disease; renal disease; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated and IgE-mediated allergic conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 95; DB 2; Length 140; 100.0%; Pred. No. 5.8e-07; Live 0; Mismatches 0; Indels
                                                                                                                                                            /label= CDR
/note= "complementarity determining region"
                                                                                                                                                                                                                                               region"
                                                                                                                                                                                                                                                                                                        /note= "complementarity determining region"
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nonoclonal antibody; MAb; interleukin-4; IL-4; allergy.
                                                                                                                                                                                                                                               /note= "complementarity determining
                                                                                                       . .19
|abel= Sig_peptide
                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sylvester DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
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93US-00136783.
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                                                                                                                                                                                                                       /label= CDR
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                                                                                                                                                                                                                                                                .129
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                      .86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Holmes S, Gross MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-123387/16.
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14-OCT-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of a particularly preferred heavy chain variable region of a humanised antibody of the present invention. In this sequence, the complementarity determining regions originate from murine monoclonal antibody 10D5 and the framework regions originates from human germaline VH segment DP-28 and J segment JH4. Novel humanised antibodies of the invention have CDRs from 10D5 and human framework sequences. These humanised antibodies from 10D5 and human framework sequences. These humanised antibodies have binding affinities (affinity and epitope location) approximately the same as those of the mouse 10D5 antibody. The invention includes antibodies, single chain antibodies, and their fragments, as well as nucleotide sequences, vectors, transformed host cells, and methods of using the humanised antibody to treat, prevent, alleviate, reverse or otherwise ameliorate symptoms and/or pathology associated with Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral amyloid anglopathy, and to inhibit formation or reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New humanized 10D5 antibody, useful for the manufacture of a medicament for treating Down's syndrome, clinical or pre-clinical Alzheimer's disease or cerebral amyloid angiopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 95; DB 6; Length 123; 100.0%; Pred. No. 5.1e-07; ive 0; Mismatches 0; Indels
                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR70190 standard; protein; 140 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 9; 52pp; English.
                                                                                                              .35
.a= "CDR1"
                                                                                                                                                            52. .67
/note= "CDR2"
100. .112
/note= "CDR3"
                                                                                                                                                                                                                                                                                                                                                26-APR-2002; 2002WO-US011854.
                                                                                                                                                                                                                                                                                                                                                                                        30-APR-2001; 2001US-0287653P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 HIYWDDDKRYNPSLKS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse MAb 3B9 heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIYWDDDKRYNPSLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Conservative
                                                                                                                                           'note=
                                                                                                                                                                                                                                                                                                                                                                                                                              (ELIL ) LILLY & CO ELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hinton PR, Vasquez M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-183836/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 123 AA;
                                                                                                                                                                                                                                                                  WO200288307-A2
                   Mus sp.
Homo sapiens.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
20-SEP-1995
                                                                                                                                                                                                                                                                                                        07-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                      Region
                                                                                                                                                              Region
                                                                                                                                                                                                    Region
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Gaps

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**%%%%%%%%%** 

8

Mus sp.

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This sequence represents the heavy chain of the murine 3B9 antibody of the invention. The antibody is a chimeric or humanised interleukin-4 (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic asthma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft versus host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                          Recombinant IL4 antibodies useful for tratment of allergic rhinitis, atopic ashthma and anaphylactic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanized antibody; antibody engineering; monoclonal antibody; MAb;
interleukin-4; IL-4; allergy.
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/label= CDR
/note= "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /100. 130
/label= CDR
/note= "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 95; DB 2; Length 140; 100.0%; Pred. No. 5.8e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "complementarity determining region"
                                                                                                       Gross MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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/label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR70192 standard; protein; 141 AA.
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                                                 (SMIK ) SMITHKLINE BEECHAM PLC. (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                Claim 24; Fig 2; 50pp; English.
93US-00136783.
              94WO-US010308
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93US-00136783.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 HIYWDDDKRYNPSLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 HIYWDDDKRYNPSLKS
                                                                                                     Sylvester DR, Holmes SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
                                                                                                                                      WPI; 1999-370482/31.
                                                                                                                                                           N-PSDB; AAX79520
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 140 AA;
14-OCT-1993;
              07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
20-SEP-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9507301-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents the heavy chain variable region of murine interleukin-4 (IL-4) antibody 189: The sequences are used in the production chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis, atopic athma, anaphylactic shock, rheumatoid archritis, host dermatitis, atopic archma, anaphylactic shock, rheumatoid archritis, host diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans
                                                                                                                                                                                                                                                                                                                                                                      DNA molecules encoding recombinant antibodies useful for treating IL4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody, interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 95; DB 2; I 100.0%; Pred. No. 5.8e-07; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heavy chain sequence for murine 3B9 antibody.
                                                                                                                                                                                                                                                                                 Gross MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY18121 standard; protein; 140 AA.
                                                                                                                                                                                                                         (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Fig 2; 50pp; English.
                                                                                                                                                   93US-00117366.
93US-00136783.
94WO-US010308.
                                                                                                                    95US-00483632
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                                                                                                                                                                                                                                                                                 Holmes SD, Sylvester DR,
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        -mediated conditions.
                                                                                                                                                                                                                                                                                                              WPI; 1999-429500/36.
N-PSDB; AAX85885.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 140 AA;
                                                                                                                                                   07-SEP-1993;
14-OCT-1993;
                                                                                                                    07-JUN-1995;
                                                                                                                                                                                        07-SEP-1994;
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                                              US5928904-A
                                                                                 27-JUL-1999
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AAY18121;

RESULT 17 AAY1812:

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Mus sp.

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(SMIK ) SMITHKLINE BEECHAM PLC.
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14-OCT-1993;
07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                          Holmes
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                                                                                                                                                                                                                                                                                                               A humanized antibody heavy chain variable region and signal sequence is given in AAR70192. The signal sequence is also provided in AAR70193. The Schwances of the construct are identical to the native CDRs of mouse anti-human IL-4 MAb 1B9 (AAR70198-200). (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                        Chimeric and humanised IL-4 monoclonal antibodies (mabs), derived from high affinity mabs - useful in treatment of IL-4-mediated and \lg E-mediated allergic conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric antibody; antibody engineering; monoclonal antibody; MAb; interleukin-4; IL-4; allergy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 95; DB 2; Length 141; 100.0%; Pred. No. 5.9e-07; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "complementarity determining region"
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/label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cocation/Qualifiers
                                                                                   Gross MS, Sylvester DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR70191 standard; protein; 141 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric antibody 3B9 heavy chain
                                                                                                                                                                                                                                                                                Disclosure; Fig 4; 97pp; English,
                 (SMIK ) SMITHKLINE BEECHAM CORP.
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93US-00136783.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIYWDDDKRYNPSLKS 87
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/label= CDR
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/label= CDR
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/label= CDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16; Conservative
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                                                                                                                             WPI; 1995-123387/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                  N-PSDB; AAQ83493
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 141 AA;
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                                                                                   Holmes S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR70191;
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AAR70191
XX
AC AAR705
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AC AAR705
DT 25-MAJ
DT 26-MAJ
EPT Region
FPT REGION
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                                                                                                                                                                               A human/mouse chimeric antibody heavy chain variable region was constructed (given in AAR70191) that contained the mouse anti-human IL-4 MAD 389 variable region including 3 CDRs (AAR70198-200) and a human antibody signal peptide (AAR70193). The construct was used for humanized antibody production. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heavy chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin E-mediated allergic reaction; allergic rintintis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.
                                                                                Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated and IgE-mediated allergic conditions.
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heavy chain variable region of humanised murine IL-4 antibody 3B9.
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                                                                                                                                                                                                                                                                                                                                      Length 141;
                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                      100.0%; Score 95; DB 2; 1
100.0%; Pred. No. 5.9e-07;
                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY23770 standard; protein; 141 AA.
                                                                                                                                                 Disclosure; Fig 3; 97pp; English.
 Sylvester
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93US-00136783.
94WO-US010308.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        HIYWDDDKRYNPSLKS
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 16; Conservative
Gross MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-429500/36.
                               WPI; 1995-123387/16
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Gaps

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This sequence represents the light chain of the chimeric 3B9 antibody of the invention. The antibody is a chimeric or humanised interleukin-4 (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE) mediated diseases. The antibodies are useful for the treatment of albergic disorders such as allergic rhinitis, conjunctivitis, atopic asthma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft versus host disease
             atopic dermatitis, atopic asthms, anaphylactic shock, rheumatoid arthritis, host-versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans. (Updated on 17-OCT-2003 to standardise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease.
   B-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant IL4 antibodies useful for tratment of allergic rhinitis,
                                                                                                                                                                   100.0%; Score 95; DB 2; Length 141; 100.0%; Pred. No. 5.9e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 95; DB 2; Length 141; 100.0%; Pred. No. 5.9e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric 3B9 monoclonal antibody heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atopic ashthma and anaphylactic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gross MS;
                                                                                                                                                                                                                                                                                                                                                     AAY18125 standard; protein; 141 AA.
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                                                                                                                                                                                                                                                         72 HIYWDDDKRYNPSLKS
                                                                                                                                                                                                                                                                                                                                                                                                                         11-AUG-1999 (first entry)
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                                                                                                                                                                                                     16; Conservative
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Best Local Similarity
                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                   Sequence 141 AA;
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                                                                                                  os field)
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             The present sequence represents the heavy chain variable region of a humanised murine interleukin-4 (IL-4) antibody 389. The specification describes chimmeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic asthma, anaphylactic shock, rheumarcid arthritis, versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents the heavy chain variable region of murine/human interleukin-4 (IL-4) chimeric antibody 3B9. The specification describes chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA molecules encoding recombinant antibodies useful for treating IL4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heavy chain variable region; interleukin-4; IL-4; antibody 389; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin E-mediated allergic reaction; allergic rhinitis; conjunctivitis; atopic dermetitis; atopic dermetitis; atopic dermetitis; atopic atopic asthma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.
                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                      Length 141;
                                                                                                                                                                                                                                                                                   0; Indels
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Pred. No. 5.9e-07;
                                                                                                                                                                                                                                                                                   Mismatches
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(SMIK ) SMITHKLINE BEECHAM PLC.
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93US-00136783.
94WO-US010308.
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                                                                                                                                                                                                                                                                                                                                         72 HIYWDDDKRYNPSLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                     Sequence 141 AA;
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14-OCT-1993;
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The present invention relates to new humanized immunoglobulin (Ig) light chain (LC) or heavy chain (HC) comprising variable region complementarity determining regions from 3D6/10D5 Ig LC or HC variable region sequence, and variable framework region from human acceptor Ig LC or HC sequence. The invention is useful for preventing or treating an amyloidogenic disease or Alzheimer's disease in a patient. The invention is also useful for in vivo imaging amyloid deposits in a patient. The present amino acid sequence represents a mouse 3D6/10D5 variable light (VL) chain or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3D6; heavy chain variable region; immunoglobulin; complementarity determining region; CDR; 10D5; variable framework region; neuroprotective; nootropic; gene therapy; amyloidogenic disease;
                                                Mouse, humanized, immunoglobulin; Ig; light chain; LC; heavy chain; HC; variable region complementarity determining region; 3D6; 10D5; variable framework region; amyloidogenic disease; Alzheimer's disease; amyloid deposit; variable light chain; VL; variable heavy chain; VH; nootropic; neuroprotective; inhibitor of beta amyloid accumulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel light/heavy chain of humanized immunoglobulin for treating amyloidogenic disease, has 3D6/10D5 variable region complementarity determining regions and variable framework region from human acceptor immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine 10D5 immunoglobulin heavy chain variable region SEQ ID NO:16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 142; Fig 10; 171pp; English.
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                                                                                                                                                                                                                                                                                                  06-DEC-2001; 2001WO-US046587.
                                                                                                                                                                                                                                                                                                                                       06-DEC-2000; 2000US-0251892P.
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               Mouse 10D5 VH protein.
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                                                                                                                                                                                                                                                                                                                                                                        (NEUR-) NEURALAB LTD (AMHP ) WYETH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-519658/55.
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                                                                                                                                                                                                                        WO200246237-A2.
                                                                                                                                                                                     Mus musculus.
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Best Local Simi
Matches 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents the heavy chain of the humanised 389 antibody of the invention. The antibody is a chimeric or humanised interleukin-4 (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic dermartisis, atopic asthma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft versus host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                              Antibody, interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allargic disorder, allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tratment of allergic rhinitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Mismatches 0;
                                                                                                                                                                                                                                                           Heavy chain sequence for humanised 3B9 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 95; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant IL4 antibodies useful for
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                                                                                                                                              AAY18117 standard; protein; 141 AA
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93US-00136783.
94WO-US010308.
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                                   Sylvester DR, Holmes SD,
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Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 141 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-SEP-1993;
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07-SEP-1994;
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RESULT 24 ABG76934

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Length 142; 0; Indels

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The invention relates to a novel humanised immunoglobulin light or heavy chain. The humanised immunoglobulin light or heavy chain comprises:

variable region complementarity determining regions (CDR's) from the 3D6 immunoglobulin light chain variable region sequence of 132 amino acids fully defined in the specification (ADR88406), or heavy chain variable region sequence of 131 amino acids fully defined in the specification (ADR88408); or from the 10D5 immunoglobulin light chain variable region sequence of 131 amino acids given in the specification (ADR88418) or conservation (ADR88408); or from the 10D5 immunoglobulin light chain variable region sequence of 142 amino acids fully defined in the specification (ADR88420); and a variable framework region from a chuman acceptor immunoglobulin light or heavy chain sequence, provided that at least one framework residue is substituted with the corresponding amino acid residue from the mouse 306 or 10D5 light or heavy chain variable region sequence, where the framework residue that non-covalently binds antigen directly, a residue adjacent to a CDR, a CDR on-covalently binds antigen directly, a residue adjacent to a CDR, and may have a use in gene therapy. The composition and methods are constituted and may have a use in gene therapy. The composition and methods are constituted and moctropic activity, and may have a use in gene therapy. The composition and methods are constituted and moctropic activity, and may have a use in gene therapy of manunoglobulin, immunoglobulin, immunoglobuli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New humanized antibodies that recognize beta amyloid peptides, useful for preventing or treating amyloidogenic diseases, such as Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chain, or its domain. The present sequence immunoglobulin heavy chain variable region.
                           1. .19
/label= signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 85; SEQ ID NO 16; 176pp; English
                                                                                                     /label= mature protein
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                               12-MAR-2003; 2003US-00388389
                                                                                                                                                                                                                                                              12-MAR-2004; 2004WO-US007503
                                                                            .142
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                                                                                                                                                                                                                                                                                                                                                                (NEUR-) NEURALAB LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-668880/65.
N-PSDB; ADR88419.
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                                                                                                                                                                                                          23-SEP-2004
  Key
Peptide
                                                                            Protein
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Query Match
100.0%; Score 95; DB 8; Length 142;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 1 HIYWDDDKRYNPSLKS 16 ò

Gaps

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71 HIYWDDDKRYNPSLKS

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RESULT 26

Mammalian amyloid antibody, heavy chain variable region SEQ ID No:59. ADZ08834 standard; peptide; 142 AA. 16-JUN-2005 (first entry) ADZ08834; ADZ0883 SEX B X B X B X

New isolated mammalian anti-amyloid antibodies useful for treating amyloid-associated disorders, such as Alzheimer's disease, cancer, allergies, autoimmune disease, Parkinson's disease, multiple sclerosis, amyloid-associated disorder; Alzheimers disease, cancer; allergy; autoimmune disease; Parkinsons disease; autoimmune disease; Parkinsons disease; acquired immune deficiency syndrome; multiple sclerosis; migraine; dementia; infection; nootropic; neuroprotective; cytostatic; antiallergic; Immunosuppressive; antiparkinsonian; antimigraine; antimicrobial; anti-HIV; heavy chain variable region. 28-MAR-2003; 2003US-0458469P. 28-MAR-2003; 2003US-0458474P. 28-MAR-2003; 2003US-0458509P. 26-MAR-2004; 2004WO-US009522 28-MAR-2003; 2003US-0458510P Mercken M, Benson JM; migraine and dementia. (CENZ ) CENTOCOR INC. (MERC/) MERCKEN M. (BENS/) BENSON J M. WPI; 2005-242565/25. WO2005028511-A2. N-PSDB; ADZ08836 31-MAR-2005. Mammalia.

Claim 5; SEQ ID NO 59; 306pp; English.

The invention relates to at least one isolated mammalian amyloid antibody comprising at least one variable region comprising at least one heavy chain and at least one light chain, of a fully defined sequence of SEQ ID NOS: 48, 49, 59, 60, 69, 70, 79 and 80, respectively. Also described are: (i) at least one isolated mammalian amyloid antibody that binds to the same region of an amyloid polypeptide as an antibody comprising at least one heavy chain or light chain complementarity determining region (CDR) that least one isolated mammalian amyloid antibody, comprising at least one isolated mammalian amyloid antibody, comprising at least one isolated mammalian amyloid antibody, comprising at least one solated mammalian amyloid antibody comprising at least one solated mammalian amyloid antibody comprising at least one isolated mammalian amyloid antibody comprising at least one of any of the isolated mammalian amyloid antibodic acid encoding at least one of any of the isolated mucleic acid encoding an amyloid antibody, (vi) a method of sequence of SEQ ID NO: 52, 61, 62, 71, 72, 81 and 82, (iv) an isolated mucleic acid encoding an amyloid antibody, (vi) a method of an amyloid antibody, (vi) a method of an isolated mucleic acid encoding an amyloid antibody, (vi) a method of the isolated mammalian amyloid antibodies of an isolated mucleic acid encoding an amyloid antibodies mentioned, and at least one pharmaceutical carrier or diluent, (vii) an anti-idiotype antibodies mentioned, (ix) a method of diagnosing or treadment that specifically binds at least one amyloid antibody or fragment that specifically binds at least one of the antibodies mentioned, where the device comprising at least one amyloid antibody, (vi) an article of maning and encoded and antibody or the confirming at least one amyloid antibody, (vi) an article of maning or and antibody or incomprising at least one amyloid antibody, (vi) an article of maning or and a pharmaceutical or diagnostic use, comprising packaging material and a container comprising a solution or a lyophilized form of at least one of the amyloid antibodies mentioned; and (xii) a method of producing at least one of the isolated mammalian amyloid antibodies, comprising providing a host cell or transgenic animal or transgenic plant or plant cell capable of expressing the antibody in recoverable amounts. The methods and compositions of the present invention are useful for 

Gaps

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Monoclonal antibody; 10D5; complementarity determining region; CDR; mouse; human; humanised antibody; antibody; Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
location) approximately the same as those of the mouse 10D5 antibody. The invention includes antibodies, single chain antibodies, and their fragments, as well as nucleotide sequences, vectors, transformed host cells, and methods of using the humanised antibody to treat, prevent, alleviate, reverse or otherwise amellorate symptoms and/or pathology associated with Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "light chain variable region, claimed in Claim 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New humanized 10D5 antibody, useful for the manufacture of a medicament for treating Down's syndrome, clinical or pre-clinical Alzheimer's disease or cerebral amyloid anglopathy.
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/note= "the mature light chain is claimed in Claim 5"
                                                                                                                                                                     Length 453;
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                                                                                                                                                                 100.0%; Score 95; DB 6; I
100.0%; Pred. No. 2.1e-06;
tive 0; Mismatches 0;
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/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                     ABP58289 standard; protein; 472 AA
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. "CDR1"
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/note= "CDR2"
119. .131
/note= "CDR3"
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(first entry)
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                                                                                                                                                                               Local Similarity
les 16; Conserv
                                                                                                                                         Sequence 453 AA;
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Chimeric.
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31-MAR-2003
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              associated disorders, such as Alzheimer's disease, cancer, allergies, autoimmune disease, Parkinson's disease, AIDS, multiple sclerosis, migraine, dementia and infections. This sequence represents a heavy chain variable region useful in the antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is the protein sequence of the heavy chain of a humanised antibody of the present invention. In the variable portion, the complementarity determining regions (CDRs) originate from murine monoclonal antibody 1005 and the framework region originates from human germline VH segment DP-28 and 3 segment JH4. Novel humanised antibodies of the invention have CDRs from 1005 and human framework sequences. These humanised antibodies have binding affinities (affinity and epitope
                                                                                                                                                                                                                                                                                                                                                                                      Monoclonal antibody; 10D5; complementarity determining region; CDR; mouse; human; humanised antibody; antibody; Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New humanized 10D5 antibody, useful for the manufacture of a medicament for treating Down's syndrome, clinical or pre-clinical Alzheimer's
                                                                                                                                         Gaps
 producing therapeutic compositions and devices for treating amyloid-
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                                                                                                            Length 142;
                                                                                                           Score 95; DB 9; Length 14
Pred. No. 5.9e-07;
Mismatches 0; Indels
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/note= "light chain variable region"
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                                                                                                            100.0%;
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/note= "CDR2"
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/note= "CDR3"
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                                                                                                                                                                                             71 HIYWDDDKRYNPSLKS
                                                                                              Query Match
Best Local Similarity 100...
And 16; Conservative
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                                                                                  Sequence 142 AA;
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Chimeric.
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Chimeric.
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                              The present sequence is the protein sequence of the heavy chain of a humanised antibody of the present invention. In the variable portion, the complementarity determining regions (CDRs) originate from murine monoclonal antibody 10D5 and the framework region originates from human germline VH segment DP-28 and J segment JH4. Novel humanised antibodies of the invention have CDRs from 10D5 and human framework sequences. These humanised antibodies have binding affinities (affinity and epitope location) approximately the same as those of the mouse 10D5 antibody. The invention includes antibodies, single chain antibodies, and their cargments, as well as nucleotide sequences, vectors, transformed host cells, and methods of using the humanised antibody to treat, prevent, alleviate, reverse or otherwise ameliorate symptoms and/or pathology associated with Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical Alzheimer's disease or (pre-)clinical Alzheimer's disease or ceduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the protein sequence for the heavy chain variable region (VH) of M130, a murine monoclonal antibody (MAb) that binds to Staphylococcus aureus but not to Staphylococcus haemolyticus or Staphylococcus epidermidis. M130 is produced by hybridoma 11-232.3 IE9 (ATCC PTA-3659), which was obtained by immunising mice with UV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New medicament comprising at least one MAb that binds to peptidoglycan (PepG) of gram-positive bacteria, useful for treating staphylococcal infections, including nosocomial infections.
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                                                                                                                                                                                                                                                                       100.0%; Score 95; DB 6; Length 472; 100.0%; Pred. No. 2.2e-06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M130; monoclonal antibody; antibody; Staphylococcus aureus; peptidoglycan; infection; antibacterial.
                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monoclonal antibody M130 heavy chain variable region.
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          Disclosure; Page 13-15; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Foster S,
                                                                                                                                                                                                                                                                                                                                                                                                             ABR62961 standard; protein; 119 AA.
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21-DEC-2001; 2001US-034344P.
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                                                                                                                                                                                                                                                                                                                                                  86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                        1 HIYWDDDKRYNPSLKS
                                                                                                                                                                                                                                                                                                                                       71 HIYWDDDKRYNPSLKS
                                                                                                                                                                                                                                                                                  Local Similarity 100.
nes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BIOS-) BIOSYNEXUS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-587257/55.
N-PSDB; ACF79291.
                                                                                                                                                                                                                                                Sequence 472 AA;
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                                                                                                                                                                                                                        field)
                                                                                                                                                                                                                                                                                                                                                                                                                                      ABR62961;
                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
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inactivated whole S. aureus and subcloning by limiting dilution. It is an example of Mabs of the invention that bind to the peptidoglycan of Grampositive bacteria, and which are useful for treating staphylococcus infections. The antibodies also bind to whole bacteria and enhance phagocytosis and killing of the bacteria in vitro and block nasal colonisation by Grampositive bacteria in vitro and block nasal that have been cloned and human/mouse chimeric antibodies were produced that have the MI30 variable regions and human constant regions. These chimeric antibodies, referred to as Al30, retain the ability to bind to S. aureus peptidoglycan, and are expected to have a reduced human antimouse antibody response in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monoclonal antibody; 10D5; complementarity determining region; CDR; mouse; human; humanised antibody; antibody; Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                   Score 91; DB 7; Length 119;
Pred. No. 2.1e-06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humanised 10D5 antibody heavy chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label= Met, Val,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'label= Val, Ala
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note= "CDR3"
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/note= "CDR1"
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/note= "(
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Matches 15; Conserv
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The invention relates to humanized immunoglobulin (Ig) light or heavy chains comprising variable region complementary determining regions (CDRs) from the 1284 Ig variable region sequence and variable framework regions from the light or heavy chain or heavy chain or heavy chain sequence. The humanized Ig light or heavy chain or its nucleic acid molecule is useful for preventing or treating an amyloidogenic disease in humans, associated with amyloid deposits of Abeta in the brain, e.g., Alzheimer's disease, Down's syndrome or mild cognitive impairment, all characterized by cognitive impairment. The variable region sequence is useful in producing a three-dimensional image of a 1284 Ig, 1284 Ig chain or its domain. A humanized antibody is useful for reducing plaque or neuritic burden in a subject. The present sequence represents a mouse 1284 antibody variable heavy chain mature peptide sequence
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                                             comprising variable
ole framework regions,
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amyloidogenic disease; antibody; 12B4v1.
                                        New humanized immunoglobulin light or heavy chains comprisin region complementary determining regions and variable framew useful for preventing or treating e.g., Alzheimer's disease.
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                                                                                                                                 Example 5; Fig 2A-B; 122pp; English
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WPI; 2003-779077/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 123 AA;
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                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of a preferred heavy chain variable region of a humanised antibody of the present invention. In this sequence, the complementarity determining regions (CDRs) originate from murine monoclonal antibody 10D5 and the framework region originates from human germline VH segment DP-28 and J segment JH4. Novel humanised antibodies of the invention have CDRs from 10D5 and human framework sequences. These humanised antibodies have binding affinities (affinity and epitope location) approximately the same as those of the mouse 10D5 antibody. The invention includes antibodies, single chain antibodies, and their fragments, as well as nucleotide sequences, vectors, transformed host cells, and methods of using the humanised antibody to treat, prevent, alleviate, reverse or otherwise ameliorate symptoms and/or pathology cassociated with Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical Alzheimer's disease or (pre-)clinical Alzheimer's disease or category (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral anyloid anglopathy, and to inhibit formation or case and control of the commentation or case and control of the commentation or case and control of the case and case and control of the case and control of the case and case an
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                                                                                                                                                                                                                                       New humanized 10D5 antibody, useful for the manufacture of a medicament for treating Down's syndrome, clinical or pre-clinical Alzheimer's disease or cerebral amyloid angiopathy.
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                                                                                                                                                                                                                                                                                                                                Claim 3; Page 8; 52pp; English
                      26-APR-2002; 2002WO-US011854
                                                               30-APR-2001; 2001US-0287653P
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                                                                                                          (ELIL ) LILLY & CO ELI
                                                                                                                                                     Hinton PR, Vasquez M;
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Best Local S
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The invention relates to humanized immunoglobulin (Ig) light or heavy chains comprising variable region complementary determining regions (CDRS) from the 12B4 Ig variable region sequence and variable framework regions from a human acceptor Ig light chain or neavy chain sequence. The humanized Ig light or heavy chain or its nucleic acid molecule is useful for preventing or treating an amyloidogenic disease in humans, associated with amyloid deposits of Abeta in the brain, e.g., Alzhelmer's disease, bown's syndrome or mild cognitive impairment, all characterized by cognitive impairment. The variable region sequence is useful in producing a three-dimensional image of a 1284 Ig, 12B4 Ig chain or its domain. A humanized antibody is useful for reducing plaque or neuritic burden in a subject. The present sequence represents the humanised 1284WHV1 sequence
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humanized Ig light or heavy chain or its nucleic acid molecule is useful for preventing or treating an amyloidogenic disease in humans, associated with amyloid deposits of Abeta in the brain, e.g., Alzheimer's disease, Down's syndrome or mild cognitive impairment, all characterized by cognitive impairment. The variable region sequence is useful in producing a three-dimensional image of a 12B4 Ig, 12B4 Ig chain or its domain. A humanized antibody is useful for reducing plaque or neuritic burden in a subject. The present sequence represents the humanised 12B4VHV1 mature
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Pred. No. 2.2e-06;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                      HIYWDEDKRYNPSLKS 67
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                                                                                                                                                                                                                      Query Match 95.8
Best Local Similarity 93.8
Matches 15, Conservative
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                                                                                                                                                                                         Sequence 123 AA;
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Sequence 142 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New humanized immunoglobulin light or heavy chains comprising variable region complementary determining regions and variable framework regions, useful for preventing or treating e.g., Alzheimer's disease.
                                                                                                                                                                                                                                           Immunoglobulin; Ig; neuroprotective; nootropic; gene therapy; vaccine; amyloidogenic disease; antibody.
                            Gaps
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 Length 142;
Score 91; DB 7; I
Pred. No. 2.6e-06;
                         1; Mismatches
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                                                                                                                                           AAY42957 standard; protein; 142 AA.
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21. .142
/note= "mature pr
51. .56
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.86 =--
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                                                                                                                                                                                                                      Mouse 12B4 antibody VH region.
 95.8%;
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                          15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NEUR-) NEURALAB LTD.
(AMHP ) WYETH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heavy chain sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-779077/73.
         Best Local Similarity
Matches 15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ACF58516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003077858-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 142 AA;
                                                                                                                                                                                             12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-SEP-2003.
                                                                                                                                                                    AAY42957;
  Query Match
                                                                                                                                                                                                                                                                                                                Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Basi G,
                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                      Mus sp.
                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                       Region
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                                                                                                               RESULT 34
AAY42957
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JP06141885-A
                                                                                                                                                                                                                                           05-NOV-1992;
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                                                                                                                                                                                                                     05-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-AUG-2004
                                                      08-FEB-1995
                                                                                                                                                                                              24-MAY-1994
                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADP71373;
                                AAR54105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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AAR54105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to humanized immunoglobulin (Ig) light or heavy chains comprising variable region complementary determining regions (CDRs) from the 12B4 Ig variable region sequence and variable framework regions from a human acceptor Ig light chain or heavy chain sequence. The humanized Ig light or heavy chain or its nucleic acid molecule is useful for preventing or treating an amyloidogenic disease in humans, associated with amyloid deposits of Abeta in the brain, e.g., Alzheimer's disease, Down's syndrome or mild cognitive impairment, all characterized by a three-dimensional image of a 12B4 Ig, 12B4 Ig chain or its domain. A humanized antibody is useful for reducing plaque or neuritic burden in a subject. The present sequence represents a chimeric 12B4VH region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New humanized immunoglobulin light or heavy chains comprising variable region complementary determining regions and variable framework regions, useful for preventing or treating e.g., Alzheimer's disease.
                                                                                                                                                                                                                              Immunoglobulin, Ig; neuroprotective; nootropic; gene therapy; vaccine; amyloidogenic disease; antibody; 12B4; chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.8%; Score 91; DB 7; Length 142; 93.8%; Pred. No. 2.6e-06; ive 1; Mismatches 0; Indels
         Length 142;
                               0; Indels
       Score 91; DB 7;
Pred. No. 2.6e-06;
1; Mismatches 0
                                                                                                                                   AAY42972 standard; protein; 142 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example, Fig 4A-D; 122pp; English
                                                                                                                                                                                                       Chimeric 12B4VH region sequence.
        95.8%;
                                                                 12-MAR-2003; 2003WO-US007715.
                                                                                                                                                                                                                                                                                                                                                           12-MAR-2002; 2002US-0363751P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 HIYWDDDKRYNPSLKS 16
                                                                                                                                                                                 (first entry)
                                                      1 HIYWDDDKRYNPSLKS
    Query Match
Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 (NEUR-) NEURALAB LTD. (AMHP ) WYETH.
                                                                                                                                                                                                                                                                                                                                                                                                                   Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-779077/73.
                                                                                                                                                                                                                                                               Chimeric - Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ACF58540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 142 AA;
                                                                                                                                                                                                                                                                                        WO2003077858-A2.
                                                                                                                                                                                 12-FEB-2004
                                                                                                                                                                                                                                                                                                               25-SEP-2003
                                                                                                                                                           AAY42972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                    Basi G,
                                                                                                                        AAY42973
ID AA
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RESULT 36

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           naked binding material; short consensus complement receptor; SCR1; SCR2; cancer; Cytostatic; CD55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant anti-HIV monoclonal antibody - capable of neutralising strains which can not be neutralised by anti-IIIB and IIIMN antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDR sequence 2 for the heavy chain of 105AD7 anti-idiotypic antibody.
                                                                                                                                                                        Human; mouse; murine; heavy; light; chain; monoclonal; antibody;
complementarity determining region; CDR; IgG; kappa; IIIB; IIIMN;
polymerase chain reaction; primer; amplify; PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.7%; Score 90; DB 2; I
93.8%; Pred. No. 3.5e-07;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 14; 23pp; Japanese.
                                                                                                                                    Humanised anti-HIV MAb fragment #3
AARS4105 standard; protein; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADP71373 standard; peptide; 22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                92JP-00322476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          92JP-00322476.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 HIYWDDDKRYNPSLKS 16
                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 HIYWDDDXHYNPSLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 93.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1994-205040/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2004048413-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-JUN-2004
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The sequences given in AAR54101-02 represent the heavy and light chains respectively of the humanised monoclonal antibody (WAb) of the invention. The antibody has the ability to neutralise human immunodeficiency virus. The antibody is classified as IgG kappa and has the sequence RIGPGR or RVGPGR in the principal neutralising domain. The antibody may be used to the neutralise the clinically separate strains which cannot be neitralised by the neutralising antibodies against IIIB and IIIMN strains. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequences given in AAR54103-11 are fragments of the heavy and light chains of the humanised monoclonal antibody (MAb) of the invention. The
                                                                                                                                                                                                                                                                                                Recombinant anti-HIV monoclonal antibody - capable of neutralising strains which can not be neutralised by anti-IIIB and IIIMN antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant anti-HIV monoclonal antibody - capable of neutralising strains which can not be neutralised by anti-IIIB and IIIMN antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; mouse; murine; heavy; light; chain; monoclonal; antibody;
complementarity determining region; CDR; IgG; kappa; IIIB; IIIMN;
polymerase chain reaction; primer; amplify; PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.7%; Score 90; DB 2; Length 122; 93.8%; Pred. No. 3.1e-06; ive 0; Mismatches 1; Indels
                                                                                                                                                                             (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Page 13; 23pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 14; 23pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR54110 standard; protein; 122 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Humanised anti-HIV MAb fragment #8.
                                                                                        92JP-00322476.
                                                                                                                                     92JP-00322476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92JP-00322476.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1994-205040/25.
                                                                                                                                                                                                                           WPI; 1994-205040/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                     N-PSDB; AAQ68709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 122 AA;
JP06141885-A.
                                                                                                                                     05-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JP06141885-A.
                                                                                        05-NOV-1992;
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                                             24-MAY-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-MAY-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR54110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR54110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a naked binding material which binds to both short consensus complement receptor (SCR1) and SCR2 and/or an active both short consensus complement receptor (SCR1) and SCR2 and/or an active agent as a combined preparation for simultaneous, separate or sequential use in the treatment of cancer. The material and the nucleic acid encoding the material are useful in the preparation of a medicament for the neutralization of CDS5, for the enhancement of complement deposition on a tissue, and for treating cancer, which involve administering the material to the subject, which is ammal. The cancer is one or more of colorectal, breast, ovarian, cervical, gastric, lung, liver, skin and material to the presence of inhe material is useful for identifying an agent capable of inhibiting CDS5, which involve bringing into contact a candidate agent with at least a portion of SCR1 and SCR2 of CDS5, and determining the extent to which the candidate agent in the absence of the material bods of the deposition on a cell sample to the material to SCR1 and SCR2 of CDS5, and determining the amount of complement deposition on a cell sample of in the presence and absence of the candidate agent. Which bind both SCR1 and SCR2 of CDS5, and/or determining the amount of complement deposition on a cell sample of the assay method is useful in the manufacture of a medicament for the treatment of cancer. The presence expresents a CDR sequence for the heavy chain of 105AD7 anti-idiotypic antibody.
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                                                                                                                                                 Naked binding material useful for treating cancer, and for neutralizing CD55 binds to both short consensus complement receptor SCR1 and SCR2 and/or active agent as combined preparation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, mouse, murine; heavy, light, chain, monoclonal, antibody,
complementarity determining region, CDR; IgG; kappa, IIIB, IIIMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.7%; Score 90; DB 8; Length 22; 93.8%; Pred. No. 4.9e-07; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 5; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR54101 standard; protein; 122 AA.
                   (CANC-) CANCER RES TECHNOLOGY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52. .67
/label= CDR2
100. .111
/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 HIYWDDDKRYNPSLKS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 HIYWDDDKRYSPSLKS 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31. .37
/label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Humanised MAb H-chain.
                                                                                                        WPI; 2004-441153/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2003
08-PEB-1995
                                                                Durrant GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR54101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
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 antibody has the ability to neutralise human immunodeficiency virus. The antibody is classified as IgG kappa and has the sequence RIGPGR or RVGPGR in the principal neutralising domain. The antibody may be used to neutralise the clinically separate strains which cannot be neitralised by the neutralising antibodies against IIIB and IIIMN strains
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid encoding peptide derived from antibody 105AD7 - used to induce an immune response for treatment and prevention of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                      Monoclonal antibody 105AD7; complementarity determining region; CDR; human; immune response; treatment; cancer.
                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117. .132
/note= "complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "complementarity determining region 2"
                                                                                                                    Length 122
                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                         Monoclonal antibody 105AD7 heavy chain variable region.
                                                                                                                    Score 90; DB 2; 1
Pred. No. 3.1e-06;
                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8. .54
note= "complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "encoded by GTG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "encoded by GGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CANC-) CANCER RES CAMPAIGN TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                  AAW26239 standard; protein; 148 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 1A; 32pp; English.
                                                                                                                    94.7%;
                                                                                                                                                                                16
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96GB-00004321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97WO-GB000591
                                                                                                   Query Match
Best Local Similarity 93.8%,
Best Local Similarity 93.8%,
                                                                                                                                                                                                          52 HIYWDDDKHYNPSLKS
                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                               HIYWDDDKRYNPSLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .132
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                                                                                         Sequence 122 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spendlove I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                             02-APR-1998
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29-FEB-1996;
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                                                                                                                                                                                                                                                                                                                AAW26239;
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the fragments, equivalents and mimetics are used to stimulate an immune response to a tumour antigen, for the treatment or prevention of tumours. Transfected host cells are used to produce this peptide and the vectors can be used to generate the peptide in vivo for stimulation of an immune response. The peptide contains promiscuous helper epitopse which stimulate a response against tumour antigens other than gp72. These epitopes may help a cytotoxic T lymphocyte response to any co-injected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptide inhibiting binding of human interleukin-6 (IL-6) to its receptor - useful for treating auto:immune disease induced or aggravated
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human interleukin-6 binding inhibitor; IL-6; rheumatoid arthritis;
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                                                                                                                                                                     Length 148;
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93.8%; Pred. No. 6.6e-06;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                Indels
                                                                                                                                                                  94.7%; Score 90; DB 2; Le llarity 93.8%; Pred. No. 3.8e-06; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hamuro J;
                                                                                                                                                                                                                                                                                                                                       Ŕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          septic shock; multiple myeloma; ss.
                                                                                                                                                                                                                                                                                                                                      AAR58612 standard; protein; 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 18; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 HIYWDDDKHYNPSLKS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94EP-00102346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93JP-00028173.
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                                                                                                                                                                                                                                                          84
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                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                              1 HIYWDDDKRYNPSLKS
                                                                                                                                                                                                                                                          HIYWDDDKRYSPSLKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Il-6 binding inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AJIN ) AJINOMOTO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1994-295777/37.
                                                                                                                                                                                Local Similarity
nes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 246 AA;
                                                                                                                                       Sequence 148 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP617126-A2.
                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2003
28-APR-1995
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                                                                                                                                                                                                                                                            69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                         antigen
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Matches
                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                         RESULT 41
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   셤
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autoimmune haemolytic anaemia; scleroderma;
                                                                                                                                 11-DEC-2003.
                                                                     Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                 Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 44
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ID ADF7
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셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an engineered CD44 antibody for inducing the differentiation and wither of leukemia cells, the gene in the heavy chain and light chain variable region of monoclonal antibody H144a of CD44, the polypeptide coded by said gene, the carrier containing said gene, and the application of said gene and polypeptide in preparing medicines for diagnosing and treating leukemia and disclosed. The present sequence represents the amino acid sequence of the mouse CD44 antibody V segment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anti-CD16A antibody; mouse; 3G8 antibody; humanised anti-CD16A antibody; immune response; haemostatic; antirheumatic; antiarthritic; dermatological; immunosuppressive; antiinflammatory; antianaemic; vasotropic; nephrotropic; neuroprotective; antipsoriatic; uropathic; ophthalmological; antiasthmatic; inflammatory response; autoimmune disease; idiopathic thrombocytopenic purpura; rheumatoid arthritis; systemic lupus erythematosus;
                                                                                                                      antibody engineering; CD44; leukemia; hematological disease; neoplasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                     Engineering antibody against CD44 for inducing leukemia cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.6%; Score 88; DB 9; Length 121; 93.8%; Pred. No. 6.4e-06; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                             (HEMA-) HEMATOLOGY INST CHINESE MEDICINE ACAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hu3G8VH-1 amino acid sequence SEQ ID NO:104.
                                                                                                                                                                                                                                                                                                                                                                  Claim 2; SEQ ID NO 2; 19pp; Chinese.
                                     AEA37667 standard; protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADF71905 standard; protein; 118 AA.
                                                                                                  Mouse CD44 antibody V segment.
                                                                                                                                                                                                                  18-DEC-2003; 2003CN-01107583.
                                                                                                                                                                                                                                       18-DEC-2003; 2003CN-01107583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 HIYWDDDKRYNPSLKS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 HIYWDDGKRYNPSLKS 67
                                                                                                                                                                                                                                                                                                                                                differentation and necrosis.
                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15; Conservative
                                                                                                                                                                                                                                                                                                    WPI; 2005-173920/19.
N-PSDB; AEA37666.
                                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 121 AA;
                                                                                                                                                                                                                                                                                 Song G;
                                                                                                                                                    Mus musculus.
                                                                              28-JUL-2005
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                                                                                                                                                                         CN1552735-A
                                                                                                                                                                                             08-DEC-2004
                                                                                                                                 cytostatic
                                                          AEA37667;
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                                                                                                                                                                                                                                                                                Han Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                  RESULT 42
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                            AEA37667
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The present invention describes an anti-CD16A antibody (I) comprising a VH domain comprising complementarity determining regions (CDRs) derived from the mouse 308 antibody light chain or a humanised anti-CD16A antibody (II) that lacks effector function and comprises all six CDRs of couse antibody 308. Also described is a method (MI) for reducting a deleterious immune response in a mammal in need of such reduction, which involves administering to the mammal a CD16A binding protein comprising comperciation from a human 1gG heavy chain, where the For region carried from a human ligh have been chence binding to an FC antiarthritic, dermatological, immunosuppressive, antiinflammatory.

CC effector ligand (I) and (II) have haemostatic, antirheumatic, antianaemic, vasotropic, nephrotropic, neuroprotective, antipsoriatic, antianaemic, ophthalmological and antiasthmatic activities. (I) or (II) is cusful for reducing a deleterious immune response in a mammal which involves administering to the mammal (I) or (II). The deleterious immune cuseful for reducing a deleterious immune response is an inflammatory response caused by autoimmune disease such as clatopathic thrombocytopenic purpura (ITP), rheumatolous (AMA), scleroderma, autoantibody trigged urticaria, pemphigus, vasculitis corpatic arthritis, ankylosing spondare, which intravenous (MS), psoriatic arthritis, ankylosing spondare, which intravenous corporatic arthritis, and sease, polymyositis and dermatomyce immunorlobulin (IVIC) therawn of all parcit as thms. The new new remains a mammal and mammal which and mammal and mamma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel anti-CD16A antibody comprising complementarity determining regions derived from mouse 3G8 antibody and humanized anti-CD16A antibody that lacks effector function, useful for treating deleterious immune response.
autoantibody trigged urticaria; pemphigus; vasculitis syndrome; systemic vasculitis; Godgasture's syndrome; multiple sclerosis; psoriatic arthritis; ankylosing spondylitis; Sjogren's syndrome; Kowasaki's disease; polymyositis; dermatomyositis; allergic asthma.
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Pred. No. 9e-06;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; SEQ ID NO 104; 103pp; English
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nes 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ų,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-042985/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 118 AA;
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                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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Sequence 118 AA;

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anti-CD16A antibody; mouse; 3G8 antibody; humanised anti-CD16A antibody; immune response; haemostatic; antirheumatic; antiarthritic; dermatological; haemostatic; antirheumatic; antianaemic; vasotropic; nephrotropic; antiportective; antiportatic; uropathic; ophthalmological; antiasthmatic; inflammatory response; autoimmune disease; idiopathic thrombocytopenic purpura; rheumatoid arthritis; systemic lupus erythematosus; autoimmune haemolytic anaemia; scleroderma; autoimtopy trigged urticaria; pemphigus; vasculitis syndrome; systemic vasculitis; Goodpasture's syndrome; multiple sclerosis; psoriatic arthritis; ankylosing spondylitis; Sjogren's syndrome; Reiter's syndrome; Kowasaki's disease; polymyositis; dermatomyositis; Hu3G8VH-5 amino acid sequence SEQ ID NO:109. Tuaillon N; 29-MAY-2003; 2003WO-US017111. 30-MAY-2002; 2002US-0384689P. 10-JAN-2003; 2003US-0439320P. Li H, (first entry) (MACR-) MACROGENICS INC. Johnson LS, Huang L, WPI; 2004-042985/04. WO2003101485-A1. allergic asthma Homo sapiens. 26-FEB-2004 11-DEC-2003 Synthetic. ADF71910; Mus sp. 

Novel anti-CD16A antibody comprising complementarity determining regions derived from mouse 3G8 antibody and humanized anti-CD16A antibody that lacks effector function, useful for treating deleterious immune response.

Claim 12; SEQ ID NO 109; 103pp; English.

the present invention describes an anti-ULIGA antibody (1) comprising a decrease and domain comprising complementarity determining regions (CDRs) derived from the mouse 368 antibody light chain or a humanised anti-CD16A derived from the mouse 368 antibody light chain or a humanised anti-CD16A antibody (II) that lacks effector function and comprises all six CDRs of mouse antibody 368. Also described is a method (M1) for reducting of deleterious immune response in a mammal in need of such reduction, which involves administering to the mammal a CD16A binding protein comprising an Fc region derived from a human 1gG heavy chain, where the Fc region lacks effector function or is modified to reduce binding to an Fc effector ingand (1) have haemostatic, antituteumatic, antiarthritic, dermatological, immunosuppressive, antiinflammatory, antianaemic, vasotropic, nephrotropic, neuroprotective, antiporiatic, antianaemic, vasotropic, nephrotropic, neuroprotective, antiporiatic, antianaemic, vasotropic, nephrotropic, neuroprotective, antiporiatic, or useful for reducing a deleterious immune response in a mammal which involves administering to the mammal (1) or (II). The deleterious immune response is an inflammatory response in an animal which involves administering to the mammal (1) or (II). The deleterious immune cresponse is an inflammatory response clused by autofinmune disease such as idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA), systemic lupus erythematosus (SLE), autoimmune haemolytic anaemia (AHA), systemic lupus erythematosus (SLE), eutoimmune haemolytic anaemia (AHA), systemic vasculitis, ankylosing spondylltis, Sjogren's syndrome, systemic vasculitis, ankylosing spondylltis, Sjogren's syndrome, syndrome, systemic vasculitis, ankylosing spondylltis, sjogren's syndrome, and also for treating diseases susceptible to treatment with intravenous immunoglobulin (IVIG) therapy e.g., allergic asthma. The present sequence immunospone in the exemplification of the present invention. The present invention describes an anti-CD16A antibody (I) comprising a

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-CD16A antibody; mouse; 3G8 antibody; humanised anti-CD16A antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune response; hadmostatic; antirheumatic; antiarthritic; dermatological; immunosuppressive; antinflammatory; antianaemic; owasotropic; nephrotropic; neuroprotective; antipsoriatic; uropathic; ophthalmological; antiasthmatic; inflammatory response; autoimmune disease; idiopathic thrombocytopenic purpura; rheumatoid arthritis; systemic lupus erythematosus; autoimmune haemolylic anemia; solaroderma; autoantibody trigged urticaria; pemphigus; vasculitis syndrome; systemic vasculitis; Goodpasture's syndrome; multiple sclerosis; psoriatic arthritis; ankylosing spondyllitis; Sjogren's syndrome; syndrome
                                                                                                Gaps
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                               Length 118;
                                                                                          0; Indels
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                        91.6%; Score 87; DB 8;
87.5%; Pred. No. 9e-06;
tive 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                               ADF71908 standard; protein; 448 AA.
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Query Match
Best Local Similarity 87.35,
--hes 14; Conservative
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uropathic, ophthalmological and antiasthmatic activities. (I) or (II) is useful for reducing a deleterious immune response in a mammal which involves administering to the mammal (I) or (II). The deleterious immune response is an inflammatory response caused by autoimmune disease such as idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA), scytemic lupus erythematosus (SLE), autoimmune haemolytic anaemia (AHA), scleroderma, autoantibody trigged urticaria, pemphigus, vasculitis syndrome, systemic vasculitis, Goodpasture's syndrome, multiple sclerosis (MS), psoriatic arthritis, ankylosing spondylltis, Sjogren's syndrome, Rowasaki's disease, polymyositis and dermatomyositis and also for treating diseases susceptible to treatment with intravenous immunoglobulin (IVIG) therapy e.g., allergic asthma. The present sequence is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                           91.6%; Score 87; DB 8; Length 448; 87.5%; Pred. No. 3.8e-05; ive 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADF71912 standard; protein; 448 AA.
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10-JAN-2003; 2003US-0439320P.
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Best Local Similarity 87.5
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                        Sequence 448 AA;
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Disclosure; SEQ ID NO 111; 103pp; English

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The present invention describes an anti-CD16A antibody (I) comprising a VH domain comprising complementarity determining regions (CDRs) derived from the mouse 308 antibody light chain or a humanised anti-CD16A derived from the mouse 308 antibody light chain or a humanised anti-CD16A antibody (II) that lacks effector function and comprises all six CDRs of mouse antibody 368. Also described is a method (MI) for reducting a deleterious immune response in a mammal in need of such reducting, which involves administering to the mammal a CD16A binding protein comprising an FC region derived from a human 1gG heavy chain, where the FC region lacks effector function or is modified to reduce binding to an FC effector ligand. (I) and (II) have haemostatic, antirheumatic, antiarthritic, dermatological, immunosuppressive, antipheamatory, antipheamatory, confident and antiasthmatic activities. (I) or (II) is antiarthritic, ophthalmological and antiasthmatic activities. (I) or (III) is useful for reducing a deleterious immune response in a mammal which response is an inflammatory response caused by autoimmune disease such as idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RAA), systemic lupus erythematosus (SLE), autoimmune haemolytic anaemia (AHA), systemic vasculitis, ankylosing spondyllitis, Sjogren's syndrome, systemic vasculitis, ankylosing spondyllitis, Sjogren's syndrome, systemic vasculitis, ankylosing spondyllica, syndrome, systemic vasculitis, ankylosing spondyllica, syndrome, systemic vasculitis, ankylosing spondyllica, theratomycallum (IVIG) therapy e.g., allergic asthma. The present sequence constitution immunoglobulin (IVIG) therapy e.g., allergic asthma. The present sequence
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87.5%; Pred. No. 3.8e-05;
rative 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 448 AA;
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Homo sapiens.
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Matches
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Homo sapiens
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                                                                  Synthetic.
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ABG67188
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                                                                                                                                                                                                                                 The present invention describes an anti-CD16A antibody (1) comprising a VH domain comprising complementarity determining regions (CDRs) derived from the mouse 308 antibody heavy chain and a VL domain comprising CDRs derived from the mouse 308 antibody light chain or a humanised anti-CD16A antibody (II) that lacks effector function and comprises all six CDRs of couse antibody 368. Also described is a method (MI) for reducting a deleterious immune response in a mammal in need of such reducting, which involves administering to the mammal a CD16A binding protein comprising a RF cergoin derived from a human 1gG heavy chain, where the RC region lacks effector function or is modified to reduce binding to an FC effector ligand. (I) and (II) have heemostatic, antitheumatic, antianaemic, vasotropic, nephrotropic, neuroprotective, antiphematic, antianaemic, vasotropic, nephrotropic, neuroprotective, antiphematic, curopathic, ophthalmological and antiasthmatic activities. (I) or (II) is useful for reducing a deleterious immune response in a mammal which involves administering to the mammal (ITP), rheumatoid arthritis (RA), systemic luguas erythematous (SLB), autoimmune haemolytic ansenda (AHA), selectoderma, autoantibody trigged utricaria, pemphigus, vasculitis syndrome, systemic vasculitis, ankylosing spondylitis, Slogren's syndrome, syndrome, Kowasaki's disease, polymyositis and also for treating diseases susceptible to treatment with intravenous immuned in mammal (IVI) therapy e.g., allergic asthma. The present sequence is mannal strain of the present sequence is an intending disease susceptible to treatment the present sequence is mammal of the present sequence.
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                                                                                                                                         Novel anti-CD16A antibody comprising complementarity determining regions derived from mouse 3G8 antibody and humanized anti-CD16A antibody that lacks effector function, useful for treating deleterious immune response.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is used in the exemplification of the present invention.
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                                                                               Tuaillon N;
                                                                                                                                                                                                         Claim 9; SEQ ID NO 113; 103pp; English.
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                                                                               Li H,
30-MAY-2002; 2002US-0384689P.
10-JAN-2003; 2003US-0439320P.
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                                              (MACR-) MACROGENICS INC.
                                                                                                              WPI; 2004-042985/04
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Best Local Similarity
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The present invention describes an anti-CD16A antibody (I) comprising a VH domain comprising complementarity determining regions (CDRs) derived from the mouse 308 antibody heavy chain and a VL domain comprising CDRs derived from the mouse 308 antibody light chain or a humanised anti-CD16A antibody (II) that lacks effector function and comprises all six CDRs of couse antibody 308. Also described is a method (MI) for reduction a construction and comprises all six CDRs of involves administering to the mammal in need of such reduction, which involves administering to the mammal a CD16A binding protein comprising compared from a human IgG heavy chain, where the Fc region lacks effector function of (I) and (II) have haemostatic, antirheumatic, antianaemic, vasotropic, nephrotropic, neuroprotective, antiphamatory, antianaemic, vasotropic nephrotropic, neuroprotective, antipportatic, or uropathic thrombocytopenic numune tasponse in a mammal which involves administering to the mammal (I) or (II). The deleterious immune response is an inflammatory response caused by autoimmune disease such a diopathic thrombocytopenic purpura (ITP), rheumatoid architis (AHA), selectederma, autoantibody trigged urticaria, pemphigus, vasculitis clarantic architits, ankylosing spondylitis, Sjogren's syndrome, systemic vasculitis and diseases succeptible to treatment with intravence and also for treating diseases succeptible to treatment with intravence immunely and alsomer as promoved.
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is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel anti-CD16A antibody comprising complementarity determining regions derived from mouse 3G8 antibody and humanized anti-CD16A antibody that lacks effector function, useful for treating deleterious immune response.
psoriatic arthritis; ankylosing spondylitis; Sjogren's syndrome;
Reiter's syndrome; Kowasaki's disease; polymyositis; dermatomyositis;
allergic asthma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 115; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-MAY-2003; 2003WO-US017111.
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Best Local Similarity 87.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Huang L,
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95WO-US007372. 94US-00259321.

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anti-protein C monoclonal antibody HPC-4 heavy chain variable region. HPC-4 recognises the activation peptide region (AAR88106) of the heavy chain of protein C, a vittamin K-dependent plasma protein zymogen. Protein C is converted to activated protein C (APC) by cleavage between the Arg-Leu prevents protein C activation to APC by binding to this region. HPC-4 prevents protein C activation to APC by binding to this region. The DNA sequences encoding the variable regions of the heavy and light chains of the antibody (AAT09299-302) were used to construct humanised antibodies using the PCR primars AAT09303-9. The humanised antibodies are useful as inhibitors of coagulation and can be used for the treatment of tumours by inhibiting the anticoagulant activity of APC by preventing conversion of
                                                                                                                                                                                                           Calcium-binding monoclonal antibody immunoreactive with Protein C - inhibits Protein C anticoagulant activation by thrombin-thrombomodulin, e.g. for treating tumours.
                                                                                                                                                                                                                                                                                                                            This is the amino acid sequence of the mature peptide from the murine
                                                                                                                                                                                                                                                                                       Claim 2; Page 29; 41pp; English.
                                                                              (OKLA-) OKLAHOMA MED RES FOUND.
                                                                                                                                                      WPI; 1996-049681/05.
N-PSDB; AAT09300.
                                                                                                                   Rezaie A, Esmon CT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprising different groups of peptides each group being capable of raising, in an infected individual, an antibody able to bind to the hypervariable 1 (HVR1) region of the envelope protein E2 of the infecting HCV strain. The different groups of peptides are administered sequentially to raise antibodies, helper T-lymphocytes, and cytotoxic T-lymphocytes which are cross-reactive to the HVR1 region of the infecting HCV. The vaccines are useful for preventing and treating chronic HCV infections. ABG67186-ABG67189 represent variable regions of human 1gG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a hepatitis C virus (HCV) vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus (HCV) vaccines able to raise antibodies, helper 'lymphocytes and/or cytotoxic T lymphocytes able to bind to the hypervariable 1 region of the infecting HCV strain.
                                                                      Hepatitis C virus vaccine; HCV; hypervariable region 1; HVR1; envelope protein E2; antibody; helper T-lymphocyte; IgG1; cytotoxic T-lymphocyte; HCV infection; virucide; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 121;
                                     Human IgG1 antibody heavy chain variable region 15H4VH.
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Pred. No. 2.3e-05;
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                                                                                                                                                                                                                                                                  07-DEC-2001; 2001WO-GB005421.
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18-DEC-2000; 2000GB-00030789.
(first entry)
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                                                                                                                                                                                                                                                                                                                                                            (ALLA/) ALLAIN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 121 AA;
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 24-SEP-2002
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Score 84; DB 2; Length 120
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RESULT 50 AAR88109 ....

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Epitope, activation, heavy chain, protein C; vitamin K; plasma protein, zymogen, cleavage, mouse, humanised antibody, variable region, light chain, inhibition, anticoagulant, coagulation, tumour.

Mus musculus WO9534652-A1

21-DEC-1995.

Murine anti-Protein C MAb HPC-4 VH gamma mature peptide.

(first entry)

25-JUL-1996

AAR88109;

AAR88109 standard; peptide; 120 AA

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Cipate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
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Gibeavy chain V region (DP-76) - human (fragment)
Gibecies: Homo sapiens (man)
Gibate: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
Gibate: 22-So 26936
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26936
A;Reference number: S26936
A;Reference preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-41 <TOM>
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C;Accession: S18556
R;Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; Hk
EMBO J. 10, 3641-3645, 1991
A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: clu
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       Length 107;
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   Score 84; DB 2; Length 107
Pred. No. 4.5e-06;
1; Mismatches 1; Indels
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87.5%; Pred. No. 6.8e-06;
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C, Species: Mus musculus (house mouse)
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   Query Match
Best Local Similarity 87.5%;
Matches 14; Conservative
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A49442
Ig heavy chain V region (50.1) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Date: 21-U1-1995 #sequence_revision 21-U1-1995 #text_change 21-Jan-2000
C; Jacession: A49442
R; Stura, E.A.; Stanfield, R.L.; Fieser, G.G.; Silver, S.; Roguska, M.; Hincapie, L.M.; SPCOTEINS 14, 499-508, 1992
A; Title: Crystallization, sequence, and preliminary crystallographic data for an antipep A; Reference number: A49442
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: DNA
A; Residues: 1-107 <STU
A; Cross-references: UNIPARC:UPIO0001768FD
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 7-91/Domain: immunoglobulin homology <IMM>
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(5) Species: Mus musculus (house mouse)
(5) Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
(5) Accession: $11740
(6) Accession: $11740
(7) Accession: $11740
(8) Accession: Bata Library, May 1990
(8) Reference number: $11740
(9) Accession: $11740
(1) Accession: $11740

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Best Local Similarity 100.
Matches 16; Conservative
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Best Local Similarity 80.0%;
Matches 12; Conservative
2 IYWDDDKRYNPSLKS 16
                                                                                                                      2 IYWDDDKRYNPSLKS 16
                                                                                                                                                 72 IYWNDDKRYSPSLKS 86
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Query Match
Best Local Similarity 86.7
Matches 13; Conservative
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54 LYWDDDKRFSPSLKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A02093
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                    A; Accession: S1856
A; Accession: S1856
A; Status: translation not shown
A; Molecule type: DNA
A; Residues: 1-118 <SHI>
A; Cross-references: UNIPARC:UPI0000115FEC; EMBL:X62108; NID:g37840; PIDN:CAA44018.1; PID
A; Cross-references: UNIPARC:UPI0000115FEC; EMBL:X62108; NID:g37840; PIDN:CAA44018.1; PID
C; Genetics:
A; Introns: 16/1
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 1-19/Domain: signal sequence #status predicted <SIG>
F; 20-118/Product: Ig heavy chain V region (VII-5b) #status predicted <MAT>
F; 34-116/Domain: immunoglobulin homology <IMM>
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A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residuae: 1-138 cCHA>
A; Cross-references: UNIPARC:UPI00001160FA; EMBL:X69861; NID:933084; PIDN:CAA49495.1; PIL
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heteroterramer; immunoglobulin
F; 30-114 / Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain - human
CiSpecies: Homo sapiens (man)
CiDate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
CiAccession: 831513
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
Richastagner, P. Demaison, C.; Theze, J.; Zouali, M.
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autc
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Ig heavy chain V region precursor (VII-5) - human (fragment)
C;Species: Homo aspiens (man)
C;Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 21-Jul-2000
C;Accession: 818555
R;Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; Famio, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; Famio, E.Physical map of the 3' region of the human immunoglobulin heavy chain locus: C; Maccession: 818555
M;Accession: 818555
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C;Keywords: heterotetramer; immunoglobulin
C;Reywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-119/Product: Ig heavy chain V region (VII-5) #status predicted <MAT>
F;34-118/Domain: immunoglobulin homology <IMM>
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     A;Reference number: S18551; MUID:92037524; PMID:1935893
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A; Residues: 1-119 <SHI>
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C;Accession: A02093
R;Curningham, B.A.; Pflumm, M.N.; Rutishauser, U.; Edelman, G.M.
Rpcc. Natl. Acad. Sci. U. S.A. 64, 997-1003, 1959
A;Title: Subgroups of amino acid sequences in the variable regions of immunoglobulin hea A;Reference number: A02093; MUID:70114712; PMID:5264153
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A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: blocked amino end; heterotetramer; immunoglobulin
F;15-100/bomain: immunoglobulin homology <IMM>
F;15-100/bomain: immunoglobulin homology <IMM>
F;11/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #statu
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Arthritis A rheumatoid factor from a normal individual encoded by VH2 and V kappa II gene A; Reference number: A49002; MUID:92352481; PMID:1322670
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A;Experimental source: EBV-transformed lymphoblastoid cell line SSH23
A;Note: sequence extracted from NCB1 backbone (NCBIN:110261, NCBIP:110262)
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology < IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy chain V-II region (He) - human
C;Species: Homo sapiens (man)
C;Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 09-Jul-2004
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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C;Comment: This gamma-1 chain was isolated from a myeloma protein.
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C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change
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Length 119;
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80.0%; Pred. No. 9.1e-05;
tive 3; Mismatches 0;
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Pred. No. 0.00019;
3; Mismatches 0;
Score 77; DB 2; Pred. No. 6.3e-05; 2; Mismatches 0
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Matches 11; Conservative
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A;Molecule type: mRNA
A;Residues: 1-116 <STA>
A; Molecule type: DNA
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                G.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: 13-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996
C.Accesion: Pr0174
R.Perfetti, V.; Borden, P.; Tao, M.H.; Morrison, S.L.; Kabat, E.A.
R.Perfetti, V.; Borden, P.; Tao, M.H.; Morrison, S.L.; Kabat, E.A.
R.Perfetti, V.; Borden, P.; Tao, M.H.; Morrison, S.L.; Kabat, E.A.
R.A; Reference number: Pr0174; MUD:91287738; PMID:1712074
A; Reference number: Pr0174; MUD:91287738; PMID:1712074
A; Residues: 1-143 <-PER>
A; Residues: 1-143 <-PE
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C;Species: Mus musculus (house mouse)
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 16-Aug-1996
C;Accession: B25913
R;Lawler, A.M.; Lin, P.S.; Gearhart, P.J.
R;Lawler, A.M.; Lin, P.S.; Gearhart, P.J.
A;Title: Adult B.coll repertoire is biased toward two heavy-chain variable-region genes
A;Reference number: A94148; MUID:87175692; PMID:3104915
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A;Residues: 1-140,'C',142-374 <KH2>
A;Cross-references: UNIPARC:UPI0000176F25; EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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A,Residues: 1-374 «KRA»
A;Residues: 1-374 «KRA»
A;Cross-references: UNIPARC:UPI0000176F24; EMBL:X81695
R;Khamlichi, A.A.
Bubmitted to the EMBL Data Library, September 1994
A;Reference number: S72664
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Pred. No. 0.0013;
4; Mismatches 0
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nes 13; Conservative
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Ig heavy chain V region - mouse (Species: Mus musculus (house mouse) CjSpecies: Mus musculus (house mouse) CjSpecies: 13-7an-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000 CjAccests, S.B.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A,Fitle: Antibodies that are specific for a single amino acid interchange in a protein e A,Reference number: S26309; MuID:91341421; PMID:1908510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: UNIPARC:UPI0000115F83; EMBL:X59198; NID:g52074; PIDN:CAA41908.1; PID C.Subperfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin C; Keywords: heterotetramer; immunoglobulin F;11-95/Domain: immunoglobulin homology <IMM>
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C;Species: Homo sapiens (man)
C;Date: 14-Nov-1983 #sequence_revision 22-Nov-1983 #text_change 09-Jul-2004
C;Accession: A02092
R;Gerber-Jenson, B.; Kazin, A.; Kehoe, J.M.; Scheffel, C.; Erickson, B.W.; Litman, G.W., J Immunol. 126, 1212-1216, 1981
A;Title: Molecular basis for the temperature-dependent insolubility of cryoglobulins. X.
A;Reference number: A02092; MUID:81118242; PMID:6780622
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C.Superfamily: immunoglobulin V region; immunoglobulin homology

C.Keywords: heterotetramer; immunoglobulin; pyroglutamic acid

F.15-99/Domain: immunoglobulin homology < 1WM>

F;15-99/Domain: immunoglobulin homology < 1WM>
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A;Note: this chain was derived from a monoclonal IgM cryoimmunoglobulin C;Genetics:
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A;Residues: 1-103 <LAW>
A;Cross-references: UNIPARC:UP100001768FB
A;Cross-references: UNIPARC:UP100001768FB
A;NOte: the authors translated the codon TGT for residue 11 as 6;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin
F;19-103/Domain: immunoglobulin homology <IMM>
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Local Similarity 73.3%; Pred. No. 0.005;
les 11; Conservative 2; Mismatches 2; Indels
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R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G. Y. Mol. Biol. 227, 776-798, 1995. A;Title: Biol. 227, 776-798, 1995. A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V A;Reference number: S26885; MUID:93021111; PMID:1404388
                                                                                                                                                                                                                      A;Cross-references: UNIPARC:UD1000116404; EMBL:Z12329; NID:g32875; PIDN:CAA78199.1; PID C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
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C;Species: Homo sapiens (man)
C;Date: OS-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 07-May-1999
C;Accession: 546471
R;Cook, G.P.; Tomlinson, I.M.; Walter, G.; Riethman, H.; Carter, N.P.; Buluwela, L.; Win Nature Genet. 7, 162-168, 1994
A;Title: A map of the human immunoglobulin V(H) locus completed by analysis of the telom A;Reference number: 846460; MUID:95004581; PMID:7920635
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R.Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
Arittle: Preferential utilization of conserved immunoglobulin heavy chain variable gene A36065 MUID:90349571; PMID:2117273
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C;Date: 21-Dec-1990 #sequence_revision 13-Sep-1991 #text_change 16-Dec-1998
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A;Cross-references: GDB:118731; OMIM:146910
A;Arp position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P:15-99/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-56 <COO>
A;Cross-references: UNIPARC:UP100001768FF; EMBL:Z29983
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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A;Cross-references: UNIPARC:UPI0000176977; GB:M34027
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Pred. No. 0.2;
2; Mismatches
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illarity 66.7%; Pred. No. 0.26;
Conservative 2; Mismatches
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Pred. No. 0.16;
2; Mismatches
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Best Local Similarity 66.7%;
Matches 10; Conservative
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Best Local Similarity 66.7°
Matches 10, Conservative
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les 10; Conserv
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A; Molecule type: DNA
A; Residues: 1-96 <TOM>
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                                                                                                                                                                                      Ig heavy chain V region (31-9D) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 23-Jul-1999
C;Accession: 809559
R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Bur, J. Immunol. 20, 771-777, 1990
A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie
A;Reference number: 809955; MuID:90269328; PMID:2347362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPARC:UP10000115E5E; EMBL:X51847; NID:g55247; PIDN:CAA36140.1; PID C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin homology <!MM>
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Ig heavy chain V-II region (Cor) - human (tentative sequence)

C;Species: Home sapiens (man)

C;Species: A020-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004

C;Accession: A02089

R;Press, E.M.; Hogg, N.M.

Biochem. J. 117, 641-660, 1970

A;Title: The amino acid sequences of the Fd fragments of two human gammal heavy chains.

A;Reference number: A90250; MUID:70258837; PMID:5449120
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AjCross-references: GDB:128528; OMIM:147070
AjMap position: 14q32.33-14q12.33
CjSuperfamily: immunoglobulin V region; immunoglobulin homology
CjSuperfamily: immunoglobulin Neterotetramer; immunoglobulin; pyroglutamic acid
Fj15-96/Domain: immunoglobulin homology <IMM>
Fj1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
Fj2-94/Disulfide bonds: #status experimental
Fj62/Binding site: carbohydrate (Asn) (covalent) #status experimental
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IG heavy chain V region (DP-27) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26923
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A;Residues: 1-120 <PRE>
A;Cross-references: UNIPROT:P01815; UNIPARC:UPI000012CEE9
C;Comment: This chain was isolated from an IgG1 myeloma protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 121;
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62.5%; Pred. No. 0.086;
Live 3; Mismatches
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52 NIWWNDDKYYNSVLKS 67
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  2 IYWDDDKRYNPSLKS 16
                                                         67
                                  53 INWDDDNRYSPSLRS
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Best Local Similarity 62.5
Matches 10; Conservative
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A; Regidues: 1-121 <REI>
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Best Local &
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R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region (DP-71 / VH 4.11 / 4.15) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: 2-Nov-1993 #sequence revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26906; S09421; S12415
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A;Tille: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Risanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A.Title: The smaller human V(H) gene families display remarkably little polymorphism.
A.Reference number: S09421, MUID:90059975; PMID:2511001
A.Reference: DNA
A.Rocession: S09421
A.Status: preliminary; translation not shown
A.Rolecule type: DNA
A.Rolecule type: DNA
A.Roses-references: UNIPARC:UPI000004CF81; EMBL:X56355
A.Roces-reference: UNIPARC:UPI000004CF81; EMBL:X56355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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C;Superfantly: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-84/Domain: immunoglobulin homology (fragment) <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

54.7%; Score 52; DB 2; Length 115;
Best Local Similarity 62.5%; Pred. No. 0.5;
Matches 10; Conservative 2; Mismatches 4; Indels
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keyworda: heterotetramer; immunoglobulin homology
F;15-97/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                A; Reference number: S23716; MUID: 92031262; PMID:1718404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 HIYWDDDKRYNPSLKS 16
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50 YIYYSGSTNYNPSLKS 65
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Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                   A; Accession: S23718
A; Molecule type: mRNA
A; Residues: 1-84 < HAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-97 < TOM>
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A; Residues: 1-97 <SA2>
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S12416
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19 heavy chain V region (YAC-3) - human (55pecies: Homo sapiens (man) (7. Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999 (7. Date: 20-Feb-1995 #sequence_revision 20-Feb-1999  
Nature Genet. 7, 162-168, 1994  
Nature Genet. 7, 162-168,
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A;Accession: S78053
A;Molecule type: mRNA
A;Residues: 1-115 <HAR>
A;Cross-references: UNIPARC:UPI000011558B; EMBL:X54443; NID:g37816; PIDN:CAA38310.1; PID
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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S26924
Ig heavy chain V region (DP-28) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26924
B;Tomlinson, I.N.; Walter, G; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups
A;Reference number: S26885; MUID:93021117; PMID:1404388
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C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 55.8%; Score 53; DB 2; Length 96; Local Similarity 66.7%; Pred. No. 0.28; se 10; Conservative 2; Mismatches 3; Indels
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Pred. No. 0.23;
2; Mismatches
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                                                                              36 IDWDDDKFYSTSLKT 50
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                                       IYWDDDKRYNPSLKS 16
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A,Molecule type: DNA
A,Residues: 1-96 <TOM>
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Ig heavy chain V-J region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Mono Sayté4
C;Accession: S57464
R;Paterson, G.; Wilson, G.; Kennedy, P.G.E.; Willison, H.J.
A;Description: Analysis of anti-GMI ganglioside IgM antibodies cloned from motor neuropa A;Reference number: S57408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo gapiens (man)
C;Species: Homo gapiens (man)
C;Date: 05-Jun-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
C;Accession: B26340
G;Accession: B26340
J; Wal. Biol. 190, 529-541, 1986
J; Mol. Biol. 190, 529-541, 1986
A;Atitle: Organization and evolution of variable region genes of the human immunoglobulin A;Accession: B26340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPARC:UP100001137AD; EMBL:X87897; NID:9871273; PIDN:CAA61148.1; PI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Introns: 16/1
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heteroterramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-116/Product: Ig heavy chain V region 71-4 #status predicted
F;34-116/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             c, sucrons: 100/2
A; Introns: 100/2
C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Superfamily: immunoglobulin homology <!MM>
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:||:
50 XIYYSGSTNYNPSLKS 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 YIYYTGNTNYNPSLKS 67
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Best Local Similarity
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Best Local Similarity
Matches 9; Conserv
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A;Molecule type: mRNA
A;Residues: 1-115 <PAT>
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S44125
Ig lambda chain V region - human
C; Species: Homo sapiens (man)
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
R; Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
A; Decension: Idiotypic vaccination against human B-cell lymphoma: rescue of variable national symplements in the special symplement of variable national symplements in the symplement 
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512412
19 heavy chain V region (4.12) - human
C;Species: Home sapiens (man)
C;Species: Home sapiens (man)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 1: Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
A;Reference number: S09421; MUID:90059975; PMID:2511001
A;Reference number: S09421; MUID:90059975; PMID:2511001
A;Residues: 1-99 - SAN>
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>
                            Title: The smaller human V(H) gene families display remarkably little polymorphism.
Reference number: S09421; MUID:90059975; PMID:2511001
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                            A;Title: The smaller human V(H) gene tamilies Gibylogy remutations A;Reference number: 809421; MUID:90059975; PMID:2511001
A;Reference number: 812416
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-97 < SAN>
A;Residues: 1-97 < SAN>
A;Cross-references: UNIPROT:09UL73; UNIPARC:UPI0000176E65; EMBL:X56360
C;Superfamily: immunoglobulin homology cIMM>
F;15-97/Domain: immunoglobulin homology < IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 50; DB 2; Length 97;
Pred. No. 0.85;
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Best Local Similarity 56.2.
Local 9; Conservative
EMBO J. 8, 3741-3748, 1989
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A;Molecule type: mRNA
A;Residues: 1-140 <RES>
A;Cross-references: UNIPPARC:UPI0000176E83; EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;46-128/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26922
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26922
A;Status: preliminary
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A,Residues: 1-97 - AMAN>
A,Residues: 1-97 - AMAN>
A,Residues: 1-97 - AMAN>
A,Cross references: UNIPROT: Q9UL/3; UNIPARC: UPI0000176COC
A,Note: the authors translated the codon TAT for residue 50 as Thr
C,Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C,Superfamily: immunoglobulin homology but the codon TAT for residue 50 as Thr
C,Reywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 49; DB 2; Length 96; Pred. No. 1.2; 4; Mismatches 3; Indels
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3
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Ig heavy chain V region (DP-26) - human (fragment)
                                                                                                                                                                                                                                                    h Similarity 56.2%; Pred. No. 1.3; 9; Conservative 2; Mismatches
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69 YIYYSGSTNYNPSLKS
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Best Local Similarity 56.2
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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hes 9; Conserv
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A; Residues: 1-96 <TOM>
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Matches
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A. Mol. Biol. 190, 529-541, 1986
A.Title: Organization and evolution of variable region genes of the human immunoglobulin A.Title: Organization and evolution of variable region genes of the human immunoglobulin A.Reference number: A26340
A.Molecule type: DNA
A.Note: the authors translated the codon GAG for residue 25 as Gln
A.Note: the authors translated the codon GAG for residue 25 as Gln
A.Note: the authors translated the codon GAG for residue 25 as Gln
A.Note: the authors translated the codon GAG for residue 25 as Gln
A.Note: the authors translated the codon GAG for residue 25 as Gln
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A.Note: the authors translated the codon GAG for residue 25 as Gln
A.Note: the authors translated the codon GAG for residue 25 as Gln
A.Note: the authors translated the codon GAG for residue 25 as Gln
A.Note: the authors translated the codon GAG for residue 25 as Gln
A.Note: the authors translated the codon GAG for residue 25 as Gln
A.Note: the authors translated the codon GAG for residue 25 a
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Modecule type: DNA
A,Reaidues: 20-118 <TOM>
A,Cross-references: UNIPARC:UPI000011641A, EMBL:Z12366; NID:g32950, PIDN:CAA78236.1; PID
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Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: Sil690
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
Submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from 1
A;Reference number: Sil585
A;Accession: Sil690
A;Status: preliminary
A;Acteus mRNA
A;Acteus mRNA
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C; Keywords: heteroterramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-118/Product: Ig heavy chain V-II region 71-2 #status predicted <MAT>
F;34-118/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.6%; Score 50; DB 2; Length 118; 56.2%; Pred. No. 1.1; tive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 HIYWDDDKRYNPSLKS 16
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55 YIYYSGSTNYNPSLKS
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Best Local Similarity 56.2
Matches 9; Conservative
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reveals about fifty groups of V
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R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A;Title: The smaller human V(H) gene families display remarkably little polymorphism. A;Reference number: S09421; MUID:90059975; PMID:Z511001
A;Accession: S12413
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J. Mol. Biol. 227, 776-799, 1992
A,Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V A,Teference number: S26885; MUID:93021117; PMID:1404388
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C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999 C;Accession: $26903; $12413 R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G. J. Mol. Biol. 227, 776-798, 1992 A;Title: The repertoire of human germline V(H) sequences reveals about fifty A;Reference number: $26885; MUID:93021117; PMID:1404388
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 25-Oct-1996 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes. A;Reference number: S26800; MUID:92201299; PMID:1348029
A;Accession: S26801
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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A;Note: designated 4.13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 50.5%; Score 48; DB 2; Best Local Similarity 56.2%; Pred. No. 1.8; Matches 9; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 48; DB;
Pred. No. 1.8;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translation not shown A;Molecule type: DNA
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Best Local Similarity 56.2
Matches - 9; Conservative
                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-98 < TOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-99 <WEN>
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A;Molecule type: DNA
A;Residues: 1-99 <TOM>
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$1244

Ig heavy chain V region (4.14) - human
C;Species: Home sapiens (man)
C;Species: Home sapiens (man)
C;Species: Home sapiens (man)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C;Date: 1.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A;Reference number: S09421; MUID:90059975; PMID:2511001
A;Reference number: S09421; MUID:90059975; PMID:2511001
A;Residues: 1-98 cSAN>
A;Residues: 1-98 cSAN>
A;Residues: 1-98 cSAN>
A;Residues: 1-98 cSAN>
A;Residues: 1-98 cSAN>
A;Residues: 1-98 cSAN>
A;Cross-references: UNIPARC:UPI0000176E64; EMBL:X56358
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                       Ig heavy chain precursor V-II region (Cess) - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C;Accession: A02090
R;Takahashi, N.; Noma, T.; Honjo, T.
Proc. Natl. Acad. Sci. US.A. 81, 5194-5198, 1984
A;Title: Rearranged immunoglobulin heavy chain variable region (V-H) pseudogene that del A;Reference number: A02090; MUID:84298107; PMID:6089186
A;Accession: A02090
A;Accession: A02090
A;Molecule type: mRNA
A;Residues: 1-147 cTAK>
A;Residues: 1-147 cTAK>
A;Cross-references: UNIPROT:P04438; UNIPARC:UPI000012CEF0
A;Note: the sequence was determined from the differentiated gene
A;Note: the authors translated the codon GGG for residue 16 as Trp, TGG for residue 142
As Ser, and CAG for residue 147 as Ser
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A;Gross-references: GDB:128528; OMIM:147070
A;Gene: GDB:128528; OMIM:147070
A;Map position: 14q32.33-14q32.33
A;Introns: 15/3
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin homology
E;1-19/Domain: signal sequence Hestatus predicted <AGT>
E;20-147/Product: Ig heavy chain V-II region (Cess) #status predicted <AMT>
E;34-118/Domain: immunoglobulin homology <IVM>
E;34-118/Domain: immunoglobulin homology <IVM>
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56.2%; Pred. No. 1.8;
tive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
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226903
Ig heavy chain V region (DP-68 / 4.13) - human (fragment)
C;Species: Homo sapiens (man)
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2; Mismatches
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IDWDDDKYYGTSLET 86
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Best Local Similarity 60.v-
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Best Local Similarity
Matches 9; Conserv
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C;Accession: E14964
R;Sanz, I; Casali, P.; Thomas, J.W.; Notkins, A.L.; Capra, J.D.
A; Tmumnol. 142, 4054-4061, 1989
A;Title: Nucleotide sequences of eight human natural autoantibody V-H regions reveals app. A;Reference number: A92830; MUID:89235232; PMID:2497188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C'Species: Homo sapiens (man)
C'Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: 859912
R;Sahota, S.; Hamblin, T.; Oscier, D.G.; Stevenson, F.K.
R;Sahota, S.; Hamblin, T.; Oscier, D.G.; Stevenson, F.K.
A;Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of multiging A;Reference number: 869909; MUID:94335315; PMID:8057663
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                                                                                                                                                                                                                                                                                                                                                                        C'Species: Homo sapiens (man)
C'Date: 07-Sep-1990 #sequence_revision 23-Nov-1991 #text_change 16-Aug-1996
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C;Date: 13.Jan-1995 #sequence_revision 13.Jan-1995 #text_change 23.Jul-1999
C;Accession: S31514
R;Chastagner, P.; Demalson, C.; Theze, J.; Zouali, M.
                                                                      Gaps
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A.Molecule type: mRNA
A.Residues: L1 - 65AN>
A.Cross-references: UNIPARC:UPI0000176BFE; GB:M26997
A.Note: the authors translated the codon GCT for residue 42 as 7
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heteroterramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
         Length 116;
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                                                                      5; Indels
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A, Status: preliminary, nucleic acid sequence not shown
A, Modecule type: mRNA
A; Residues: 1-122 <SAH>
                                                                                                                                                                                                                                                                                                                                              Ig heavy chain precursor V-IV region (Ab26) - human
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      50.5%; Score 48; DB 2
56.2%; Pred. No. 2.1;
ive 2; Mismatches
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9; Conservative
                                                                                                                                                                  43 YIYYSGSTYYNPSLKS
                                                                                                                               1 HIYWDDDKRYNPSLKS
                                                                  9; Conservative
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                                      Best Local Similarity
Matches 9; Conserv
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Matches 9; Conserv
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         Query Match
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A; Residues: 1-116 <MCI>
A; Cross-references: UNIPARC; UPI00001161C0; EMBL; X75024; NID: 9404313; PIDN: CAA52932.1; PI C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin
F; 6-90/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>
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537456
19 mu chain - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37456
R;McIntooh, R.S., Tandon, N.; Weetman, A.P.
submitted to the EMBL Data Library, September 1993
A;Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from A;Reference number: S37453
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Ig heavy chain V region - human C;Species: Homo sapiens (man)
C;Species: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accesion: S26802
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A;Reference number: S26802
A;Reference number: S26802
A;Reference number: S26802
A;Reference number: S26802
A;Accession: S26602
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Best Local Similarity 56.20,
Best Local Similarity 56.20,
Best Local Similarity 56.20,
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A; Residues: 1-99 <WEN>
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A, Molecule type: DNA
A, Residues: 1-99 <WEN>
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A,Status: preliminary
A,Molecule type: mRNA
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R;Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990

Bytitle: Nucleotide sequences and three-dimensional modelling of the VH and VL domains o A;Reference number: S09710; MUD:90262535; PMID:2111699

A;Accession: S09711
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
                                                                                                                                                                                                                     Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
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R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A;Reference number: $26800; MUID:92201299; PMID:1348029
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C;Superfaaily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotteramer: immunoglobulin
F;34-118/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49.5%; Score 47; DB 2; ilarity 50.0%; Pred. No. 3.9; Conservative 3; Mismatches
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71 YIYYSGSTNYNPSLRS 86
                                           84
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                                       70 LYNDGDTGYNPALKS
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nes 8; Conserv
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Matches 9; Conserv
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A;Molecule type: mRNA
A;Residues: 1-146 <HUG>
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A; Residues: 1-99 < WEN>
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                                                                                                                                                      RESULT 46
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                               A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autch Reference number: 531509
A;Reference number: 531509
A;Reference number: 531514
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-128 <CHA>
A;CTOSS-references: UNIPARC:UPIO0001160FB; EMBL:X69862; NID:g33086; PIDN:CAA49496.1; PILC
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;22-106/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-144 <DUE:
A;Cross-references: UNIPARC:UPI0000116726; EMBL:Z49169; NID:g794095; PIDN:CAA89038.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>
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554228
Grand Heavy chain V region precursor - sheep (fragment)
Grand Heavy chain V region precursor - sheep (fragment)
Gracession: Solution of the same of the state (domestic sheep)
Gracession: S54228
Albeotription: Sheep immunoglobulin mu heavy chain variable region sequence.
Alreadion: S54228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
49.5%; Score 47; DB 2; Length 128;
Best Local Similarity 56.2%; Pred. No. 3.4;
Matches 9; Conservative 1; Mismatches 6; Indels
submitted to the EMBL Data Library, December 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 HIYWDDDKRYNPSLKS 16
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Best Local Similarity 60.01
Best Local 9; Conservative
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$12418
Ig heavy chain V region (4.18) - human
$1,5pecies: Homo saptens (man)
$1,5pecies: Homo saptens (man)
$2,5pecies: Homo saptens (man)
$2,5pecies: Homo saptens (man)
$2,5pecies: Homo saptens (man)
$2,5pecies: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
$2,5aaz, 1.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
$3,7a1-3749, 1989
$4,7tle: The smaller human V(H) gene families display remarkably little polymorphism.
$4,Reference number: $09421; MUID:90059975; PMID:2511001
$4,Restue: preliminary; translation not shown
$4,Restue: preliminary; translation not shown
$4,Residues: 1-99 <SAN>
$4,Residues: 1-99 <SAN>
$4,Residues: 1-99 <SAN>
$5,Residues: 1-99 <SAN>
$6,Residues: 1,09 <SAN>
$7,Residues: 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,000 <\table 1,0
                                                        A;Cross-references: UNIPARC:UPI0000116484; EMBL:214236; NID:g37702; PIDN:CAA78605.1; PID C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;15-99/Domain: immunoglobulin homology <!MM>
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M.; Goldfarb, I.S.; Ikemateu, H.; Burastero, S.B.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
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S78056
G. S78056
C. Species: Homo sapiens (man)
C. Species: Homo sapiens (man)
C. Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 31-Dec-2004
C. Accession: S78056; S23721
B. Harindranath, N. S. S78051
A. Reference number: S78051
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A. Reference number: S78056
A. Reference number: S78051
A. Residues: 1-100
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48.4%; Score 46; DB 2; Length 100;
Best Local Similarity 60.0%; Pred. No. 3.7;
Matches 9; Conservative 1; Mismatches 5; Indels
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48.4%; Score 46; DB 2; Length 99;
Best Local Similarity 60.0%; Pred. No. 3.7;
Matches 9; Conservative 1; Mismatches 5; Indels
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C; Superfamily: immunoglobulin homology
C; Keywords: immunoglobulin
F:19-100/Domain: immunoglobulin homology (fragment) < IMM>
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A, Reference number: $23716; MUID:92031262; PMID:1718404
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR.2004 (TrEMBLrel. 6, Last annotation update)
Anti-human Fc gamma receptor III 3G8 gamma heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=BALB/c;
PubMed=15059139; DOI=10.1111/j.1365-2141.2004.04893.x;
PubMed=15059139; DOI=10.1111/j.1365-2141.2004.04893.x;
Bruenke J., Fischer B., Barbin K., Schreiter K., Wachter Y., Mahr K., Titgemeyer F., Niederweis M., Peipp M., Zunino S.J., Repp R., Valerius T., Fey G.H.;
"A recombinant bispecific single-chain Fv antibody against HLA class II and FcgammaRIII (CD16) triggers effective lysis of lymphoma
                                                                                                                                                                                                                                           100.0%; Score 95; DB 2; Length 485; 100.0%; Pred. No. 2.4e-06; .ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 91.6%; Score 87; DB 2; Best Local Similarity 87.5%; Pred. No. 1e-05; Matches 14; Conservative 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ensembl; ENSMUSG0000057010; Mus musculus. GO; GO:0004872; F:receptor activity; IEA. InterPro; IPR007110; Ig-like. InterPro; IPR003596; Ig-v. SMART; SM00406; IGV; I... PROSITE; PS50835; IG_LIKE; 1.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF07654; C1-8et; Z.
SWART; SW00409; IG; 3.
SWART; SW00407; IGc1; 3.
SWART; SW00406; IGv; 1.
PROSITE; PS00299; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cells.";
Br. J. Haematol. 125:167-179(2004).
EMBL; AX173025; AA018227.1; -; mRNA.
HSSP; P01822; 1ANN.
SMR; Q811U5; 1-118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                             100.08;
                                                                                                                                                                                                                                                                                                                          1 HIYWDDDKRYNPSLKS 16
                                                                                                                                                                                                                                                                                                                                                69 HIYWDDDKRYNPSLKS 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 HIWWDDDKRYNPALKS 67
                                                                                                                                                                                                                                                           Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                        Q811U5 MOUSE
ID Q811U5 MOUSE PRELIMINARY;
AC Q811U5;
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O9UL96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Fragment).
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
                                                                                                                                                                                                                                             Query Match
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Q9UL96 HUMAN
ID Q9UL96 HI
AC Q9UL96;
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Matches
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XI TISSUB-Manmary tumor. WAP-TGF alpha model. 7 months old;

XI Staubberg R.L.; Feingold E.A.; Grouse L.H., Derge J.G.;

XI Staubberg R.L.; Feingold E.A.; Grouse L.H., Derge J.G.;

XI Altschul S.F.; Zeeberg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;

Altschul S.F.; Zeeberg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;

Altschul S.F.; Jordan H.; Moore T., Max S.I.; Wang J., Heich F.;

A Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;

A Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.;

A Bosak S.A.; Morley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;

XI Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;

XI Nilalon D.X.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;

XI Helton E.; Ketteman M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;

A Rahasley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;

Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.;

Butterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smailus D.E.;

Rodriguez A.C.; Grimwood J.; Schmutz J.; Marra M.A.;

                     Q55964 pongo pygma
Q5618 mattus norv
Q6038 methanococc
Q47736 plasmodium
G5ulro lactobacill
Q86890 epidinium c
Q7mzh8 photorhabdu
Q50499 brachydanio
Q43nk1 pseudomonas
Q7xy2 plasmodium
G5rdv2 pongo pygma
Q6447 motultured
Q7zwg1 brachydanio
Q57wg1 brachydanio
Q648by0 tetraodon n
Q4msy0 tetraodon n
Q4msy1 bacillus ch
Q4msy4 bacillus ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Wouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
        0876e1
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TISSUE-Mammary tumor. WAP-TGF alpha model, 7 months old;
NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases EMBL, BC093517, APH93517.1; -; mRNA.
InterPro; IPR003599; Ig. Ig. InterPro; IPR007510; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 485 AA
                                                                                                                                                            0504E9 BRARE
093NK1 PSESY
04ZT80 PSESY
07RJX5 PLAYO
05RDV2 PONPY
06Q947 GAMM
07ZWG1 BRARE
                                                                                 Q4Y736 PLACH
Q5ULRO 9CAUD
Q86S90 9CILI
Q7MZH8 PHOLL
                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                      Q4MSG4_BACCE
Q6HLK7_BACHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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10-MAY-2005 (TrEMBLrel. 30, La
10-MAY-2005 (TrEMBLrel. 30, La
LOC238447 protein (Fragment).
Name=LOC238447;
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Q561M5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
    STRAIN=Mix FVB/N;
      MOUSE
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RESULT 1

981 982 983 984 996 999 999 999 999 999 999 999

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Gaps

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HV2E HUMAN
ID HV2E HUMAN
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MEDINE-2138257; PubMed-12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
M. Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Bronstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Mulaky S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley N.A., Sedergren E.J., Lu X., Gibbs R.A.,
Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
                                                                                                      Homo sapions (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                             'Myosin-reactive autoantibodies in rheumatic carditis and normal
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0
                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.3%; Score 82; DB 2; Length 121
93.3%; Pred. No. 6.3e-05;
iive 1; Mismatches 0; Indels
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                   Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035018; AAD56254.1; -; mRNA.
HSSP; P01820; 1A7N.
SMR; Q9UL96; 1-121.
SMR; Q9UL96; 1-121.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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  Created)
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QSBE53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 IYWDDDKRYSPSLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00406; IGV; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Name=LOC544903;
                                                                                                                                                                                           NCBI_TaxID=9606;
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Local Sim
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SEQUENCE
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Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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MEDLINE=70114712; PubMed=5264153;
MIDLINE=70114712; PubMed=5264153;
MIDLINE=70114712; PubMed=5264153;
"Subgroups of amino acid sequences in the variable regions of immunoglobulin heavy chains.";
Proc. Natl. Acad. Sci. U.S.A. 64:997-1003(1969).
-!- MISCELLANEOUS: This gamma-1 chain was isolated from a myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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STRANTHEFUB/N; TISSUE=Colon;
NIH MGC Project;
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC092066; ARH92066.1; -; mRNA.
GO; GO:0003823; F:antigen binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SEQUENCE 487 AA; $2616 MW; 839E85363A764CF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A02093; G1HUHE.
                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0003823; F:immune response; NAS.
InterPro; IPR00710; Ig-like.
InterPro; IPR03596; Ig-v.
SMART; SM00406; IGv; I.
PR051TF; PS26385; IG IIKE; I.
Direct protein sequencing; Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
11-MAY-2005 (Rel. 47, Last annotation update)
1g heavy chain V-II region HE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; 1FR001597; 19-1; interPro; 1FR001597; 19-1; interPro; 1FR001506; 19-4; InterPro; 1FR001506; 19-4; Pfam; PF07654; C1-set; 2-8MART; SM00400; 1G4; 3-8MART; SM00400; 1G4; 3-8MART; SM00400; 1G4; 1-8MART; SM00400; 1-8MART; SM00400; 1-8MART; SM00400; 1-8MART; SM00400; 1-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 HIYWDDDKRYNPSLKS 16
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                                                                                                             and mouse cDNA sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Richards R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Rownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Frange C., A Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Wilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Anting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schnerch A., Schein J.B., Jones S.J.M., Marra M.A., Touchman G.M., Marra M.A., Touchman G.M., Marra M.A., Touchman J.W., Marra M.A., Touchman J.W., Waslake U., Smailus D.E., Schnerch A., Schein J.B., Jones S.J.M., Marra M.A., Touchman G.M., Marra M.A., Touchman G.M., Marra M.A., Touchman G.M., Marra M.A., Touchman G.M., Marra M.A., Touchman G.W., Marra M.A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones G.M., Marra M.A., Schein J.B., Jone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Spleen;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUES-51-6-7.

NIH MGC Project;
Submitted (ARR-2005) to the EMBL/GenBank/DDBJ databases.
REMEL; BC092586; AAH92586.1; -; mRNA.
RO; GO:0003823; F:antigen binding; IEA.
RICEPTO: IPR003599; Ig.
RICEPTO: IPR003597; Ig.-1ike.
RICEPTO: IPR003597; Ig.-1ike.
RICEPTO: IPR003597; Ig.-1ike.
RICEPTO: IPR003597; Ig.-1ike.
RICEPTO: IPR003596; Ig.-V.
RICEPTO: IPR003596; Ig.-V.
RICEPTO: IPR003596; Ig.-V.
RICEPTO: IPR00409; IG; 2.
RICEPTO: IPR00409; IG; 2.
RICEPTO: IPR00409; IG; 2.
RICEPTO: IPR00409; IG; 2.
RICEPTO: IPR03596; IGV; 1.
DR SWART; SW00409; IG ICV; 1.
DR ROSITE; PS00396; IG INW; 5943BIAFDD14C460 CRC64;
                                                                                                                                                                            Score 76; DB 1; Length 121;
Pred. No. 0.00056;
3; Mismatches 0; Indels
                                 Ig-like.
Pyrrolidone carboxylic acid.
                                                                                   121 121
121 AA; 13483 MW; 88A5082C273753B4 CRC64;
Immunoglobulin V region, Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                617 AA.
                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                               80.0%;
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                                                                                                                                                                                                                                                                                                                                2 IYWDDDKRYNPSLKS 16
                                                                                                                                             Query Match
Best Local Similarity 80.0%
The 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q56983_RAT PRELIMINARY;
056983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOC314521 protein.
Name=LOC314521;
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                              DOMAIN
MOD_RES
NON_TER
SEQUENCE
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TISSUE-Glandular pool- thyroid;

WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METAUBDERG R.L., Feligoold E.A., Grouse L.H., Derge d.G.,

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METAUBDERG R.L., Peligoold E.A., Grouse L.H., Derge d.G.,

Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MISCHOR, L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

MARA S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

Bosak S.A., McEran P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Myllalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahesley N., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

M. Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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      Length 617;
                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC092449; AAH92449.1; -; mRNA.
SEQUENCE 493 AA; 53157 MW; 5B037BEE5BSB2ADF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
      76.8%; Score 73; DB 2; 75.0%; Pred. No. 0.0092; iive 3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                 493 AA.
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                                                                                                                        1 HIYWDDDKRYNPSLKS 16
                                                                                                                                                            :||||| |||||:
71 NIWWDDDKYYNPSLKN 86
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ID Q569J1 HUMAN PRELIMINARY;
AC Q569J1;
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Query Match
Best Local Similarity 75.0
Matches 12, Conservative
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Best Local Similarity 80.0°
Matches 12; Conservative
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QSVLR6;
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGHAl protein.
Name=IGHAl;
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ID QSVLR6
AC QSVLR6
DT 01-FEB
DT 01-FEB
DE BWK3.
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SEQUENCE
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Litman G.W.; "Molecular basis for the temperature-dependent insolubility of cryoglobuling. X. The amino acid sequence of the heavy chain variable region of McE.";
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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MEDLINE-81118242; PubMed=6780622;
Gerber-Jenson B., Kazin A., Kehoe J.M., Scheffel C., Erickson B.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7. Immunol. 126:1212-1216(1981).
-!- MISCELLANEOUS: This chain was derived from a monoclonal IgM cryoimmunoglobulin.
-!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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                                                                                                                                        A Koami K., Yamakita S., Irino T., Osaka M.;

Koami K., Yamakita S., Irino T., Osaka M.;

"Cloning of a novel leukemia-related gene.";

L submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AY158661; AA017784.1; -; mRNA.

SMR; Q5VLR6; 251-460.

R G0; G0:003823; F:antigen binding; IEA.

R InterPro; IPR003199; Ig -1ike.

R InterPro; IPR003599; Ig -01.

R InterPro; IPR003599; Ig -01.

R InterPro; IPR003599; Ig -01.

R InterPro; IPR003596; Ig -01.

R SMART; SM00409; IG; 3.

R SMART; SM00409; IG; 3.

R SMART; SM00406; IG; 1.

R PROSITE; PS50835; IG LIKE; 4.

R PROSITE; PS50835; IG LIKE; 4.

R PROSITE; PS002290; IG MHC; UNKNOWN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.6%; Score 68; DB 2; Length 482; 68.8%; Pred. No. 0.044; ive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL 1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO:0005976; C:extracellular region; NAS.
GO:0003823; F:antigen binding; NAS.
GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 125 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|:|:||| |||||:
71 NIWWNDDKYYNPSLKN 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 68.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A02092; MHHUMC.
HSSP; P01820; 1A7N.
SMR; P01817; 1-125.
                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                             STRAIN=DONRYU
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P01817;
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STRAIN-FVB/N; TISSUE-Colon;

X STRAIN-FVB/N; TISSUE-Colon;

X Straubberg R.L.; Feingold E.A.; Groube L.H.; Derge J.G.;

X Klausherg R.L.; Feingold E.A.; Groube L.H.; Derge J.G.;

X Klausherg R.L.; Feingold E.A.; Groube L.H.; Derge J.G.;

X Rlausher R.D.; Colling F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;

A ltschul S.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Histeh F.;

A pokins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Histeh F.;

A paletcon M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;

Rownstein M.J.; Usdin T.B.; Toshiyuki S.; Carninci P.; Prange C.;

R Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.;

Bosak S.A.; Morley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;

Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;

X Nollalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;

R Pahey J.; Helton E.; Ketteman M.; Madan A.; Rouffard G.G.;

R Nahing M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;

R Daksley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;

R Datiguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.;

R Daterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smailus D.E.;

R Daterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smailus D.E.;

R Daterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smailus D.E.;

R Daterfield M. Schein J.E.; Jones S.J.M.; Marra M.A.;

R Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
0
                                                                                                                                                                                                                                                                                                                                                              Length 125;
                                                                                                                                                                                                                     Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH MGC Project; Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                            1 1 Pyrrolidone carboxylic ac:
125 125
125 AA; 13785 MW; 7AlADF4C40F47BB5 CRC64;
SMART; SMO0406; IGV.
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region; Pyrrolidone carboxylic acid.
DOWAIN 1 113 Pyrrolidone carboxylic acid.
NOD_RES 1 1 Pyrrolidone carboxylic ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                              68.4%; Score 65; DB 1; 73.3%; Pred. No. 0.031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   485 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, BC092065; AAH92065.1; -; mRNN.
GO, GO:0003823; F:antigen binding; IEA.
InterPro; IPR007110; Ig-like.
InterPro; IPR00359; Ig_c1.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003506; Ig_W.
Fam, PF07554; C1-8et; Z.
SMART; SM00409; IG; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 IYWDDDKRYNPSLKS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QSBES4 MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                              Query Match 68.4
Best Local Similarity 73.3
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 INWDDDNRYSPSLRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCS44903 protein.
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145 AA

PRT;

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STRAIN-3D7;
Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,
Harris B., Lennard N., Hall N., Akkin R., Chillingworth C., Doggett J.,
Ornond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL844509; CAD52342.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 145 AA; 16762 MW; 099740DB29FD5B16 CRC64;
                                                                                                  Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                  01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein MAL13P1.106.
Name=MAL13P1.106;
          Q8IEB8_PLAF7 PRELIMINARY;
                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                           NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kinase; Pyruvate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=5825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                         04XWY4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                               Press E.M., Hogg N.M.; "The amino acid sequences of the Fd fragments of two human gamma-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A02089; GIHUCO.
HSSP; P01820; 1A7N.
GO; GO: 00005576; C: extracellular region; NAS.
GO; GO: 0000953; P: antigen binding; NAS.
GO; GO: 0000855; P: immune response; NAS.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR007586; Ig-v.
SWART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein.
-!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. J. 117:641-660(1970).
-!- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 55; DB 1; Length 120;
Pred. No. 1.1;
2; Mismatches 3; Indels
                                                                     Score 62; DB 2; Length 485;
Pred. No. 0.39;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pyrrolidone carboxylic acid. N-linked (GlcNAc. . .).
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13226 MW; 158A8B29AE7EEB98 CRC64;
                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Ig heavy chain V-II region COR.
Homo saplens (Human).
                                                                                                                                                                                                                 120 AA.
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                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=70258837; PubMed=5449120;
                                                                      / Match 65.3%;
Local Similarity 62.5%;
hes 10; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.9%;
66.7%;
                                                                                                                        1 HIYWDDDKRYNPSLKS 16
                                                                                                                                       2 IYWDDDKRYNPSLKS 16
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Best Local Similarity 66.70,
Best Local 10; Conservative
                                                                                                                                                                                                                STANDARD;
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94
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22
120
120 AA,
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                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                          heavy chains.";
                                                                                                                                                                                                                HV2B HUMAN P01815;
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NON TER
SEQUENCE
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Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
James K., Rutherford K., Harris B., Harris D., Churcher C.,
Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
Bldwell S.L., Rajandream M.A., Carucci D.J. Yates J.R., Kafatos F.C.,
Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,
"A comprehensive survey of the Plasmodium life cycle by genomic,
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transcriptomic, and proteomic analyses.";
Science 307:82-86(2005).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium chabaudi.
Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium
Score 51; DB 2; Length 145;
Pred. No. 5.9;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 51; DB 2; Length 357; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                        13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Phosphoenolpyruvate carboxykinase, putative (Fragment).
ORFNames=PC001162.02.0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     357 AA; 40167 MW; E58913F2A8FAEF0F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preliminary data.
EMBL; CAAJ01002543; CAH78577.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 AA.
                                                                                                                                                                                                                                                                                               357 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 315 HIGWDNKEDYNASLKT 330
  53.7%;
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56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 HIYWDDDKRYNPSLKS 16
                                                                                                                                                                                                                                                                                            Q4XWY4_PLACH PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q86SX2 HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 56.2
Matches 9; Conservative
                                                      8; Conservative
                                                                                                         3 YWDDDKRYNPSL 14
                                                                                                                                          25 YLDDDNRYNPTM 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
Q86SX2 HUMAN
ID Q\overline{0}6SX2 HI
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53 IDWDDDKYYNTSLET 67

RESULT 12 Q8IEB8\_PLAF7

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Last sequence update)
Last annotation update)
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llarity 56.2%; Pred. No. 8;
Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-AUG-1987 (Rel. 05, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
1g heavy chain V-II region SESS precursor.
Homo sapiens (Human).
             97 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 AA
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HSSP; P01820; 1G7I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   not related to HLA DRB1*0401.";
Mol. Immunol. 0:0-0(1997).
EMBL; AF035802; AAB88534.1; -; mRNA.
SMR; O43234; 1-96.
ENBEMB; ENSG00000196662; Homo sapiens.
                                                                                                   01-JUN-1998 (TrEMBLrel. 06, Last seq
01-0C0T-2003 (TrEMBLrel. 25, Last ann
Rheumatoid factor RF-ET13 (Fragment)
Homo sapiens (Human).
         PRT;
                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=84298107; PubMed=6089186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR007110; Ig-1ike.
InterPro; IPR003596; Ig_v.
SWART; SW00406; IGv; 1.
NON TER 1 1
NON TER 97 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-1987 (Rel. 05, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SO HIPANDEKSYSTSLKS 65
                                                                  01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 HIYWDDDKRYNPSLKS
         043234_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
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tes 9; Conserv
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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P04438;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches
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01-0708-2003 (TrEMBLrel. 24, Created)
01-0708-2004 (TrEMBLrel. 24, Last sequence update)
01-0708-2004 (TrEMBLrel. 26, Last sequence update)
01-0708-2004 (TrEMBLrel. 26, Last annotation update)
Pull-length cDNA clone CSOBD10047M19 of B cells (Ramos cell line) of Homo sapiens (Human) (Fragment).
Homo sapiens (Human) (Fragment).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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53.8%; Pred. No. 51;
iive 3; Mismatches 3; Indels
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Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX248300; CAD62627.1; -; mRNA.
HSPP; P01820; 1G7J.
SMR; Q86SX2; 33-129.
Ensembl; ENSG00000130076; Homo sapiens.
InterPro; IPR001110; Ig-like.
InterPro; IPR001110; Ig-like.
SMART; SM04406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=B cells;
Li W.B., Gruber C., Jessee J., Polayes D.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
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Viruses; deDNA viruses, no RNA stage; Caudovirales.
VGBI_TaxID=310539;
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484 WDDDRHYNDDVRS 496
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Q5G7N6;
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Best Local Similarity 53.8
Matches 7; Conservative
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Best Local Similarity
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RESULT 16

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not ö nouso agricus, indumann. Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae, Borretzen M., Natvig J.B., Thompson K.M.; "Heterogenous RP structures between and within healthy individuals are Takahashi N., Noma T., Honjo T.; "Rearranged immunoglobulin heavy chain variable region (VH) pseudogene that deletes the second complementarity-determining region."; Proc. Natl. Acad. Sci. U.S.A. 81:5194-5198(1984). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae, Gaps ö Length 97; Indels 97 AA; 10748 MW; DDCOBF47B9AA812D CRC64; GO; GO:0005576; C:extracellular region; NAS. GO; GO:0003823; F:antigen binding; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; IG-11ke. InterPro; IPR003596; IG\_V. 

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Pfam; PF00561; Abhydrolage 1; 1
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Neopera; Endoprerygota, Diptera; Nematocera; Culicoidea; Culicidae;
Anophelinae; Anopheles.
NCBI_TaxID=7165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ranson H., Nikou D.;

"Cytochrome P4508 from the malaria vector, Anopheles gambiae.";

"Cytochrome P4508 from the malaria vector, Anopheles gambiae.";

Submitted (SEP-2004) to the EMBL/GenBank/DDBU databases.

"C. - SIMILARITY: Belongs to the cytochrome P450 family.

EMBL; AV145209; AAU93476.1; -; mRNA.

GO; GO:0004497; F:metal ion binding; IEA.

R GO; GO:0004497; F:metal ion binding; IEA.

R GO; GO:0004497; F:metal ion binding; IEA.

R GO; GO:000418; P:electron transport; IEA.

R InterPro; IPR0012401; EP4501.

R Pfam; PF00067; P450; 1.

R PRINTS; PR00463; EP4501.

R PRINTS; PR00463; EP4501.

R PRINTS; PR00463; EP4501.

R PRINTS; PR00463; P450.

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C SEQÜENCE 167 AA; 19140 MW; 38415B74D793A4A7 CRC64;
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                                                                             Ig heavy chain V-II region SESS. V segment.
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05JEL9_10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
ABC-type phosphate transport system, periplasmic component.
OrderedLocusNames=TK1864;
                                                                                                                                                                                                                           51.6%; Score 49; DB 1; Length 147;
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                                                                                                                                                                                                                                                                   4; Indels
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SMART; SM04406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin domain; Immunoglobulin V region; Signal.
SIGNAL
                                                                         20 147 Ig heavy chain V-II region 20 118 V segment. 119 132 D segment. 131 147 147 147 AA; 16323 MW; FCBCDB3D00FB6666 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
CST-OCM-COMP P450 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anopheles gambiae (African malaria mosquito)
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2; Mismatches
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Best Local Similarity 60...
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QSXNU6;
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YWSEPKRFNPS 83
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STRAIN=CBS 2159 / IFO 1267 / NRRL Y-1140 / WM37;

PUDOM B., Sherman D., Fischer G., Durrens P., Casaregola S.,

Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,

Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,

Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,

Boisrame A., Roszul R., Lemaire M., Lesur I., Ma L., Muller H.,

Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,

Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,

Nellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,

Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,

Zeniou-Meyer M., Zivanovic Y., Bolotin-Pukuhara M., Thierry A.,

Micher P., Souciet J.-L.,

Micher C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,

Micher P., Souciet J.-L.,

Micher P., Weisenbach J.,

Micher P., Souciet J.-L.,

Micher P., Weisenbach J.,

Micher P., Souciet J.-L.,

Micher P., Weisenbach J.,

Micher P., Weisenbach J.,

Micher P., Souciet J.-L.,

Micher P., Weisenbach J.,

Micher P., Weisenbach J.,

Micher P., Souciet J.-L.,

Micher P., Souciet J., J.,

yrococcus kodakaraensis (Thermococcus kodakaraensis).
Archaea, Euryarchaeota, Thermococci; Thermococcales, Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                           STRAIN=KOD1;
PubMed=15710748; DOI=10.1101/gr.3003105;
Fukui T., Atomi H., Kanai T., Matsumi R., Fujiwara S., Imanaka T.;
"Complete genome sequence of the hyperthermophilic archaeon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to spl P53264 Saccharomyces cerevisiae YGRIIOw singleton.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Res. 15:352-363 (2005).

EMBL, AP006878; BAD86053.1; -; Genomic DNA.

GO; GO:0005315; F:inorganic phosphate transporter activity; IEA.

GO; GO:0015114; F:phosphate transporter activity; IEA.

GO; GO:0005215; F:transporter activity; IEA.

GO; GO:0006817; P:phosphate transport; IEA.

GO; GO:0006817; P:phosphate transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermococcus kodakaraensis KOD1 and comparison with Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.6%; Score 49; DB 2; Length 383; 69.2%; Pred. No. 34; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    383 AA; 41427 MW; 9C1DAA349C7EC179 CRC64;
                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    426 AA
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EMBL; CR382122; CAH02499.1; -; Genomic_DNA.
GO; GO:0003824; P:catalytic activity; IEA.
InterPro; IPR000073; A/b hydrolase.
InterPro; IPR000073; Ser_estrs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR005673; Peri-phosph.
InterPro; IPR006059; SBP bac_1.
Pfam; PP01547; SBP_bac_1; 1.
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OCCVD3;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Klauener R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buttow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                     Anopheles gambiae str. PEST.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelinae; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                  The Anopheles gambiae Sequence Committee;

The Anopheles gambiae Sequence Committee;

Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.

-I-CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

-I-SIMILARITY: Belongs to the cytochrome P450 family. REMBL; AABD01008811; EAL41693.1; -; Genomic_DNA.

R GO; GO:0004697; F:metal ion binding; IEA.

R GO; GO:0004497; F:metal ion binding; IEA.

R GO; GO:0004497; F:monooxygenase activity; IEA.

R GO; GO:0004497; F:metal ion binding; IEA.

R InterPro; IPR001128; Cytochrome_P450.

R InterPro; IPR002401; EP4501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                               The Anopheles gambiae Sequence Committee;
"Anopheles gambiae re-annotation.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.6%; Score 49; DB 2;
63.6%; Pred. No. 44;
iive 2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                    ORFNames=ENSANGG00000004170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00067; p450; 1.
PRINTS; PR00463; EP4501.
PRINTS; PR00465; EP4501V.
PRINTS; PR00385; P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGGMX1 HUMAN PRELIMINARY;
QGGMX1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
TISSUE=Spleen;
                                                                                                                                              NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                         STRAIN=PEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 23
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelinae; Anopheles.
NCBI_TaxID=180454;
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                                                        2; Length 426;
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PRINTS; PR00465; EP4501V.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME P450; UNKNOWN 1.
Heme; Iron; Metal-binding; Monooxygenase; Öxidoreductase.
NON TER 462 462
                                                                                         4; Indels
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                    49040 MW; 8529866FE5286586 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                462 AA; 53171 MW; 5677B1D7CC28CA27 CRC64;
                                                                                                                                                                                                                                                                                    01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ENSANGRO0000005415 (Fragment)
ORFNames=ENSANGG000004170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
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EMBL; AARAB1008BII.; EAA04974.2; -; Genomic_DNA.
GO; GO:0004497; F:monooxygenase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR001128; Cytcchrome_P450.
InterPro; IPR002401; EP4501V.
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                                                    51.6%; Score 49; DB 46.7%; Pred. No. 38; ive 4; Mismatches
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Anopheles gambiae Sequence Committee;
                                                                                                                                                                                                                                                    PRT;
                                                                                                                                               |:|||:| :| |:
408 HLYWDNDSFFNNVLR 422
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01-FEB-2005 (TYEMBLYEL 29,
01-FEB-2005 (TYEMBLYEL 29,
01-FEB-2005 (TYEMBLYEL) 29,
                                                                                                                         1 HIYWDDDKRYNPSLK 15
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                                 Ouery Match
Best Local Similarity 46.77
Triconservative
                                                                                                                                                                                                                                                 Q7QHX0 ANOGA PRELIMINARY;
Q7QHX0;
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                    426 AA;
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Les 7; Conserv
Complete proteome.
SEQUENCE 426 AA
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Best Loc Matches

ठ 셤 RESULT 22 QSTW91\_ANC

44444

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Gaps

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Score 48; DB 2; Length 549; Pred. No. 71; 3; Mismatches 2; Indels

50.5%;

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549 AA; 61796 MW; 780AA922BED46F0A CRC64;
              P:response to copper ion; IEA.
                                                                                                                                                                     Query Match
Beet Local Similarity 58.33,
7; Conservative
         GO; GO:0046688; P:response
InterPro; IPR007348; CopC.
InterPro; IPR008457; CopD.
                                                                                                                                                                                                                                                                                                                   330 HMYWDMIKRFSP 341
                                                                                                                                                                                                                                                                                         1 HIYWDDDKRYNP 12
                                                                            Pfam; PF04234; CopC;
Pfam; PF05425; CopD;
Complete proteome.
SEQUENCE 549 AA; 6
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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A.Y. Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Shevchenko Y., Souffard G.G., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
Chu L., Mazur M., Golteman B., Larsen N., D'Souza M., Walumas T.,
Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
Overbeek R., Kyrpides N.C.;
Genome sequence of Bacillus cereus and comparative analysis with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
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                                                                                                                                                                                                                                                                                                                             TISSUE-Spleen;
Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL: BC073773; AAH73773.1; -; mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDB9D CRC64;
                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AE017003, AAP08812.1, -; Genomic_DNA. GO; GO:0019866; C:inner membrane; IEA. GO; GO:0016021; C:innegral to membrane; IEA. GO; GO:0042597; C:periplasmic space; IEA. GO; GO:0005507; F:copper ion binding; IEA. GO; GO:0006878; P:copper ion homeostasis; IEA. GO; GO:0006878; P:copper ion homeostasis; IEA. GO; GO:0006825; P:copper ion transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  549 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001359; IG.
InterPro; IPR007110; IG-11ke.
InterPro; IPR007110; IG-11ke.
InterPro; IPR003597; IG_C1.
InterPro; IPR003595; IG_C1.
InterPro; IPR003595; IG_V.
Fam; PF07654; C1-set; 3.
SWART; SW00409; IG; 2.
SWART; SW00406; IG; 2.
PR0SITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNRNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 HIYWDDDKRYNPSLKS 16
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                                                                                                                                                                                                                                    and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copper resistance protein. OrderedLocusNames=BC1838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :||:
71 YIYYSGSTYYNPSLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QBIEX3_BACCR PRELIMINARY;
Q81EX3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 56.2
1es 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus cereus group.
NCBI_TaxID=226900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 423:87-91(2003)
                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
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081EXZ BAC
10081EXZ BAC
1001-JU
DT 01-JU
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                                                                                                                                                glutamine permease.
OrderediocusNames=DEHAOGO5632g;
OrderediocusNames=DEHAOGO5632g;
Debaryomyces hansenii (Yeast) (Torulaspora hansenii).
Bukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomyceteles; Saccharomycetescee; Debaryomyces.
                                                                             25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to CA1373|CaAGP1 Candida albicans CaAGP1 asparagine and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.5%; Score 48; DB 2; Length 572; 50.0%; Pred. No. 74; 3; Indels iive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00124; AA_Dermease; 1.
TIGREAMS; TIGR00913; 2A0310; 1.
PROSITE; PS00218; AMINO_ACID_PERMEASE 1; 1.
COMPLETE STOCKTORNE; Transmembrane; Transport.
SEQUENCE 572 AA; 63267 NW; 6557C233AC08CF33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; CR382139; CAG90220.1; -; Genomic_DNA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0015020; C:membrane; IEA.
GO; GO:0015359; F:amino acid permease activity; IEA.
GO; GO:0006865; P:amino acid transport; IEA.
GO; GO:0006810; P:transport; IEA.
                                           572 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002293; AA/rel permeasel.
InterPro; IPR004840; AAC permease.
InterPro; IPR004841; Permease region.
InterPro; IPR004762; Yeast AA perm.
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Best Local Similarity 50.00,
Best Local Similarity 50.00,
RESULT 25
QGBJSB DEBHA
ID QGBJSB_DEBHA PRELIMINARY;
AC QGBJSB;
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Gaps

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Indels

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RESULT 26

GGLZD6 MET

10 GGLZD6

AC GGLZD6

AC GGLZD6

DT 05-JU

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MEDLINE=22373777; PubMed=12447439; DOI=10.1038/nature01183; Peng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J., Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y., Weng Q., Zhang L., Lu Y., Wu J., Lu Y., Zhang L., Su Z., Fan D., Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J., Wu W., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H., Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y., Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang Y., Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W., Hu D., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y., Hu B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
InterPro; IPR000719; Prot kinase.
InterPro; IPR000279; Ser Lhr pkin AS.
InterPro; IPR002290; Ser Lhr pkin AS.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR001245; Tyr pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence and analysis of rice chromosome 4.";
Nature 420:1316.320(2002).
-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; ALG06684; CAE03570.2; -; Genomic_DNA.
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SMART; SM00220; Trc; 1.

SMART; SM00219; Trrc; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00108; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; UNKNOWN 1.

ATP-binding; Kinase; Nucleotide-binding; Serine-protein kinase; Transferase.

SEQUENCE 778 AA; 84453 MW; 7A76578AAE91338B CRC64;
                                                                                                                                                                                                                                                                                                                                              01-OCT-2003 (TrEMBLrel. 25, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
OSJNBA0065110.15 protein.
Name=OSJNBA0065110.15;
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                                                                                                                                                                                                                                                                                        778 AA
      Mismatches
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207 WDDDEEFDPTTRS 219
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ID Q7XPL1_ORYSA PRELIMINARY;
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ID 099JUO MOUSE PRELIMINARY;
AC 099JUO;
                                                                  4 WDDDKRYNPSLKS 16
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      Conservative
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Best Local Similarity
8; Conserve
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   Matches
                                                                                                                                                                                                                            RESULT 28
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X PubMed=15466049; DOI=10.1128/JB.186.20.6956-6969.2004;

A Handrickson E.L., Kaul R., Shou Y., Bovee D., Chapman P., Chung J., Comway de Macario E., Dodsworth J.A., Gillett W., Graham D.E., W. Hackett M., Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J., M. Andjor T.A., Moore B.C., Porat I., Palmeiri A., Rouse G., Saenphimmachak C., Soell D., Van Dien S., Wang T., Whitman W.B., A. Aria Q., Zhang Y., Larimer F.W., Olson M.V., Leigh J.A.; R. "Complete genome sequence of the genetically tractable R. Tydrogenotrophic methanogen Methanococcus maripaludis."; R. Mydrogenotrophic methanogen Methanococcus maripaludis."; DR EMBL; BAS97220; CAF2049.1, -; Genomic_DNA.

DR GO: GO:0004812; F:ENNA ligase activity; IEA.

KW Aminoacyl-tRNA synthetase; Complete proteome; Signal.

FIGNAL 1. 20. PARCANA CROKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis briggsae.
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The C.briggsae Sequencing Consortium;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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EMBL: CARCO1000012; CASS9024.1; -; Genomic_DNA.

Inter: PTRR010733; DUF1308.

PANTHER; PTRR13379; DUF1308; 1.

Pfam; PF07000; DUF1308; 1.

Hypothetical protein.

SEQUENCE 400 AA; 45670 MW; 9AFD1B91C98A3D2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    Archaea; Buryarchaeota; Methanococci; Methanococcales;
                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Aminoacyl-tRNA synthetase, class II precursor.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein CBG02301.
                                                                                                                                                             288 AA
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                                                                                                                                                             PRT;
                                                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 HIYWDDDK-RYNPSLKS 16
                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                              OrderedLocusNames=MMP0693;
Methanococcus maripaludis.
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                                                                                                                                                  QELZD6 METMP PRELIMINARY;
QELZD6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 52.9
170 YWDQNTKYNPDI 181
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CAEBR

Matches

ઠે a RESULT 27
G0621X9
CAE
ID Q0621X
AC Q0621X
AC Q0621X
DT 25-0C
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NUCLEOTIDE SEQUENCE.
                                             NCBI_TaxID=10090;
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  STRAIN-EVUBNI, TISSUE-Mammary tumor. C3;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Straubberg R.L., Feingold E.A., Grouee L.H., Derge J.G.,
Altsuberg R.L., Zeeberg B., Magner L., Shemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
B Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Robers S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman U.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
T "Generation and initial analysis of more than 15,000 full-length human
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                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 46, Last sequence update)
13-SEP-2005 (Rel. 46, Last annotation update)
Ribosomal protein S6 kinase beta 2 (EC 2.7.1.37) (S6K-beta 2) (70 kDa ribosomal protein S6 kinase beta 2) (70-S6KB) (p70 ribosomal S6 kinase beta)
Name-Rps6kb2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI, MGII192743; Rps6kb2.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

GO; GO:000468; P:protein serine/threonine kinase activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR000961; Pkinase.

Pfan; PF00433; Pkinase.

ProDom; PD000001; Prot kinase; 1.

SNART; SM00133; S. TK.X; 1.

Nucleotide-binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.; Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC005694; AAH05694.1; -; mRNA. MGI:1927343; Rps6kb2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 AA; 22968 MW; 228A8B586D7AE30B CRC64;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       || ||| || || 53 HINWDDLLARRVDPPFRPSLQS 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences."
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                                                                                                                Muridae; Murinae; Mus.
                                                                     (Mouse)
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Best Local Similarity
                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                            NCBI TaxID=10090;
                                         Rps6kb2 protein.
                                                        Name=Ros6kb2:
                                                                        Mus musculus
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Designation of the project, Metacase, Concludes, Craintes, Norder, Scharles, Memmahis, Butherlay, Burthordrogizee, Giltres, Rodentia, Sciurognathi, Merchaforines, States, Sta
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Neisseriaceae; Neisseria.
                          NCBI_TaxID=242231;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polerovirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Human rectum tumor;

Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

R SDM J. Memann S.,

R BMBL; BX538077; CAD98001.1; -; mRNA.

R SNR; PO1820; 1G74.

R SNR; PRO31010; 1G-11ke.

R InterPro; IPR0013006; 1G-MHC.

R InterPro; IPR001596; 1G-MHC.

R InterPro; IPR001596; 1G-MHC.

R Pfam; PR07654; C1-set; 2.
                                                                                                                                                                                                                    Gaps
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Putative UDP-N-acetylmuramyl-tripeptide synthetase (EC 6.3.2.13).
OrderedLocusNames-NGO1541;
Neisseria gonorrhoeae (strain ATCC 700825 / PA 1090).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
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                                                                                       Proton acceptor (By similarity).
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53.3%; Pred. No. 1.3e+02;
tive 5; Mismatches 2; Indels
                                                                                                                                                                         Length 485;
                                                                                                                                                                                                                  4; Indels
                                                                                                           99 ATP (By similarity).
53538 MW; 396929ADABOF6CB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Hypothetical protein DKFZp686C02218 (Fragment).
                    Protein kinase.
ATP (By similarity).
Pro-rich.
                                                                                                                                                                       48.4%; Score 46; DB 1; 1
45.5%; Pred. No. 1.3e+02;
tive 2; Mismatches 4,
Serine/threonine-protein kinase; Transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2003 (TrEMBLrel. 25, Created)
                                                                                                                                                                                                                                                                                     330 HINWDDLLARRVDPPFRPSLQS 351
                                                                                                                                                                                                                                                          1 HIYWDD-----DKRYNPSLKS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 IYWDDDKRYNPSLKS 16
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84 IYYNENTYYSPSLKS 98
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Best Local Similarity 53.3.
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QSF6LO;
                                                                                                                                                                   Query Match
Best Local Similarity 45.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             Q72374 HUMAN PRELIMINARY;
                                          81
485
194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                             485 AA;
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                      DOMAIN
NP BIND
COMPBIAS
ACT SITE
BINDING
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O72374

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DE BUKAX

OCC BUKAX

OCC BUKAX

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             NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

Lewis L.A., Gillaspy A.F., McLaughlin R.E., Gipson M., Ducey T.F.,

Lewis L.A., Gillaspy A.F., McLaughlin R.E., Gipson M., Ducey T.F.,

Song L., Lin S., Yuan X., Najar E., Zhan M., Ren Q., Zhu H., Qi S.,

Kenton S.M., Lai H., White J.D., Clifton S., Roe B.A., Dyer D.W.;

"The complete genome sequence of Neisseria gonorrhoeae.";

Submitted (NAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AR004969; AAW90177.1; -; Genomic_DNA.

GO; GO:0006765; F:UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-. ..; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20318675; PubMed=10859394; Smith G.R., Borg Z., Lockhart B.E.L., Braithwaite K.S., Gibbs M.J.; Smith G.R., Borg Z., Lockhart B.E.L., Braithwaite K.S., Gibbs M.J.; Sugarcane yellow leaf virus: a novel member of the Luteoviridae that probably arose by inter-species recombination."; Gen. Virol. 81:1865-1869(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein (Fragment).
Sugarcane yellow leaf virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.4%; Score 46; DB 2; Length 492
50.0%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Borg Z., Braithwaite K.S., Smith G.R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ491131; CAD36539.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        492 AA; 53010 MW; 9EDOCF2865C86A20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  524 AA; 58837 MW; 89372CE19C0DB394 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.4%; Score 46; DB 2; I 63.6%; Pred. No. 1.4e+02; tive 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     524 AA
                                                                                                                                                                                                                                                              InterPro; IPRO0516; MurE.
InterPro; IPR004101; Mur ligase_C.
InterPro; IPR004101; Mur ligase_C.
InterPro; IPR0012137; UDP-NACM_Alig.
Pfam; PF01225; Mur ligase; 1.
Pfam; PF02875; Mur ligase_C; 1.
PIRSF; PIRSF001562; UDP-NACM_Alig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ::[||| |: || |
64 VFWDDDGRFAWNPEWK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome; Ligase. SEQUENCE 492 AA; 53010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q7T6H2_9LUTE PRELIMINARY;
Q7T6H2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Best Local Similarity
8; Conserve
[1]
NUCLEOTIDE SEQUENCE
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Q70417 9LUTE PRELIMINARY,
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Q704KS;
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Best Local Similarity 63.6
Matches 7; Conservative
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Rassaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X., Smith G., Rott P.;
Smith G., Rott P.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ621181; CAF18407.1; -; Genomic_DNA.
Interpro; IRPR00382; Peptidase_S39B.
Pfan; PF02122; Luteo ORF2;
PRINTS; PR00913; LVIRUSORF2.
NOW PRINTS; PR00913; LVIRUSORF2.
NOW TER
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Smith G., Rott P.;
Submitted (NOV-03) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ621182; CAF18410.1; -; Genomic_DNA.
InterPro; IPR000382; Peptidase_S39B.
Pfam, PF02122; Luteo_ORF2; 1.
Hypothetical protein.
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                                                                                                                            0704G6;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein (Fragment).
Sugarcane yellow leaf virus.
Viruses; seRNA positive-strand viruses, no DNA stage; Luteoviridae;
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Sugarcane yellow leaf virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
Polerovirus.
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48.4%; Score 46; DB 2; Length 525;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 525 AA; 58860 MW; D4AEC9C9A2F086E7 CRC64;
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                                                                                             525 AA.
                                                                                    PRT;
                                                                                    Q704G6_9LUTE PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                            TISSUE-Leaf;
Rassaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X., Smith G., Rott P.;
Smith G., Rott P.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ621175; CAF18386.1; -; Genomic_DNA.
EMBL, AJ621175; CAF18386.1; -; Genomic_DNA.
EMBL, AJ621275; Luteo ORF2; 1.
PRINTS; PR00913; LUTEO ORF2; 1.
Hypothetical protein.
Hypothetical protein.
NON_TER 5.25
SEQÜENCE 5.25 AA; 58746 MW; DC638C04B08714B3 CRC64;
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Rassaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X., Smith G., Rott P.;

Smith G., Rott P.;

Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AJ621169; CAF18368.1; -; Genomic_DNA.

InterPro; IFR000382; Peptidase_S39B.

PFam, PF02122; Luteo ORF2; 1.

PRINTS; PR00913; LUTEUSORF2.

Hypothetical protein.

NON_TER 1 1

NON_TER 525 S25

SEQÜENCE 525 AA; 58642 MW; 0D8933C444B23F3D CRC64;
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                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein (Fragment).
Sugarcane yellow leaf virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
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Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
Polerovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 525;
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Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels
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05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein (Fragment)
525 AA
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RESULT 38

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TISSUE-Leaf;
Rassby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X., Smith G., Rott P.,
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ621162; CAF18347.1; -; Genomic_DNA.
InterPro; IPR00382; Peptidase_S39B.
Pfam; PF02122; Luteo_CRF2; 1.
                                                                                                                                                                                                                                                                                                                             TISSUBLEATE,
Rassaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X.,
Smith G., Rott P.,
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AJG21161, CAF18344.1; -; Genomic_DNA.
InterPro; IPR000382; Peptidase_S39B.
Fram; PF02122; Luteo_ORF2; 1.
PRINTS; PR0913; LVIRUSORF2.
Capaid protein; Hypothetical protein; Structural protein.
                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Sugarcane yellow leaf (Fragment).
Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein (Fragment).
Sugarcane yellow leaf virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 525;
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Capsid protein; Hypothetical protein; Structural protein.
NON TER 1 1 1 NON TER 525 525
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48.4%; Score 46; DB 2; Length 525
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels
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63.6%; Pred. No. 1.4e+02;
ive 1; Mismatches 3; Indels
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  525 AA.
PRT;
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Q704M6;
Q704M9_9LUTE PRELIMINARY;
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Matches 7; Conservative
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                                                                                                                                                                                                                                                       NCBI_TaxID=94290;
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Q704M3 9LU
ID Q704M
  DE REPORTED DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DEL PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DEL PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DE LA PROPERTO DEL PROPERTO DEL PROPERTO DE LA PROPERTO DE LA PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO DEL PROPERTO 
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EMBL, AJ621160; CAF18341.1; -; Genomic_DNA.

InterPro; IPR000382; Peptidase_S19B.

Pfam, PF02122; Lutec_ORF2; 1.

Capsid protein; Hypothetical protein; Structural protein.
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                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein (Fragment).
Sugarcane yellow leaf virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein (Fragment).
Sugarcane yellow leaf virus.
Viruses; sskNA positive-strand viruses, no DNA stage; Luteoviridae;
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Pred. No. 1.4e+02;
1; Mismatches 3; Indels
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525 AA; 59015 MW; E3B3E6BA686152B6 CRC64;
                          525 A.A.
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                          PRT;
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Q704N5 9LUTE PRELIMINARY;
Q704N5;
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Best Local Similarity 63.6'
Tr Conservative
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Q704N2_9LUTE PRELIMINARY;
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Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                             TISSUE=Leaf;
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NON TER
SEQUENCE
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Q704M9_9LUTE
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ઠે В RESULT 39
CO 704N2
DI 07704N
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NUCLEOTIDE SEQUENCE.

TISSUE-Leaf;
Rassaby L., Royr M., Borg Z., Braithwaite K., Mirkov E., Perrier X., Smith G., Rott P.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ621165; CAPIS156_11; -; Genomic_DNA.
InterPro; IPR000382; Peptidase_S19B.
Fram; PP02122; Luteo ORP2; 1.
PRINTS; PR00913; LVIRUSORP2.
Capsid_protein; Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ621166; CART8359-1; -; Genomic_DNA.
InterPro; IPR000382; Peptidase_S39B.
PRINTS; PR00913; IVTENSORE2.
Capsid protein; Hypothetical protein; Structural protein.
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
14-Ypothetical protein (Tremandament).
Sugarcane yellow leaf virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein (Fragment).
Sugarcane yellow leaf virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                            48.4%; Score 46; DB 2; Length 525; 63.6%; Pred. No. 1.4e+02; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 525;
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525 AA; 58820 MW; 1F51DC03A8DB2F40 CRC64;
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525 AA; 58848 MW; C3BAC1B90BA2F0E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.4%; Score 46; DB 2; I 63.6%; Pred. No. 1.4e+02;
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Q70411 91UTE
D Q70411 91UTE PRELIMINARY; PRT;
AC Q704111;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
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Q704L4;
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Best Local Similarity 63.0
Tr Conservative
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                                                                                                                              NCBI_TaxID=94290;
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                                                                                                               Polerovirus
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SEQUENCE
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Rassaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X., Smith G., Rott P., Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ621163; CAF18350.1; -; Genomic_DNA.
InterPro; IPR000382; Peptidase_S39B.
Pfam; PF02122; Luteo_ORF2; 1.
PRINTS; PR00913; LVIRUSORF2.
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Rassaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X., Smith G., Rotte P.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ621164; CAF18353.1; -; Genomic_DNA.
InterPro; IPR000382; Pepridase_S39B.
Pfam; PF02122; Luteo_ORF2; 1.
PRINTS; PR00913; Luteo_ORF2; 1.
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                                                               Hypothetical protein (Fragment).
Sugarcane yellow leaf virus.
Viruses; BSRNA positive-strand viruses, no DNA stage; Luteoviridae;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein (Fragment).
Sugarcane yellow leaf virus.
Viruses; seRNA positive-strand viruses, no DNA stage, Luteoviridae,
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525 AA; 58789 MW; E12E4FADE48A1A34 CRC64;
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               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Pred. No. 1.4e+02;
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Q704M0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 63.6
nes 7; Conservative
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Matches 7; Conservative
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                                                                                                                                               NCBI_TaxID=94290;
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                                                                                                                            Polerovirus
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RESULT 43
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RESULT 44 Q704L7 9LU ID Q704L AC Q704L

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Gaps

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TISSUE-Leaf;
Rassaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X., Smith G., Rott P.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ621171; CAF18374.1; -; Genomic_DNA.
InterPro; IPR000382; Peptidase_S39B.
Pfam; PF02122; Luteo ORP2;
PRINTS; PR00913; LVIRUSORP2.
Capsid protein; Hypothetical protein, Structural protein.
                                                                                                                                                                                                                                             TISSUE-Leaf;
Rassaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X., Smith G., Rott P., Suth P., Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ621170, CAF18371.1; -; Genomic_DNA.
Interpro, IPR000392; Peptidase_S39B.
Pfam; PF02122; Luteo_ORF2; 1.
PRINTS; PR00913; LVIRUSORF2.
Capsid protein; Mypochetical protein; Structural protein.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein (Fragment).
Sugarcane yellow leaf virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
                                                                                                Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 525;
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63.6%; Pred. No. 1.4e+02;
tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        525
58889 MW; 46231937027492AG CRC64;
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525 AA; 58846 MW; E774B1B7C83B4699 CRC64;
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Last sequence update)
Last annotation update)
   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                   Hypothetical protein (Fragment). Sugarcane yellow leaf virus.
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Q704J9;
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0704J6_9LUTE PRELIMINARY;
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Q704J6_9LU
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                                                                                                                                                                                                                                                                    TISSUE=Leaf;
Rassaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X., Smith G., Rott P.;
Submitted G., Rott P.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ621167; CAP18362.1; -; Genomic_DNA.
InterPro; IPR000382; Peptidase_S39B.
Ffam; PF02122; Luteo ORF2; 1.
PRINTS; PR001913; LVIEUSORF2.
Capsid protein; Hypothetical protein; Structural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Leaf;
Rassaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X.,
Smith G., Rott P.,
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
BMBL, AJ621168; CAF18365.1; -; Genomic_DNA.
InterPro; IPR000382; Peptidase_339B.
Pfam; PP02122; Luteo ORP?;
PRINTS; PR00913; LVIRUSORP2.
Capsid protein; Hypothetical protein.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein (Fragment).
Hypothetical protein (Fragment).
Varancane yallow leaf virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
                                                                                                                          Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
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63.6%; Pred. No. 1.4e+02;
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525 AA; 58817 MW; E612C70F75A29AA9 CRC64;
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525 AA; 58823 MW; EB9CB74C9FA4B6AC CRC64;
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
65-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein (Fragment)
Sugarcane yellow leaf virus.
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05-JUL-2004 (TrEMBLrel. 27, Last Sequence update)
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63.6%; Pred. No. 1.4e+02;
iive 1; Mismatches 3;
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Q704K2;
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NCBI_TaxID=94290;
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VI TISSUE-Leaf;

A Rassaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X.,

Smith G., Rott P.;

Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.

La Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.

R EMBL; AJ621172; CAP18377.1; -; Genomic_DNA.

R InterPro; IPR000382; Peptidase_S19B.

PRINTS; PR00913; LVIRUSORF2.

R Capsid protein; Hypothetical protein; Structural protein.

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PT NON_TER 525

SSC SEQUENCE 525 AA; S8721 MW; 70943818E8BD7875 CRC64;
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Hypothetical protein (Fragment).
Sugarcane yellow leaf virus.
Viruses; BSRNA positive-strand viruses, no DNA stage; Luteoviridae;
Polerovirus.
NCBI_TAXID=94290;
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March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   March   Marc	scFV \ Random Human Secret BoNT/P BoNT/P Anti-t Non-na Human KPI (-4	Aay68092 Kunitz pr Aay68135 Kunitz pr Aay68068 Kunitz pr Aay68073 Kunitz pr Aay68085 Kunitz pr Aay68134 Kunitz pr Aay68132 Kunitz pr Aau09242 Human KPI Aau09248 Human KPI Aau09259 Human KPI Aau09259 Human KPI Aau09259 Human KPI Aau09259 Human KPI Aau09295 Human KPI	Adulto 25 Authan addition 1 Adulto 25 Authan addition 24 Add 252 1 Humanised Add 252 1 Humanised Add 252 1 Emunoglo Add 252 1 Emunoglo Add 252 1 Emunoglo Add 252 1 Emunoglo Add 252 1 Emunoglo Add 252 1 Humanised Add 252 1 Humanised Add 252 1 Humanised Add 252 1 Humanised Add 252 1 Humanised Add 252 1 Humanised Add 252 1 Humanised Add 252 1 Humanised Add 252 1 Humanised Add 252 1 Humanised Add 253 1 Humanised Add 253 1 Humanised Add 253 1 Humanised Add 253 1 Humanised Add 253 1 Humanised Add 253 1 Humanised Add 253 1 Humanised Add 253 1 Humanised Add 253 1 Humanised Add 253 1 Humanised Add 253 1 Humanised Add 253 1 Humanised Add 253 1 Humanised Add 253 1 Humanised Add 253 1 Humanised Add 253 1 Humanised Add 253 1 Humanised Add 253 1 Humanised Add 253 1 Humanised Add 253 1 Humanised 253 1	Abg31432 Humani Kay Abg31433 Amino aci Aae28016 Human mod Aae28045 Human mod Aae28057 Human mod Aae28057 Human mod Aae28053 Human mod Aae28053 Human mod Aae28053 Human mod Abu6224 Respirato Abu62251 Respirato Abu62251 Respirato Abu62252 Respirato Abu6225 Respirato Abu6225 Respirato Abu6225 Respirato Abu6225 Respirato Abu6225 Respirato Abu6225 Respirato Abu6325 Respirato Abu6325 Respirato Abu6325 Respirato Abu6325 Respirato Abu6325 Respirato Abu6325 Respirato Abu6326 Respirato Abu6326 Respirato Abu53756 SYNAGIS a Ade33736 SYNAGIS a Ade35760 SYNAGIS a Ade35760 SYNAGIS a Ade35760 SYNAGIS a Ade35760 SYNAGIS a Ade35760 SYNAGIS a Ade35760 SYNAGIS a Ade35760 SYNAGIS a Ade36910 RSV antib Adi56918 RSV antib
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3B9 was positive. cDNA clones of the 3B9 light and heavy chains were cloned into pGEM7f+ and transformed into E. coli DH5-alpha. A heavy chain cDNA clone was sequenced (AAQ83491) that encoded the protein given in AAR70190. 3 CDRs (AAR70198-200) were identified. (Updated on 25-MAR-2003 to correct PN field.)

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Gaps

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100.0%; Score 66; DB 2; Length 11; 100.0%; Pred. No. 0.00026;

0; Mismatches

11; Conservative 1 RETVEYWYFDV 11 

Local Similarity

Best Loca Matches

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Query Match

Sequence 11 AA;

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Experimen
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Anti-VEGF
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    Adl17583
Adw10893
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                               ABP61260
ABP61270
ABP61268
                                           ADG31814
AEA40801
AAB0G386
AAB0G396
AAB0G396
AAB0G399
AAB0G393
AAB0G3893
AAB0G3893
AAB0G3893
AAB0G3893
AAB0G3893
    ADL17583
ADW10893
AAW70699
AAW70701
AAW70613
AAW70691
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## ALIGNMENTS

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Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated and IgE-mediated allergic conditions.
                                                                                                        Chimeric antibody; humanized antibody; antibody engineering; monoclonal antibody; MAb; interleukin-4; IL-4; allergy; CDR; complementarity determining region.
                                                                                                                                                                                                                                                                                     Gross MS, Sylvester DR;
                  AAR70200 standard; protein; 11 AA.
                                                                                                                                                                                                                                                        BEECHAM CORP. BEECHAM PLC.
                                                                                                                                                                                                                            93US-00117366.
93US-00136783.
                                                                                                                                                                                                          94WO-US010308
                                                        (revised)
(first entry)
                                                                                      WAb 3B9 heavy chain CDR,
                                                                                                                                                                                                                                                                                                        WPI; 1995-123387/16.
                                                                                                                                                                                                                                                        (SMIK ) SMITHKLINE (SMIK ) SMITHKLINE
                                                                                                                                                                                                        07-SEP-1994;
                                                                                                                                                                  WO9507301-A1
                                                                                                                                                                                                                            07-SEP-1993;
14-OCT-1993;
                                                        25-MAR-2003
20-SEP-1995
                                                                                                                                                                                     16-MAR-1995.
                                                                                                                                                                                                                                                                                      Holmes S,
                                      AAR70200;
                                                                                                                                               Мив вр.
RESULT 1
          AAR70200
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Spleen cells from mice immunized with human IL-4 were used to prepare hybridomas, which were screened for anti-IL-4 MAb secretion. Only clone

Disclosure; Page 58; 97pp; English.

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New DNA molecules encoding recombinant antibodies useful for treating 1L4-mediated conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a complementarity determining region antibody 189. The specification describes chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in the rapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin E-mediated allergic reactions e.g. allergic rendities, conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host-versus-graff disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans
                                                                                                                                 Heavy chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin E-mediated allergic reaction; allergic rhinitis; conjunctivitis, atopic dermatitis; atopic asthma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy; complementarity determining region.
                                                                                                   CDR of the heavy chain variable region of antibody 3B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sylvester DR, Gross MS;
AAY23777 standard; peptide; 11 AA
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                                                                                                                                                                                                                                                                                                                                                                                                           93US-00136783.
94WO-US010308.
                                                                                                                                                                                                                                                                                                                                                                                              93US-00117366
                                                                                                                                                                                                                                                                                                                                                             95US-00483632
                                                                 13-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-429500/36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                             07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                             07-SEP-1993;
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07-SEP-1994;
                                                                                                                                                                                                                                                                                                                         27-JUL-1999
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                                 AAY23777;
                                                                                                                                                                                                                                                           Mus sp.
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Matches

RESULT 3

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The specification describes chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin B-mediated allorgic reactions e.g. allergic rhinitis, conjunctivitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host-versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans. The present sequence represents the heavy chain variable region of Ig NEW, and is used in the course of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New DNA molecules encoding recombinant antibodies useful for treating IL4 -mediated conditions.
                                                                                                                                                    Light chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin B-mediated allergic reaction; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic aesthma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 66; DB 2; Length 121; 100.0%; Pred. No. 0.0031;
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                                                                                                                  Heavy chain variable region of Ig NEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Col 65-66; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gross MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY18122 standard; protein; 121 AA.
       AAY23780 standard; protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                            93US-00117366.
93US-00136783.
                                                                                                                                                                                                                                                                                                                                                                                                           95US-00483632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94WO-US010308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sylvester DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-AUG-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100,
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 RETVEYWYEDV 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-429500/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAX85929.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                          07-SEP-1993;
14-OCT-1993;
07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                US5928904-A.
                                                                                 13-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                     27-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Holmes SD,
                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                     IG NEW.
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ID AAY1
XX AC AAY1
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XX III-P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a heavy chain complementarity determining region (CDR) from an antibody of the invention. The antibody is a chimeric or humanised interleukin-4 (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgB) mediated diseases. The antibodies are useful for conjunctivitis, atopic defarations as allergic rhinitis, the treatment of allergic disorders such as allergic rhinitis, the artibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft
                                                                                                                                                                                                                                                                                                                                                             Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease; complementarity determining region; CDR.
                                           Gaps
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     Score 66; DB 2; Length 11;
Pred. No. 0.00026;
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100.0%; Pred. No. 0.00026;
ive 0; Mismatches 0; Indels
                                         0; Indels
                                                                                                                                                                                                                                                                                                                              Heavy chain CDR for hIL-4 specific antibody.
                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atopic ashthma and anaphylactic shock.
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                                                                                                                                                                                                             AAY18113 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Col 47; 50pp; English.
   100.0%;
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                                                                                                                                                                                                                                                                                        (first entry)
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                     Local Similarity 100.
1es 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
                                                                             1 RETVEYWYFDV 11
                                                                                                                  RETVFYWYFDV 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     versus host disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995;
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07-SEP-1994;
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Query Match
Best Local S
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Best Local S
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Gaps

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Indels

Heavy chain sequence for humanised 3B9 antibody.

Matches

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RESULT 4

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/label= CDR
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14-OCT-1993;
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                                                                             16-MAR-1995
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                                                                                                                                                                           Holmes S,
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                      Region
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                                                                                                                                                                                                                                                                                                   the invention. The antibody is a chimeric or humanised interleukin-4 (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful
Antibody, interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allargic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease.
                                                                                                                                                                                                                                                                                           This sequence represents the heavy chain of the humanised 3B9 antibody of
                                                                                                                                                                                                                                                                                                                                                            in the treatment of autoimmune diseases and graft versus host disease
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                            Recombinant IL4 antibodies useful for tratment of allergic rhinitis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric antibody; humanized antibody; antibody engineering; monoclonal antibody; MAb; interleukin-4; IL-4; allergy.
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//label= Sig_peptide
50. .56
//label= CDR
//note= "complementarity determining region"
71. .86
                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 66; DB 2; Length 121; 100.0%; Pred. No. 0.0031; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                      atopic ashthma and anaphylactic shock
                                                                                                                                                                                             Gross MS;
                                                                                                                                                                                                                                                                      Example 3; Col 65-66; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR70190 standard; protein; 140 AA.
                                                                                                                                                                          BEECHAM CORP
                                                                                                                          93US-00117366.
93US-00136783.
94WO-US010308.
                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM PLC (SMIK ) SMITHKLINE BEBCHAM COR
                                                                                                        95US-00483636.
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                             Sylvester DR, Holmes SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse MAb 3B9 heavy chain
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                                                                                                                                                                                                               WPI; 1999-370482/31.
                                                                                                                                                                                                                         N-PSDB; AAX79527
                                                                                                                                                                                                                                                                                                                                                                                Sequence 121 AA;
                                                                                                        07-JUN-1995;
                                                                                                                                    14-OCT-1993;
07-SEP-1994;
                                                                                                                           07-SEP-1993;
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20-SEP-1995
                                                                 US5914110-A.
                                                                                     22-JUN-1999
                                               Synthetic.
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hybridomas, which were screened for anti-IL-4 MAb secretion. Only clone 3B9 was positive. cDNA clones of the 3B9 light and heavy chains were cloned into pGEM7f+ and transformed into B. coli DHS-alpha. The clones were sequenced (AAQ83490-91), and used for antibody engineering. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heavy chain variable region; interleukin-4; IL-4; antibody 389; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin E-mediated allergic reaction; allergic rhintitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated and IgB-mediated allergic conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spleen cells from mice immunized with human IL-4 were used to prepare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                   /label= CDR
/note= "complementarity determining region"
'note= "complementarity determining region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY23768 standard; protein; 140 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 2; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sylvester
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93US-00136783.
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93US-00136783.
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gross MS,
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N-PSDB; AAQ83491.
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This sequence represents the heavy chain of the murine 3B9 antibody of the invention. The antibody is a chimeric or humanised interleukin-4 (IL4) monoclonal antibody for the treatment of immunoglobulin B (IgB) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic asthma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft versus host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated and IgE-
                                                                                                                                                                                                                                                                                                                        Gaps
Recombinant II4 antibodies useful for tratment of allergic rhinitis, atopic ashthma and anaphylactic shock.
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0
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/label= Complementarity determining region"
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'label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Humanized antibody 3B9 heavy chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR70192 standard; protein; 141 AA.
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                                                     Claim 24; Fig 2; 50pp; English.
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93US-00136783.
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/label= CDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                       Conservative
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119 RETVFYWYFDV 129
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                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                 Sequence 140 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
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14-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2003
20-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR70192;
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                                                                                                                                                                                                                                                            The present sequence represents the heavy chain variable region of murine interleukin-4 (IL-4) antibody 3Bs. The sequences are used in the production chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis, atopic aethma, anaphylactic shock, rheumatoid arthritis, host diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans
                                                                                                                                                                        New DNA molecules encoding recombinant antibodies useful for treating IL4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibody, interleukin-4; IL4; immunoglobulin B; IgE mediated disease; allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 66; DB 2; Length 140; 100.0%; Pred. No. 0.0036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heavy chain sequence for murine 3B9 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                       Gross MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gross MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY18121 standard; protein; 140 AA.
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                                  SMITHKLINE BEECHAM CORP. SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                             Example 3; Fig 2; 50pp; English.
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93US-00136783.
94WO-US010308.
 94WO-US010308.
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                                                                                     Holmes SD, Sylvester DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 RETVFYWYFDV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11
                                                                                                                                                                                                -mediated conditions.
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N-PSDB; AAX79520.
                                                                                                                        WPI; 1999-429500/36.
                                                                                                                                         N-PSDB; AAX85885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 140 AA;
07-SEP-1994;
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07-SEP-1994;
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                                  (SMIK)
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Disclosure; Fig 3; 97pp; English.
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07-SEP-1994;
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                                                                                      A humanized antibody heavy chain variable region and signal sequence is given in AAR70192. The signal sequence is also provided in AAR70193. The ST sequences of the construct are identical to the native CDRs of mouse anti-human IL-4 MAD 389 (AAR70198-200). (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated and IgE-mediated allergic conditions.
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric antibody; antibody engineering; monoclonal antibody; MAb;
                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "complementarity determining region#"
                                                                                                                                                                                                                                                                                 100.0%; Score 66; DB 2; Length 141;
100.0%; Pred. No. 0.0036;
live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120. .130
/label= CDR
/note= "complementarity determining region"
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/label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR70191 standard; protein; 141 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric antibody 3B9 heavy chain.
                                              Disclosure; Fig 4; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
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mediated allergic conditions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interleukin-4; IL-4; allergy.
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(revised)
(first entry)
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                                                                                                                                                                                                                                                                                                          Local Similarity 100
1es 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 120 RETVFYWYFDV 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gross MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-123387/16.
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                                                                                                                                                                                                                                     Sequence 141 AA;
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25-MAR-2003
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                                                                                                                                                                                                                                                                                      Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New DNA molecules encoding recombinant antibodies useful for treating IL4 -mediated conditions.
A human/mouse chimeric antibody heavy chain variable region was constructed (given in AAR70191) that contained the mouse anti-human IL-4 MAD 3B9 variable region including 3 CDRs (AAR70199-200) and a human antibody signal peptide (AAR70193). The construct was used for humanized antibody production. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heavy chain variable region; interleukin-4; IL-4; antibody 389; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin B-mediated allergic reaction; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic aermax; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heavy chain variable region of humanised murine IL-4 antibody 3B9
                                                                                                                                                                                                                           ö
                                                                                                                                                                                 Length 141;
                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                   100.0%; Score 66; DB 2; 100.0%; Pred. No. 0.0036;
                                                                                                                                                                                                                         0; Mismatches
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93US-00136783.
94WO-US010308.
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                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                     120 RETVFYWYFDV 130
                                                                                                                                                                                                                                                              1 RETVEYWYFDV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-429500/36.
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Pred. No. 0.0036;

100.08;

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Best Local Similarity
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                                                                                                                                                                                                                                                      Synthetic.
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Best Local S:
Matches 11
                                                                                                                               AAY18125;
           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents the heavy chain variable region of murins/human interleukin-4 (IL-4) chimeric antibody 389. The specification describes chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis, artopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthitis, host-versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excessulin-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans. (Updated on 17-OCT-2003 to standardise
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New DNA molecules encoding recombinant antibodies useful for treating IL4
                                                                                                                                                                                                                                                                        chimeric antibody, humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin B-mediated allergic reaction; allergic refinities; conjunctivitis; acopic dermatitis; atopic asthma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.
                                                                Gaps
                                                                                                                                                                                                                                         Heavy chain variable region of murine/human chimeric antibody 3B9.
                                                                                                                                                                                                                                                               Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;
                                                                ö
                                           Length 141;
                                         Score 66; DB 2; Length 14
Pred. No. 0.0036;
Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gross MS;
                                                                                                                                                              AAY23769 standard; protein; 141 AA
endogenous IL-4 levels in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Fig 3; 50pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                          93US-00117366.
93US-00136783.
94WO-US010308.
                                          100.0%;
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                                                                                                                                                                                                         (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Holmes SD, Sylvester DR,
                              Query Match
Best Local Similarity 100.
                                                                                                  120 RETVFYWYFDV 130
                                                                                   1
                                                                                   1 RETVFYWYFDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -mediated conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-429500/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAX85886
                    Sequence 141 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 141 AA;
                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                           07-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-OCT-1993;
07-SEP-1994;
                                                                                                                                                                                                        17-OCT-2003
13-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                          US5928904-A.
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                                                                                                                                                                                    AAY23769;
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                                                                                                                                         RESULT 12
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DB 2; Length 141;

100.0%; Score 66;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the light chain of the chimeric 3B9 antibody of the invention. The antibody is a chimeric or humanised interleukin-4 (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic demarkitis, atopic asthma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft versus host disease
                                                                                                                                                                                                                                                                                                                                                                                                             Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease.
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant IL4 antibodies useful for tratment of allergic rhinitis, atopic ashthma and anaphylactic shock.
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                                                                                                                                                                                                                                                                                                                                                                  Chimeric 3B9 monoclonal antibody heavy chain.
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gross MS;
                                                                                                                                                                                                              AAY18125 standard; protein; 141 AA.
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94WO-US010308.
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                                                                                                                                                                                                                                                                                                                  11-AUG-1999 (first entry)
11; Conservative
                                                                         120 RETVFYWYFDV 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 RETVEYWYFDV 130
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                                        1 RETVEYWYFDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-370482/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAX79542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 141 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sylvester DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-SEP-1993;
14-OCT-1993;
07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-1995;
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Feng X;

11-AUG-1999

Heavy

07-JUN-1995;

US5914110-A 22-JUN-1999

Synthetic.

14-OCT-1993;

07-SEP-1993; 07-SEP-1994;

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The invention comprises a human monoclonal antibody that binds to phospholipase AZ (PLAZ). The monoclonal antibody of the invention is useful in the preparation of a medicament for the treatment of inflammatory and degenerative disorders stemming from inflammatory reactions in the joints, skin, and blood vessels, arthritis, psoriasis, asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present amino acid sequence represents a human PLAZ-specific monoclonal antibody heavy chain peptide.
                                                                                                                                                                                                                                                                                                                                                           useful for treating inflammatory conditions, e.g. arthritis, psoriasis, asthma, Alzheimer's disease, atherosclerosis, or restenosis.
                                                                                                                                                                                                                                                                                                                                   New human monoclonal antibody that binds to phospholipase A2 (PLA2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human, monoclonal antibody; phospholipase A2; PLA2; Inflammactory disorder; degenerative disorder; defencion; distintial inflammatory reaction; skin inflammatory reaction; blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alzheimer's disease; atherosclerosis; restenosis; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human phospholipase A2-specific mAb heavy chain peptide #36
                                                                                                                                                                                                                                  Lee YR, Liang ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liang ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 52; DB 8; Length 13;
Pred. No. 0.066;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; SEQ ID NO 65; 128pp; English.
                                                                                                                                                                                                                                  Chen L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADP47171 standard; peptide; 13 AA.
                                                                                                                                                                                                                              3M, Haak-Frendscho M,
Nocerini MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Landes GM, Haak-Frendscho M,
                                                                               02-DEC-2003; 2003WO-US038234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ABGE-) ABGENIX INC.
(LEXI-) LEXICON GENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32-DEC-2003; 2003WO-US038234.
                                                                                                                          02-DEC-2002; 2002US-0430724P
                                                                                                                                                                 (ABGE-) ABGENIX INC.
(LEXI-) LEXICON GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-DEC-2002; 2002US-0430724P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 78.8
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 TVPYWYFDV 11
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5 TIFYWYFDL 13
                                                                                                                                                                                                                                                                                              WPI; 2004-461119/43.
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WO2004050850-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13 AA;
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                                        17-JUN-2004
                                                                                                                                                                                                                                  Landes GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jia X,
                                                                                                                                                                                                                                                        Jia X,
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    SXCCCCCCXXX44444XXXX15X44XXXX6CCCCCCXXXX44444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the heavy chain of the humanised 3B9 antibody of the invention. The antibody is a chimeric or humanised interleukin-4 (IL4) monoclonal antibody for the treatment of immunoglobulin B (IgB) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic dermartisis, atopic asthma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autolmmune diseases and graft versus host disease
                                                                                              Antibody, interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for tratment of allergic rhinitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human; monoclonal antibody; phospholipase A2; PLA2;
inflammatory disorder; degenerative disorder;
joint inflammatory reaction, skin inflammatory reaction;
blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
Alzheimer's disease; atherosclerosis; restenosis; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human phospholipase A2-specific mAb heavy chain peptide #15.
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                                                     chain sequence for humanised 3B9 antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atopic ashthma and anaphylactic shock.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant IL4 antibodies useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADP47150 standard; peptide; 13 AA
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                                                                                                                                                                                                                                                                                                                                                                                           93US-00136783.
94WO-US010308.
                                                                                                                                                                                                                                                                                                                                                                          93US-00117366.
                                                                                                                                                                                                                                                                                                                                   95US-00483636.
                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sylvester DR, Holmes SD,
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Gaps

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Feng X;

09-SEP-2004

ADP47150;

120

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Query Match

Matches

Homo sapiens

XXXFFFXXXX000000000XX

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AAR99469 represents the variable light (VL) chain of monoclonal antibody PA1-1F10 produced by hybridoma BCCM LMBP132CB. The antibody is directed against an epitope present on cancer cells, in particular breast, ovary, lung and colorectal cancer cells. The antibody is useful for detecting cancer cell epitopes and hence in the diagnosis of cancer. The antibody can be conjugated to a cytotoxic compound and targetted to cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complementarity determining region; respiratory syncytial virus; virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine; immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant; bronchopulmonary dysplasia; congenital heart disease; congenital immunodeficiency; acquired immunodeficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody for treating respiratory syncytial virus (RSV) infection, comprises a variable heavy/light domain or complementarity determining regions 1 - 3 of variable light/heavy chains, that immunospecifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;
                                                                                                                                        Monoclonal antibody PA1-3F10 produced by hybridoma BCCM LMBP1322CB useful to target cancer cells for killing or detection.
                                                                                                                                                                                                                                                                                                                                                                                                         74.2%; Score 49; DB 2; 72.7%; Pred. No. 2.3; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human RSV antibody variable heavy domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP66387 standard; protein; 120 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LS;
                                                                                                                                                                                             Claim 4; Fig 11; 62pp; English.
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95SE-00000148.
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28-NOV-2000; 2000US-00724531.
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                                  (BIOI-) BIOINVENT INT AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MEDI-) MEDIUMMUNE INC
                                                                     Jansson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Young JF, Koenig S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 binds to RSV antigen
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                                                                                                     WPI; 1996-354478/35.
                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                        Sequence 137 AA;
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18-JAN-1995;
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                                                                    Carlsson R,
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                                                                                                                                                   The invention comprises a human monoclonal antibody that binds to phospholipase A2 (PLA2). The monoclonal antibody of the invention is useful in the preparation of a medicament for the treatment of inflammatory and degenerative disorders stemming from inflammatory reactions in the joints, skin, and blood vessels, arthritis, psoriasis, asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present amino acid sequence represents a human PLA2-specific monoclonal antibody
                                             New human monoclonal antibody that binds to phospholipase A2 (PLA2), useful for treating inflammatory conditions, e.g. arthritis, psoriasis, asthma, Alzheimer's disease, atherosclerosis, or restenosis.
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PA1-3F10; antibody; hybridoma; LMBP1322CB; cancer; target; epitope;
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note= "CDR3"
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"CDR2"
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                                                                                                                                                                                                                                                                                                                                                     Score 52; DB 8;
Pred. No. 0.066;
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|label= framework_region
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/label= framework_region
/note= "FR4"
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"FR2"
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'note= "FR3"
                                                                                                                   Example 5; SEQ ID NO 86; 128pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR99470 standard; protein; 137 AA.
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                                                                                                                                                                                                                                                                                                                                                     78.8%;
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Best Local Similarity 77.00
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/label= c
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5 TIFYWYFDL 13
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            WPI; 2004-461119/43.
                                                                                                                                                                                                                                                                                 heavy chain peptide.
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RESULT 17 AAR9947

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Gaps

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Length 137; Indels invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV, and immunostimulant activity. The polynucleotides of the invention may have a use in a vaccine, and in gene therapy. The antibody is useful for treating or ameliorating a RSV infection in a human. The antibody is also useful for preventing, treating or ameliorating one or more symptoms associated with RSV infection in a mammal, e.g. cystic fibrosis, bronchopulmonary dysplasia, congenital heart disease, congenital immunodeficiency or acquired immunodeficiency, or after a bone marrow antibody of the invention

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Gaps

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71.2%; Score 47; DB 5; Length 120; 63.6%; Pred. No. 4.4; 2; Indels ive 2; Mismatches 2; Indels

Local Similarity 63.6

Query Match Best Loca Matches

Sequence 120 AA;

The invention relates to a novel antibody comprising a variable heavy

(VH) domain, variable light (VL) domain, VH complementarity determining
region (CDR1, VH CDR2, VH CDR1, VL CDR2 or VL CDR3, where the
antibody immunospecifically binds to a respiratory syncytial virus (RSV)
antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the
invention has virucide, pulmonary, antihifilammatory, cardiant, anti-HIV,
and immunostimulant activity. The polynucleotides of the invention may
have a use in a vaccine, and in gene therapy. The antibody is useful for
treating or ameliorating a RSV infection in a human. The antibody is also
useful for preventing, treating or ameliorating one or more symptoms
associated with RSV infection in a mammal, e.g. cystic fibrosis,
bronchopulmonary dysplasia, congenital heart disease, congenital
immunodeficiency or acquired immunodeficiency, or after a bone marrow
transplant. The sequence represents a variable domain of a human RSV
antibody of the invention ö Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV; complementarity determining region; respiratory syncytial virus; virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine; immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant; bronchopulmonary dysplasia; congenital heart disease; Gaps ö Score 47; DB 5; Length 120; Pred. No. 4.4; 2; Mismatches 2; Indels congenital immunodeficiency, acquired immunodeficiency. Human RSV antibody variable heavy domain. ABP66421 standard; protein; 120 AA. Young JF, Koenig S, Johnson LS; 28-NOV-2001; 2001WO-US044807 28-NOV-2000; 2000US-00724396 28-NOV-2000; 2000US-00724531 (first entry) Local Similarity 63.0 |: :| ||||| |RDMIFNWYFDV 109 1 RETVFYWYFDV 11 (MEDI-) MEDIUMMUNE INC. Sequence 120 AA; WO200243660-A2 Homo sapiens. 04-DEC-2002 06-JUN-2002. ABP66421; 66 Query Match RESULT 19 ABP66421 Matches 8\$888888888888888888 ઠે

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The invention relates to a novel antibody comprising a variable heavy (VH) domain, variable light (VL) domain, VH complementarity determining region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the antibody immunospecifically binds to a respiratory syncytial virus (RSV) antigon, and where the antibody is not SYNAGIS (RTM). The antibody of the invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV, and immunostimulant activity. The polynucleotides of the invention may have a use in a vaccine, and in gene threapy. The antibody is useful for treating or ameliorating a RSV infection in a human. The antibody is also useful for preventing, treating or ameliorating or ameliorating one or more symptoms
                                                                                                                                                                                                                                                                                            Human, variable heavy domain, variable light domain, CDR; VH; VL, RSV, complementarity determining region; respiratory syncytial virus; virucide, pulmonary; antiinflammatory; cardiant, anti-HTV, vaccine; immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant; bronchopulmonary dysplasia; congenital heart disease; congenital immunodeficiency; acquired immunodeficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody for treating respiratory syncytial virus (RSV) infection, comprises a variable heavy/light domain or complementarity determining regions 1 - 3 of variable light/heavy chains, that immunospecifically binds to RSV antigen.
                                                                                                                                                                                                                                                          Human RSV antibody variable heavy domain.
                                                                                                                                      ABP66405 standard; protein; 120 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Young JF, Koenig S, Johnson LS,
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28-NOV-2000; 2000US-00724531.
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99 RDMIFNWYFDV 109
1 RETVFYWYFDV 11
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The invention relates to a novel antibody comprising a variable heavy (VH) domain, variable light (VL) domain, VH complementarity determining region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the antibody immunospecifically binds to a respiratory syncytial virus (RSV) antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the

Antibody for treating respiratory syncytial virus (RSV) infection, comprises a variable heavy/light domain or complementarity determining regions 1 - 3 of variable light/heavy chains, that immunospecifically binds to RSV antigen.

WPI; 2002-706803/76.

Claim 1; Page 219; 298pp; English.

12.54

Sequence 120 AA;

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The invention relates to a novel antibody comprising a variable heavy

(VH) domain, variable light (VL) domain, VH complementarity determining

region (CDR) -1. VH CDR2, VH CDR2, VI CDR2 or VI CDR3, where the

antibody immunospecifically binds to a respiratory syncytial virus (RSV)

antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the

invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HTV,

and immunostimulant activity. The polymucleotides of the invention may

have a use in a vaccine, and in gene therapy. The antibody is useful for treating or ameliorating a RSV infection in a human. The antibody is also

useful for preventing, treating or ameliorating one or more symptoms

associated with RSV infection in a mammal, e.g. cystic fibrosis,

bronchopulmonary dysplasia, congenital heart disease, congenital

immunodeficiency or acquired immunodeficiency, or after a bone marrow

transplant. The sequence represents a variable domain of a human RSV

antibody of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV; complementarity determining region; respiratory syncytial virus; virucide; pulmonary; antiinflammatory; cardiant; anti-HTV; vaccine; immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant; bronchopulmonary dysplasia; congenital heart disease; congenital immunodeficiency; acquired immunodeficiency.
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                                                                                            bone marrow
bronchopulmonary dysplasia, congenital heart disease, congenital immunodeficiency or acquired immunodeficiency, or after a bone marrow transplant. The sequence represents a variable domain of a human RSV antibody of the invention
                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                    ore 47; DB 5 ed. No. 4.4; Mismatches
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                                                                                                                                                                                                                                                                                    Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP66382 standard; protein; 120 AA.
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28-NOV-2000; 2000US-00724531.
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Best Local Similarity
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                                                                                                                                                                                                                       Sequence 120 AA;
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The invention relates to a novel antibody comprising a variable heavy (VH) domain, variable light (VL) domain, VH complementarity determining region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the antibody immunospecifically binds to a respiratory syncytial virus (RSV) antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the invention has virucide, pulmonary, antihinflammatory, cardiant, anti-HIV, and immunostimulant activity. The polynuclectides of the invention may have a use in a vaccine, and in gene therapy. The antibody is useful for reating or ameliorating a RSV infection in a human. The antibody is also useful for preventing, treating or ameliorating one or more symptoms associated with RSV infection in a mammal, e.g. cystic fibrosis, bronchopulmonary dysplasia, congenital heart disease, congenital immunodeficiency or acquired immunodeficiency, or after a bone marrow transplant. The sequence represents a variable domain of a human RSV antibody of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV; complementarity determining region; respiratory syncytial virus; virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine; immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant; bronchopulmonary dysplasia; congenital heart disease; congenital immunodeficiency; acquired immunodeficiency.
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                                                                                              Gaps
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                              Length 120;
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                                 5;
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Pred. No. 4.4;
                                                               ed. No. 4.4;
Mismatches
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                                 Score 47;
Pred. No.
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28-NOV-2000; 2000US-00724531.
                              71.2%;
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                                                                                                 Conservative
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RDMIFNWYFDV 109
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binds to RSV antigen
Query Match
Best Local Similarity
7; Conserve
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Johnson LS,
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Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 120 AA;
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                                                                                                                                            Homo sapiens.
                         13-DEC-2002
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                                                                                                                                                        Synthetic.
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   AAE28042;
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                                                                                                                                                                                               Human; immunoglobulin; IgG1; passive immunotherapy; gamma globulinaemia; vaccination; hypogammaglobulinaemia; autoimmune disease; antibacterial; immunosuppressive; lymphoid malignancy; respiratory syncytial virus; anti-RSV; systemic infection; graft-versus-host disease; cytostatic; virucide; mutant; mutant.
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  Gaps
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  Indels
                                                                                                                                                                           Human modified anti-RSV A13A11 antibody VH domain.
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 Mismatches
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                                                                                                      AAE28076 standard; protein; 120 AA.
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                                                                                                                                                   (first entry)
 7; Conservative
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RDMIFNWYFDV 109
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                       RETVFYWYFDV 11
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AAE28042 standard; protein; 120 AA.

RESULT 24
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                                                           Human; immunoglobulin; IgGl; passive immunotherapy; gamma globulinaemia; vaccination; hypogammaglobulinaemia; autoimmune disease; antibacterial; immunosuppressive; lymphoid maligancy; respiratory syncytial virus; anti-RSV; systemic infection; graft-versus-host disease; cytostatic; complementarity determining region; CDR; virucide; mutant; mutein.
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Human modified anti-RSV Ale109 antibody VH domain.
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2; Mismatches
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The invention relates to a modified immunoglobulin (IgG1) which comprises an IgG constant domain having at least one amino acid modification. The immunoglobulins are used in the treatment or prevention of a disease or disorder by passive immunotherapy for vaccinating a subject and for in vivo diagnosis of a subject. The disease and disorders include a gamma globulinaemia, hypogammaglobulinaemia, autoimmune diseases, graft-versushost, lymphoid malignancies and passive immunotherapies and also for the treatment of various systemic infections. The present sequence is human modified anti-RSV (respiratory syncytial virus) antibody VH domain (heavy
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                                                                                                                     Modified immunoglobuling useful in the treatment of autoimmune diseases, comprises at least one amino acid modification relative to a wild-type immunoglobulin constant domain.
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Pred. No. 4.4;
2; Mismatches
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                                           Ward ES;
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09-MAY-2001; 2001US-0289760P.
                                           Johnson LS,
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Best Local Similarity 63.0
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  (MEDI-) MEDIMMONE INC
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63.6%; Pred. No. 4.4;
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09-MAY-2001; 2001US-0289760P.
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09-MAY-2001; 2001US-0289760P.
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                                                                                                                                                                                                                                                                                         Dall'acqua W, Johnson LS,
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99 RDMIFNWYFDV 109
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                                                                                                                                                                                                                                                  (MEDI-) MEDIMMUNE INC
                                                                                                                                                                                                                                                                                                                                WPI; 2002-666925/71.
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hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 120 AA;
                                                          WO200260919-A2
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Homo sapiens
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                   Synthetic.
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Length 120; 2; Indels

DB 5;

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           The invention relates to a modified immunoglobulin (1gG1) which comprises an IgG constant domain having at least one amino acid modification. The immunoglobulins are used in the treatment or prevention of a disease or disorder by passive immunotherapy for vaccinating a subject and for in vivo diagnosis of a subject. The disease and disorders include a gamma globulinaemia, hypogammaglobulinaemia, autoimmune diseases, graft-versushost, lymphoid malignancies and passive immunotherapies and also for the treatment of various systemic infections. The present sequence is human modified anti-RSV (respiratory syncytial virus) antibody VH domain (heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Respiratory syncytial virus; RSV; vaccine; antibody; variable heavy domain; VH; variable light domain; VL; complementarity determining region; CDR; CDR1; CDR2; CDR3; RSV infection; cystic fibrosis; bronchopulmonary dysplasis; congenital heart disease; congenital immunodeficiency; acquired immune deficiency;
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                                                                                                                                                                                                                5; Length 120
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                                                                                                                                                                                                               Score 47; DB 5
Pred. No. 4.4;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  ABU69284 standard; protein; 120 AA.
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                                                                                                                                                                                                                71.2%;
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Matches 7; Conservative
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RDMIFNWYFDV 109
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                                                                                                                                                      chain variable region)
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                                                                                                                                                                                  Sequence 120 AA;
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The invention describes an antibody comprising a variable heavy (VH) or variable light (VL) domain or complementarity determining region (CDR), such as CDR1, CDR2, or CDR3, which immunospecifically binds to a respiratory syncytial virus (RSV) antigen and is not SYNAGIS (RTW). The antibody, pharmaceutical compositions and methods are useful for preventing, treating or ameliorating a RSV infection in patients with cystic fibrosis, bronchopulmonary dysplasta, congenital heart disease, congenital immunodeficiency, or acquired immune deficiency, or patients having had a bone marrow transplant or the elderly. This is the amino acid sequence of a respiratory syncytial virus (RSV) antibody

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antibody comprising a variable heavy (VH) or variable light (VL) domain or complementarity determining region (CDR), such as CDR1, CDR2, or CDR3, useful for preventing or treating a respiratory syncytial virus
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                                               6; Length 120;
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                                                                            2; Mismatches
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Pred. No.
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                                             71.2%;
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Best Local Similarity 63.00,
7; Conservative
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99 RDMIFNWYFDV 109
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99 RDMIFNWYPDV 109
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                                                                                                           1 RETVFYWYFDV
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Respiratory syncytial virus; RSV; vaccine; antibody; variable heavy domain; VH; variable light domain; VL; complementarity determining region; CDR; CDR1; CDR2; CDR3; RSV infection; cystic fibrosis; bronchopulmonary dysplasia; congenital heart disease; congenital immunodeficiency; acquired immune deficiency;
Respiratory syncytial virus; RSV; vaccine; antibody; variable heavy domain; VH; variable light domain; VL; complementarity determining region; CDR; CDR1; CDR2; CDR3; RSV infection; cystic fibrosis; bronchopulmonary dysplasia; congenital heart disease; congenital immunodeficiency; acquired immune deficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antibody comprising a variable heavy (VH) or variable light (VL) domain or complementarity determining region (CDR), such as CDR1, CDR2, or CDR3, useful for preventing or treating a respiratory syncytial virus
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RDMIFNWYFDV 109
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ABU69245
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                                                                                                                                                                                                                             Respiratory syncytial virus; RSV; vaccine; antibody; variable heavy domain; VH; variable light domain; VL; complementarity determining region; CDR; CDR1; CDR2; CDR3; RSV infection; cystic fibrosis; bronchopulmonary dysplasia; congenital heart disease; congenital immunodeficiency; acquired immune deficiency; bone marrow transplant.
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2; Mismatches 2; Indels
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                                                                                                                                                                                       Respiratory syncytial virus (RSV) antibody #11.
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                                                            ABU69250 standard; protein; 120 AA
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Best Local Similarity 63.00,
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                                                                                                                     New antibody comprising a variable heavy (VH) or variable light (VL) domain or complementarity determining region (CDR), such as CDR1, CDR2, or CDR3, useful for preventing or treating a respiratory syncytial virus
                                                                                                                                                                                        The invention describes an antibody comprising a variable heavy (VH) or variable light (VL) domain or complementarity determining region (CDR), such as CDR1, CDR2, or CDR3, which immunospecifically binds to a respiratory syncytial virus (KN) antigen and is not SYNAGIS (RTW). The antibody, pharmaceutical compositions and methods are useful for preventing, treating or ameliorating a RSV infection in patients with cystic fibrosis, bronchopulmonary dysplasaia, congenital heart disease, congenital immunodeficiency, or acquired immune deficiency, or patients having had a bone marrow transplant or the elderly. This is the amino acid sequence of a respiratory syncytial virus (RSV) antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    respiratory syncytial virus; RSV infection; high affinity antibody; high avidity antibody; low antibody dose; more effective prophylaxis; complementarity determining region; CDR; human.
                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                           71.2%; Score 47; DB 6; Length 120; 63.6%; Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYNAGIS antibody based heavy chain domain #13.
                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE35779 standard; protein; 120 AA
                                                                               Young JF, Koenig S, Johnson LS,
                                                                                                                                                                        Claim 1; Page 70; 165pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Johnson LS
                    28-NOV-2001; 2001US-00996288.
                                       28-NOV-2000; 2000US-00724531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-NOV-2001; 2001US-00996265
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                                                                                                                                                                                                                                                                                                                                    63.68;
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                                                                                                                                                                                                                                                                                                                                     Local Similarity 63.6
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RDMIFNWYFDV 109
                                                                                                                                                                                                                                                                                                                                                                   1 RETVFYWYFDV 11
                                                           (MEDI-) MEDIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Koenig S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (YOUN/) YOUNG J F.
(KOEN/) KOENIG S.
(JOHN/) JOHNSON L S.
                                                                                                   WPI; 2003-340947/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-874589/81
                                                                                                                                          or CDR3, useful (RSV) infection.
                                                                                                                                                                                                                                                                                                        Sequence 120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2003091584-A1
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28-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 33
ADE35779
                                                                                                                                                                                                                                                                                                                                                Matches
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Preventing, treating or ameliorating symptoms associated with respiratory syncytial virus infection in mammal by administering antibodies or their fragments that immunospecifically bind to RSV antigens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                             Disclosure; SEQ ID NO 67; 161pp; English.
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Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the SYNAGIS antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2003091584-A1
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The invention relates to a method of preventing, treating or ameliorating one or more symptoms associated with a respiratory syncytial virus (RSV) infection in a mammal. A sustained release formulation comprising one or more antibodies or their fragments that immunospecifically bind to one or more RSV antigens and a pharmaceutical composition comprising one or more RSV antigens formulated for pulmonary delivery is useful for preventing, treating or ameliorating one or more symptoms associated with a RSV infection in a mammal by administering the formulation to the mammal, or the nammal, or the nammal, or the nammal, or the nigh affinity and/or high avidity. The methods use lower doses of antibodies which immunospecifically bind to RSV which provide a more effective prophylaxis. The present sequence which emino acid sequence of a antibody chain domain based on the SYNAGIS antibody 88888888888888888888888888

Sequence 120 AA;

Gaps ö Score 47; DB 7; Length 120; Pred. No. 4.4; 2; Mismatches 2; Indels 71.2%; Local Similarity 63.0 Query Match

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|::| ||||| 99 RDMIFNWYFDV 109 1 RETVFYWYFDV 11 8 셤

RESULT 35

ADE35740 standard; protein; 120 AA. ADE35740 

(first entry) 29-JAN-2004 ADE35740;

SYNAGIS antibody based heavy chain domain #5.

respiratory syncytial virus; RSV infection; high affinity antibody; high avidity antibody, low antibody dose; more effective prophylaxis; complementarity determining region; CDR; human.

Homo sapiens. Synthetic

US2003091584-A1.

15-MAY-2003

28-NOV-2001; 2001US-00996265

28-NOV-2000; 2000US-00724396

(YOUN/) YOUNG J P. (KOEN/) KOENIG S. (JOHN/) JOHNSON L S.

Johnson LS; Koenig S, Young JF,

WPI; 2003-874589/81.

Preventing, treating or ameliorating symptoms associated with respiratory syncytial virus infection in mammal by administering antibodies or their fragments that immunospecifically bind to RSV antigens.

Disclosure; SEQ ID NO 28; 161pp; English.

The invention relates to a method of preventing, treating or ameliorating one or movre symptoms associated with a respiratory syncytial virus (RSV) infection in a mammal. A sustained release formulation comprising one or more antibodies or their fragments that immunospecifically bind to one or more RSV antigens and a pharmaceutical composition comprising one or more antibodies or their fragments that immunospecifically bind to one or more RSV antigens formulated for pulmonary delivery is useful for preventing,

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treating or ameliorating one or more symptoms associated with a RSV infection in a mammal by administering the formulation to the mammal, or the composition to the lungs of the mammal. The antibodies bind to RSV antigen with a high affinity and/or high avidity. The methods use lower which provide a more effective prophylaxis. The present sequence represents the amino acid sequence of a antibody chain domain based on the SYNAGIS antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            respiratory syncytial virus; RSV infection; high affinity antibody; high avidity antibody; low antibody dose; more effective prophylaxis; complementarity determining region; CDR; human.
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                                                                                                                                                                                                       Length 120;
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                                                                                                                                                                                                       Score 47; DB 7;
Pred. No. 4.4;
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                                                                                                                                                                                                                                          2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                        ADE35745 standard; protein; 120 AA.
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                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                              99 RDMIFNWYPDV 109
                                                                                                                                                                                                                                                                            1 RETVFYWYFDV 11
                                                                                                                                                                                  Query Match
Best Local Similarity
7; Conserve
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                                                                                                                                                                   Sequence 120 AA;
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human; liquid antibody formulation; antibody; respiratory syncytial virus; RSV; RSV infection.
                                                                                                                                                                                                                                                         RSV antibody heavy chain variable region #12
                                                                                                                                               ADI56941 standard; protein; 120 AA.
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                                                                                                                                                                                                                       (first entry)
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99 RDMIFNWYFDV 109
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                    RETVFYWYFDV
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ADI56902
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                                                                                                                                                                                                                                                                                                                                                                                                                  respiratory syncytial virus; RSV infection; high affinity antibody; high avidity antibody; low antibody dose; more effective prophylaxis; complementarity determining region; CDR; human.
                                                                                                            Gaps
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                                                                    Score 47; DB 7; Length 120;
Pred. No. 4.4;
2; Mismatches 2; Indels
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Pred. No. 4.4;
2; Mismatches 2; Indels
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                                                                                   63.68;
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Best Local Similarity 63.6%;
Matches 7; Conservative
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                                                   Query Match
Best Local Similarity 63.6.
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RDMIFNWYFDV 109
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(KOEN/) KOENIG S.
(JOHN/) JOHNSON L S.
the SYNAGIS antibody
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                                  Sequence 120 AA;
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Chang S;

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                                                                                                                                                               The invention relates to a liquid antibody formulation comprising 15 or more mg/ml of antibody, or its fragment that immunospecifically binds to a respiratory syncytial virus (RSV) antigen and histidine in an aqueous carrier. The formulation is useful for preventing, treating or ameliorating one or more symptoms associated with a RSV infection in a subject, which involves administering a prophylactically or therapeutically effective amount of the formulation. The formulation is a stable liquid formulation of an anti-RSV antibody effective in preventing or treating RSV infection. The present sequence represents the amino acid sequence of a RSV antibody heavy chain variable region.
Liquid antibody formulation, useful for treating symptoms associated with respiratory syncytial virus (RSV) infection, comprising antibody or its fragment binding immunospecifically to RSV antigen and histidine.
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                                                                                                                Claim 30; SEQ ID NO 67; 169pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADI56902 standard; protein; 120 AA.
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Best Local Similarity 63.00
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99 RDMIFNWYFDV 109
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Liquid antibody formulation, useful for treating symptoms associated with respiratory syncytial virus (RSV) infection, comprising antibody or its fragment binding immunospecifically to RSV antigen and histidine.
                                                                                                                                                                                                  The invention relates to a liquid antibody formulation comprising 15 or more mg/ml of antibody, or its fragment that immunospecifically binds to a respiratory syncytial virus (RSV) antigen and histidine in an aqueous carrier. The formulation is useful for preventing, treating or ameliorating one or more symptoms associated with a RSV infection in a subject, which involves administering a prophylactically or therapeutically effective amount of the formulation. The formulation is a stable liquid formulation of an anti-RSV antibody effective in preventing or treating RSV infection. The present sequence represents the amino acid sequence of a RSV antibody heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a liquid antibody formulation comprising 15 or more mg/mi of antibody, or its fragment that immunospecifically binds to a respiratory syncytial virus (RSV) antigen and histidine in an aqueous carrier. The formulation is useful for preventing, treating or ameliorating one or more symptoms associated with a RSV infection in a subject, which involves administering a prophylactically or therapeutically effective amount of the formulation. The formulation is a
                                                                   Liquid antibody formulation, useful for treating symptoms associated respiratory syncytial virus (RSV) infection, comprising antibody or i fragment binding immunospecifically to RSV antigen and histidine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; liquid antibody formulation; antibody;
respiratory syncytial virus; RSV; RSV infection.
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                                                                                                                                                             Claim 30; SEQ ID NO 55; 169pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADIS6925 standard; protein; 120 AA.
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99 RDMIFNWYFDV 109
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                           WPI; 2004-082183/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 120 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a liquid antibody formulation comprising 15 or more mg/ml of antibody, or its fragment that immunospecifically binds to a respiratory syncytial virus (RSV) antigen and histidine in an aqueous carrier. The formulation is useful for preventing, treating or ameliorating one or more symptoms associated with a RSV infection in a subject, which involves administering a prophylactically or therapeutically effective amount of the formulation. The formulation is a stable liquid formulation of an anti-RSV antibody effective in preventing or treating RSV infection. The present sequence represents the amino acid sequence of a RSV antibody heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                            Liquid antibody formulation, useful for treating symptoms associated with respiratory syncytial virus (RSV) infection, comprising antibody or its fragment binding immunospecifically to RSV antigen and histidine.
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human; liquid antibody formulation; antibody; respiratory syncytial virus; RSV; RSV infection.
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Pred. No. 4
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99 RDMIFNWYFDV 109
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                                                                                                                                                                                                                                                                                               (MEDI-) MEDIMMUNE INC
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 120 AA;
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RESULT 40 ADI56929

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ADT89230 standard; protein; 120 AA.
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stable liquid formulation of an anti-RSV antibody effective in preventing or treating RSV infection. The present sequence represents the amino acid sequence of a RSV antibody heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liquid antibody formulation, useful for treating symptoms associated with respiratory syncytial virus (RSV) infection, comprising antibody or its fragment binding immunospecifically to RSV antigen and histidine.
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Pred. No. 4.4;
2; Mismatches 2; Indels
                                                              DB 8; Length 120
                                                                                   2; Indels
                                                                                                                                                                                                                                                             human; liquid antibody formulation; antibody; respiratory syncytial virus; RSV; RSV infection.
                                                            Score 47; DB 8;
Pred. No. 4.4;
2; Mismatches
                                                                                                                                                                                                                                          RSV antibody heavy chain variable region #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 30; SEQ ID NO 33; 169pp; English.
                                                                                                                                                                             ADI56907 standard; protein; 120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                       Chang S;
                                                                                                                                                                                                                                                                                                                                                         16-JUN-2003; 2003WO-US018914.
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Best Local Similarity 63.00,
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RDMIFNWYFDV 109
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The present invention is based upon the development of a novel method of analysing and identifying glycoprotein (limited to immunoglobulins) degradation products. The inventors have identified a portion of the heavy chain immunoglobulin Gl (IgG1) constant domain as a site of immunoglobulin degradation. This method leads to the indentification and production of stabilised immunoglobulin molecules with increased stability and/or serum half life. The invention is useful for treating, preventing or ameliorating one or more symptoms associated with increased stability and/or serum half life. The invention is useful for treating, preventing or ameliorating one or more symptoms associated with preventing viral or bacterial antigen from binding to its host cell receptor. The invention is also useful for preventing, inhibiting or receptor. The invention is also useful for preventing, inhibiting or receptor. The invention is also useful for preventing, inhibiting or receptor. The invention is also useful for preventing, inhibiting or receptor. The invention is also useful for preventing, inhibiting or receptor. Wilms' tumour, glioma, setrocytoma, accoustic neurona, neuroblastoma and unfilammatory bowel disease and asthma. The present sequence is the humanised RSV antibody variable heavy chain (VH) domain
                                                                                                                                        renal cell carcinoma; osteogenic sarcoma; rhabdomyosarcoma;
Bwing's tumour; squamous cell carcinoma; hepatoma; Wilms' tumour; glioma;
astrocytoma; acoustic neuroma; neuroblastoma; retinoblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New modified immunoglobulin G (IgG) having modified hinge region comprising amino acid modifications corresponding to specific positions of IgG1 of wild-type, useful for treating viral infection caused by respiratory syncytial virus.
                                                                                                                                                                                                                                                                   inflammatory disorder; rheumatoid arthritis; spondyloarthropathy; inflammatory bowel disease; asthma; humanised; antibody; virucide; antibacterial; cytostatic; antinflammatory; antirheumatic; antiarthritic; variable heavy chain; VH.
                                                                                         Stabilised glycoprotein; leukaemia; neoplasms; fibrosarcoma;
Humanised RSV antibody (Ale109) VH domain protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JAN-2004; 2004US-00751744.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Respiratory syncytial virus.
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FENG J.
TOUS G.
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Score 47; DB 8 Pred. No. 4.4; 2; Mismatches

DB 8; Length 120;

Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative

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RESULT 43

RETVFYWYFDV 11

DB 8; Length 120;

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Stabilised glycoprotein; leukaemia; neoplasms; fibrosarcoma; renal cell carcinoma; osteogenic sarcoma; rhabdomyosarcoma; Ewing's tumour; squamous cell carcinoma; hepatoma; Wilma; tumour; glioma; astrocytoma; acoustic neuroma; neuroblastoma; retinoblastoma; inflammatory disorder; rheumatoid arthritis; spondyloarthropathy; inflammatory bowel disease; asthma; humanised; antibody; virucide; antibacterial; cytosteric; antiinflammatory; antirheumatic; antiantarthritic; variable heavy chain; VH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        New modified immunoglobulin G (IgG) having modified hinge region comprising amino acid modifications corresponding to specific positions of IgG1 of wild-type, useful for treating viral infection caused by
                                                                                      Humanised RSV antibody (p11d4) VH domain protein.
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                    ADT89225 standard; protein; 120 AA
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                                                                                                                                                                                                              Respiratory syncytial virus.
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                                                                (first entry)
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(FENG/) FENG J.
(TOUS/) TOUS G.
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                                                                                                                                                                                                                          sapiens.
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                                          ADT89225;
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RESULT 44
           ADT89225
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neoplasms, fibrosarcoma, renal cell carcinoma, osteogenic sarcoma, rhabdomyosarcoma, Ewing's tumour, squamous cell carcinoma, hepatoma, wilms tumour, glioma, astrocytoma, acoustic neuroma, neuroblastoma and retinoblastoma and inflammatory disorders such as rheumatoid arthritis, spondyloarthropathies, inflammatory bowel disease and asthma. The present sequence is the humanised RSV antibody variable heavy chain (VH) domain The present invention is based upon the development of a novel method of analysing and identifying glycoprotein (limited to immunoglobulins) degradation products. The inventors have identified a portion of the hinge region of the heavy chain immunoglobulin Gl (1961) constant domain as a site of immunoglobulin degradation. This method leads to the identification and production of stabilised immunoglobulin molecules with increased stability and/or serum half life. The invention is useful for treating, preventing or ameliorating one or more symptoms associated with viral infection caused by respiratory syncytial virus (RSV) in human and preventing viral or bacterial antigen from binding to its host cell receptor. The invention is also useful for preventing, inhibiting or reducing the growth or metastasis of cancerous cells such as leukaemia, Disclosure, SEQ ID NO 28; 66pp; English

Sequence 120 AA;

protein

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canalysing and identifying glycoprotein (limited to immunoglobulins)
degradation products. The inventors have identified a portion of the
hinge region of the heavy chain immunoglobuling (1 (ggd)) constant domain
as site of immunoglobulin degradation. This method leads to the
identification and production of stabilised immunoglobulin molecules with
cased stability and/or serum half life. The invention is useful for
treating, preventing or ameliorating one or more symptoms associated with
viral infection caused by respiratory syncytial virus (RSV) in human and
preventing viral or bacterial antigen from binding to its host cell
creceptor. The invention is also useful for preventing, inhibiting or
reducing the growth or metastasis of cancerous cells such as leukaemia,
neoplasms, fibrosarcoma, renal cell carcinoma, osteogenic sarcoma,
halms' tumour, glioma, astrocytoma, acoustic neuroma, neuroblastoma and
retinoblastoma and inflammatory disected such as theumatoid arthritis,
spondyloarthropathies, inflammatory bowel disease and asthma. The present
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                                                                                                                                                                                                                                                                                                                                             Stabilised glycoprotein, leukaemia, neoplasms, fibrosarcoma, renal cell carcinoma; osteogenic sarcoma, rhabdomyosarcoma; Ewing's tumour; squamous cell carcinoma; hepatoma; Wilms' tumour; glioma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention is based upon the development of a novel method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New modified immunoglobulin G (IgG) having modified hinge region comprising amino acid modifications corresponding to specific positions of IgG1 of wild-type, useful for treating viral infection caused by respiratory syncytial virus
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    astrocytoma; acoustic neuroma; neuroblastoma; retinoblastoma;
inflammatory disorder; rheumatoid arthritis; spondyloarthropathy;
inflammatory bowel disease; asthma; humanised; antibody; virucide;
antibacterial; cytostatic; antiinflammatory; antirheumatic;
antiarthritic; variable heavy chain; VH.
                                       .,
                                     2; Indels
                                                                                                                                                                                                                                                                                                           Humanised RSV antibody (Al3All) VH domain protein.
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 Score 47; DB 8;
Pred. No. 4.4;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 67; 66pp; English.
                                                                                                                                                                                                   ADT89264 standard; protein; 120 AA.
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71.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Respiratory syncytial virus.
                                                                                                                                                                                                                                                                         (first entry)
Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                              |: :| |||||
99 RDMIFNWYFDV 109
                                                                         1 RETVFYWYFDV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CASAS-FINET J.
FENG J.
TOUS G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
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(FENG/) )
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                                                                                                                                                                 RESULT 45
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Schenerman MA,
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                                                                                                protein.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                       Stabilised glycoprotein; leukaemia; neoplasms; fibrosarcoma; renal cell carcinoma; osteogenic sarcoma; rhabdomyosarcoma; Ewing's tumour; squamous cell carcinoma; hepatoma; wilms' tumour; glioma; astrocytoma; acoustic neuroma; neuroblastoma; retinoblastoma; inflammatory disorder; rheumatoid arthritis; spondyloarthropathy; antilammatory bowel disease; asthma; humanised; antibody; virucide; antibacterial; cytostatic; antilinflammatory; antirheumatic; antiantarthritic; variable heavy chain; VH.
the humanised RSV antibody variable heavy chain (VH) domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New modified immunoglobulin G (IgG) having modified hinge region comprising amino acid modifications corresponding to specific positions of IgG1 of wild-type, useful for treating viral infection caused by respiratory syncytial virus
                                                                                                               Gaps
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                                                                           Score 47; DB 8; Length 120;
Pred. No. 4.4;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                           Humanised RSV antibody (H3-3F4) VH domain protein.
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                                                                                                                                                                                                                                                    ADT89252 standard; protein; 120 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Respiratory syncytial virus.
                                                                                           63.68;
                                                                                                                                                                                                                                                                                                                (first entry)
                                                                          Query Match
Best Local Similarity 63.6
Matches 7; Conservative
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RDMIFNWYFDV 109
                                                                                                                                        1 RETVFYWYFDV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCHENERMAN M A. CASAS-FINET J. FENG J.
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                                                Sequence 120 AA;
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   sequence is
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                                                                                                                                                                                                                                                                                     ADT89252;
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                protein.
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(TOUS/)
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(CASA/)
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neoplasms, fibrosarcoma, renal cell carcinoma, osteogenic sarcoma, rhabdomyosarcoma, Ewing's tumour, squamous cell carcinoma, hepatoma, Wilms' tumour, glioma, astrocytoma, acoustic neuroma, neuroblastoma and retinoblastoma and inflammatory disorders such as rheumatoid arthritis, spondyloarthropathies, inflammatory bowel disease and asthma. The present sequence is the humanised RSV antibody variable heavy chain (VH) domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stabilised glycoprotein; leukaemia; neoplasms; fibrosarcoma; renal cell carcinoma; osteogenic sarcoma; rhabdomyosarcoma; Ewing's tumour; squamous cell carcinoma; hepatoma; wines' tumour; glioma; astrocytoma; acoustic neuroma; neuroblastoma; retinoblastoma; inflammatory disorder; rheumatoid arthritis; spondyloarthropathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New modified immunoglobulin G (IgG) having modified hinge region comprising amino acid modifications corresponding to specific positions of IgG1 of wild-type, useful for treating viral infection caused by respiratory syncytial virus.
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammatory bowel disease; asthma; humanised; antibody; virucide; antibacterial; cytostatic; antiinflammatory; antirheumatic; antiathritic; variable heavy chain; VH.
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                                                                                                                                                                                                       8; Length 120;
                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Humanised RSV antibody (A8C7) VH domain protein.
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                                                                                                                                                                                                   71.2%; Score 47;
63.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feng J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Respiratory syncytial virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                     Local Similarity 63.6
                                                                                                                                                                                                                                                                                                                        RDMIFNWYFDV 109
                                                                                                                                                                                                                                                                                 1 RETVFYWYFDV 11
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                                                                                                                                                            Sequence 120 AA;
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Wilms' tumour, glioma, astrocytoma, acoustic neuroma, neuroblastoma and rethinoblastoma and inflammatory disorders such as rheumatoid arthritis, spondyloarthropathies, inflammatory bowel disease and asthma. The present sequence is the humanised RSV antibody variable heavy chain (VH) domain
   treating, preventing or ameliorating one or more symptoms associated with
                            viral infection caused by respiratory syncytial virus (RSV) in human and preventing viral or bacterial antigen from binding to its host cell receptor. The invention is also useful for preventing, inhibiting or reducing the growth or metastasis of cancerous cells such as leukaemia, neoplasms, fibrosarcoma, renal cell carcinoma, osteogenic sarcoma, rhabdomyosarcoma, Ewing's tumour, squamous cell carcinoma, hepatoma,
                                                                                                                                                                                                                                                                                                                                               protein.
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Sequence 120 AA;

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                    Gaps
                     ;
  8; Length 120;
                     2; Indels
  Score 47; DB E Pred. No. 4.4;
                    2; Mismatches
71.2%;
                    Conservative
        Local Similarity
Nes 7; Conserv
 Query Match
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99 RDMIFNWYFDV 109 급 1 RETVFYWYFDV 유 ઠે

ADW19905 standard; protein; 120 AA. ADW19905; RESULT 48 

(first entry) 24-MAR-2005

respiratory syncytial virus infection; delivery mechanism; respiratory-gen.; virucide; vaccine; gene therapy; heavy chain variable region.

RSV antigen binding antibody variable heavy domain, SEQ ID 51.

Homo sapiens

US2005002926-A1

06-JAN-2005

26-JUL-2004; 2004US-00900230.

28-NOV-2000; 2000US-00724396. 28-NOV-2001; 2001US-00996265.

(MEDI-) MEDIMMUNE INC

Preventing, treating or ameliorating symptoms associated with a respiratory syncytial virus (RSV) infection by administering antibodies that immunospecifically bind to one or more RSV antigens. WPI; 2005-065188/07.

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Watkins JD,

Huse WD,

Johnson LS,

Koenig S,

Young JF,

Disclosure; SEQ ID NO 51; 160pp; English.

the mammal a dose of one or more antibodies or their fragments that immunospecifically binds to one or more RSV antigens, where the effective amount is less than 15 mg/kg of the antibodies or antibody fragments. The invention further comprises: a sustained release formulation comprising one or more antibodies or their fragments that immunospecifically binds The invention relates to a novel method for preventing, treating or ameliorating one or more symptoms associated with a respiratory syncytial virus (RSV) infection in a mammal. The method comprises administering to to one or more RSV antigens; and a pharmaceutical composition comprising one or more antibodies or their fragments that immunospecifically binds to one or more RSV antigens formulated for pulmonary delivery. The methods and compositions have respiratory-gen. and virucide activities.

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The antibodies can be used in the creation of a vaccine. The compositions may be used in gene therapy. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of RSV infection. This sequence represents an RSV antigen binding variable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             respiratory syncytial virus infection; delivery mechanism; respiratory-gen.; virucide; vaccine; gene therapy; heavy chain variable region.
                                                                                                                                                                                  Length 120;
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                                                                                                                                                                                Score 47; DB 9
Pred. No. 4.4;
2; Mismatches
                                                                                                                                                                                                     4.4;
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                                                                                         heavy domain of the invention.
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28-NOV-2001; 2001US-00996265.
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                                                                                                                                                                                                                               Conservative
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99 RDMIFNWYFDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2005-065188/07.
                                                                                                                                                                                                  Local Similarity
nes 7; Conserv
                                                                                                                                     Sequence 120 AA;
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                                                                                                                                                                             Query Match
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Matches
                                                                                                                                                                                                                                                                                                                                                                                     RESULT 49
ADW19887
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The invention relates to a novel method for preventing, treating or ameliorating one or more symptoms associated with a respiratory syncytial virus (RSV) infection in a mammal. The method comprises administering to the mammal a dose of one or more antibodies or their fragments that immunospecifically binds to one or more RSV antigens, where the effective amount is less than 15 mg/kg of the antibodies or antibody fragments. The invention further comprises: a sustained release formulation comprising one or more antibodies or their fragments that immunospecifically binds to one or more RSV antigens; and a pharmaceutical composition comprising one or more antibodies or their fragments that immunospecifically binds to one or more RSV antigens formulated for pulmonary delivery. The methods and compositions have respiratory-gen, and virucide activities. The antibodies can be used in the creation of a vaccine. The compositions may be used in gene therapy. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of RSV infection. This sequence represents an RSV antigen binding variable heavy domain of the invention.

Sequence 120 AA;

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The invention relates to a novel method for preventing, treating or ameliocating one or more symptoms associated with a respiratory syncytial virus (RSV) infection in a mammal. The method comprises administering to the mammal a dose of one or more antibodies or their fragments that immunospecifically binds to one or more RSV antigens, where the effective amount is less than 15 mg/kg of the antibodies or antibody fragments. The invention further comprises a sustained release formulation comprising one or more antibodies or their fragments that immunospecifically binds to one or more ARV antigens; and a pharmaceutical composition comprising one or more antibodies or their fragments that immunospecifically binds one or more RSV antigens formulated for pulmonary delivery. The methods and compositions have respiratory gen, and virucide activities. The antibodies can be used in the creation of a vaccine. The compositions may be used in gene therapy. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of RSV infection. This sequence represents an RSV antigen binding variable heavy domain of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preventing, treating or ameliorating symptoms associated with a respiratory syncytial virus (RSV) infection by administering antibodies that immunospecifically bind to one or more RSV antigens.
                                        Gaps
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                                                                                                                                                                                                                                                                                                                RSV antigen binding antibody variable heavy domain, SEQ ID 28.
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                                                                                                                                                                                                                                                                                                                                               respiratory syncytial virus infection; delivery mechanism; respiratory-gen.; virucide; vaccine; gene therapy; heavy chain variable region.
Score 47; DB 9; Length 120;
Pred. No. 4.4;
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                                      2; Indels
                                    2; Mismatches
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                                                                                                                                                                                                     ADW19882 standard; protein; 120 AA.
71.2%;
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28-NOV-2001; 2001US-00996265.
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                 Local Similarity 63.6
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RDMIFNWYFDV 109
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Matches
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Gaps

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Best Local Similarity 63.6 Matches 7; Conservative

Query Match

1 RETVFYWYFDV 11

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99 RDMIFNWYFDV 109
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Search completed: February 23, 2006, 09:40:58 Job time : 103.769 secs

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979 980 981 988 988 998 999 999 999 999 999

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A;Molecule type: DNA
A;Residues: 1.31 < WEI>
A;Cross-references: UNIPARC:UPI00001154F6; GB:S85733; NID:g246316; PIDN:AAB21560.1; PID:
A;Cross-references: spleen
A;Note: sequence extracted from NCBI backbone (NCBIN:85733, NCBIP:85761)
C;Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                   compartment after primary immunization
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: C49038
R;Weiss, U.; Zoebelein, R.; Rajewsky, K.
Eur. J. Immunol. 22, 511-517, 1992
A;Title: Accumulation of somatic mutants in the B cell compartment after pri A;Reference number: A49038
A;Stetus: preliminary
A;Accession: C49038
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-38 <WEI>
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C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: E49038
R;Weiss, U.; Zoebelein, R.; Rajewsky, K.
                                                                                                                                                                                                                                                                                    Ig lambda chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
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A;Note: sequence extracted from NCBI backbone (NCBIN:85734, NCBIP:85801)
C; Keywords: heterotetramer; immunoglobulin
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                        Length 123;
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Pred. No. 0.58;
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R;Weiss, U.; Zoebelein, R.; Rajewsky, K.
Eur. J. Immunol. 22, 511-517, 1992
A;Titler: Accumulation of somatic mutants in the B cell c
A;Reference number: A49038; WUD:92164733; PMID:1537385
A;Accession: B49038
A;Status: preliminary
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85.7%; Pred. No. 0.71
ive 1; Mismatches
                                                                         0; Mismatches
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                          71.2%; Score 47;
100.0%; Pred. No.
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                                                 Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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32 YYWYFDV 38
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25 YYWYFDV 31
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Best Local Similarity
Matches 6; Conserv
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Ig heavy chain V region (clone 165.5) - mouse (fragment)
C;Species: Museuculus (knouse mouse)
C;Species: Museuculus (knouse mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1004
R;Tillama, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J Exp. Med. 176, 761-779, 1992
A;Tillama, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1004
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A30540
Ig heavy chain V region (253.12D3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 16-Aug-1996
C;Accession: A30540
R;Clafiln, J.L.;Berry, J.
J. Immunol. 141, 4012-4019, 1988
A;Title: Genetics of the phosphocholine-specific antibody response to Streptococ A;Reference number: A30534; MUD:89035545; PMID:3141511
A;Accession: A30540
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-123 cCLA
A;Cross-references: UNTPARC;UPI0000176C34
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterocteramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>
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GUT8-2a protein -
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Pred. No. 0.11;
1; Mismatches
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F85839
E70031
T26568
T34451
A75390
T15830
PH1735
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B75022
A28771
S40612
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Best Local Similarity 72.7°
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REGCYYWYFDV 90
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F30539
Ig heavy chain V region (224.4B11) - mouse (fragment)
C;Species Mus musculus (house mouse)
C;Species Mus musculus (house mouse)
C;Accession: F30539
R;Claflin, J.L.; Berry, J.
J Immunol. 141, 4012-4019, 1988
A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneu A;Reference number: A30534; MUID:89035545; PMID:3141511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "If heavy chain V region (252.5E10) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 16-Aug-1996
C;Accession: 130539
R;Clafiln, J.L; Berry, J.
J. Immunol. 141, 4012-4019, 1988
A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneu A;Reference number: A30534; MUID:89035545; PMID:3141511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
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                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
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C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
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A;Molecule type: DNA
A;Residues: 1-592 <WOO>
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Pred. No. 2.2;
1; Mismatches
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Pred. No. 2.2;
1; Mismatches
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ilarity 85.7%;
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ilarity 85.7%;
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Query Match
Best Local Similarity
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107 YYWYFDV 113
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D49038
Ig lambda chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: D49038
R;Weiss, U.; Zoebelein, R.; Rajewsky, K.
Bur. J. Immunol. 22, 511-517, 1992
A;Title: Accumblation of somatic mutants in the B cell compartment after primary immuniz A;Reference number: A49038; MUID:92164733; PMID:1537385
A;Accession: D49038
A;Accession: D49038
A;Residues: J-58 «WEI>
A;Rosidues: 1-58 «WEI>
A;Cross-references: UNIPARC:UPIO0001154F8; GB:S85735; NID:9246320; PIDN:AAB21562.1; PID: A;Experimental source: spleen
A;Note: sequence extracted from NCBI backbone (NCBIN:85735, NCBIP:85802)
C;Keywords: heterotetramer; immunoglobulin
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G30539

Ig heavy chain V region (224.7E7) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 16-Aug-1996
C;Accession: G30539
R;Claflin, J.L; Berry, J.
J. Immunol. 141, 4012-4019, 1988
A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneu A;Reference number: A30534; MUID:89035545; PMID:3141511
A;Accession: G30539
A;Stetus: preliminary; nucleic acid sequence not shown; not compared with conceptual tra A;Molecule type: mRNA
A;Residues: 1-124 ccla>
A;Cross-references: UMFPARC:UPI0000176D23
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology clMM>
                     A;Title: Accumulation of somatic mutants in the B cell compartment after primary immuniz A;Reference number: A49038; MUID:92164733; PMID:1537385
A;Reference number: A49038
A;Reference number: B49038
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-56 <WEI>A;Cross-references: UNIPARC:UPI00001154F9; GB:S85736; NID:9246322; PIDN:AAB21563.1; PID:A;Residues: equence extracted from NCBI backbone (NCBIN:85736, NCBIP:85804)
C;Keywords: heterotetramer; immunoglobulin
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1.1;
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Pred. No.
  Immunol. 22, 511-517, 1992
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85.7%;
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Best Local Similarity 85.77
Secondary 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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YYWYFDV 58
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Best Local Similarity
Matches 6; Conserv
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R,Solin, M.L.; Kaartinen, M.
Immunogenetics 36, 306-313, 1992
A;Title: Allelic polymorphism of mouse Igh-J locus, which encodes immunoglobulin heavy c
A;Reference number: S26744; MUID:92355114; PMID:1644448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:0924P5; UNIPROT:0924R3; UNIPROT:091V67; UNIPARC:UPI0000176DD C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H. Bur. J. Immunol. 19, 1289-1295, 1989
A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl. A;Reference number: $13685; MUID:89338557; PMID:2503389
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C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-May-1997
C;Accession: 813692
R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.
Bur. J. Immunol. 19, 1289-1295, 1989
A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl
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C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig heavy chain J region JH1 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 25-Feb-1994 #sequence_revision 24-Oct-1998 #text_change 31-Dec-2004
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              Pred. No. 4.3;
3; Mismatches
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              60.08;
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A;Molecule type: DNA
A;Residues: 1-17 <SOL>
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                                                     Conservative
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    Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
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Best Local S
Matches 6
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 347-592 <LYN>
A;Cessidues: 347-592 <LYN>
C;Generics: C;Generics: A;Generics:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1313687

Ig heavy chain V region - mouse (fragment)

Ig heavy chain V region - mouse (fragment)

Ig heavy chain V region - mouse (c) Species: Must musculus (house mouse)

C; Accession: 18-Peb-1994 #sequence_revision 10-Nov-1995 #text_change 23-May-1997

C; Accession: 813687

R; Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H. Bur. J. Immunol. 19, 1289-1295, 1989

A; Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl
A; Reference number: $13685; MuID:89338557; PMID:2503389
A;Cross-references: UNIPROT:074774; UNIPARC:UPI00006C873; EMBL;AL033385; PIDN:CAA21884.
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Ig heavy chain V region (clone 202.33) - mouse (fragment)

(Species: Mus musculus (house mouse)

(Species: Mus musculus (house mouse)

C; Species: Mus musculus (house mouse)

C; Accession: PHIO06

R; Tillman, D.M.; Jou, NT.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A; Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective I A; Reference number: PH0971; MUID:92381444; PMID:1512540

A; Accession: PH1006

A; Accession: PH1006

A; Accession: Putloof

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                                           A; Experimental source: strain 972h-; cosmid c2G5
K; Lyme, M.; Rajandream, M.A.; Barrell, B.G.; Lelaure, V.; Galibert, F.
submitted to the EMBL Data Library, October 1998
A; Reference number: Z21896
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A;Introns: 14/1; 32/1
C;Superfamily: translation elongation factor Tu homology
F;178-326/Domain: translation elongation factor Tu homology <ETU>
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A;Residues: 1-111 <PEN.
A;Residues: 1-111 <PEN.
A;Croserae: UNIDARC:UPI0000176902; EMBL:X53340
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetzamer; immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.7%; Score 44; DB 2; Length 592; llarity 70.0%; Pred. No. 10; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: B cell, strain [NZB x NZW]F1
C; Superfamily: immunoglobulin v region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;10-93/Domain: immunoglobulin homology <IMM>
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llarity 87.5%; Pred. No. 4.2;
Conservative 0; Mismatches 1
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A;Residues: 1-108 <TIL>
A;Cross-references: UNIPARC:UP10000176D16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 ETVFYWYFDV 11
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57 DTVWYYYFDV 66
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Best Local Similarity
7; Conserve
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nes 7; Conserv
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Best Local S
Matches 7
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C;Accession: S13688
R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.
Bur. J. Immunol. 19, 1289-1295, 1989
A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl. A;Reference number: S13685; MUID:8933855; PMID:2503389
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Ig heavy chain V region - mouse (fragment)

Is heavy chain V region - mouse (c;Species Musculus (house mouse)

C;Species Musculus (house mouse)

C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 30-May-1997

C;Accession: S13693

R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.

A;Title: Biased immunol. 19, 1289-1295, 1989

A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl.

A;Reference number: S13685; MUID:89338557; PMID:2503389
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C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: $26463
                                  Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb_1994 #sequence_revision 10-Nov-1995 #text_change 30-May-1997
                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-110 <PEN>
A;Residues: 1-110 <PEN>
A;Cross-references: UNIPARC:UP10000176904; EMBL:X53341
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heteroterramer; immunoglobulin
F;10-93/Domain: immunoglobulin homology <IMM>
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A;Cross_references: UNIPARC:UPI0000176E3D; EMBL:X53346
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100.0%; Pred. No. 6.3;
ative 0; Mismatches
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100.0%; Pred. No. 6.3;
ive 0; Mismatches
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hes 6; Conservative
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submitted to the EMBL Data
A;Reference number: S26459
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Best Local Similarity
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-111 < KAV>
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PH1002
Ig heavy chain V region (clone 165.45) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Tille: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Restiues: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Restiues: 1-106 <TIL->
A;Cross-references: UNIPARC:UPI0000176D13
A;Cross-references: UNIPARC:UPI0000176D13
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin R;15-97/Domain: immunoglobulin F;15-97/Domain: immunoglobulin R;15-97/Domain:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ign heavy chain V region (clone 163.47) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH0987
C;Accession: PH0987
B;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Tille: Bbth IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Reference number: PH0987
A;Reference nucleic acid sequence not shown
A;Residues: 1-107 cTIL
A;Residues: 1-107 cTIL
A;Residues: UNIPARC:UPI0000176D07
A;Residues: UNIPARC:UPI000176D07
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology < IMM>
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                                  A;Cross-references: UNIPARC:UP10000176D57; EMBL:X53345
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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A;Residues: 1-101 <PEN>
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Length 111;

DB 2;

62.1%; Score 41; DB 2; 100.0%; Pred. No. 6.3;

Query Match Best Local Similarity

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(Species: Mus musculus (house mouse)

(Species: Musculus (house mouse)

(Species: Musculus (house mouse)

(Species: Musculus (house mouse)

(Species: Musculus (house)

(Species: Mu
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513690

Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C;Date: 18-Feb-1994 #sequence_revision of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the 
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S26327
G19 heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Nus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
C;Accession: S26327
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein A;Accession: S26307
A;Molecule type: mRNA
A;Residues: 1-112 <STANA

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C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
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Pred. No. 6.4;
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-91/Domain: immunoglobulin homology <IMM>
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96 YWYFDV 101
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Ig heavy chain V region (clone 202.17) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: PH1022
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Ritle: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B Cs.
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Residues: 1-112 < AIL.>
A;Rocession: PH1022
A;Residues: 1-12 < AIL.>
A;Residues: 1-12 < AIL.>
A;Residues: 1-12 < AIL.>
A;Residues: 1-12 < AIL.>
A;Residues: 1-112 < AIL.>
A;Residue
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R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H. Bur. J. Immunol. 19, 1289-1295, 1989
A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to clc: A;Reference number: $13685; MuID:89338557; PMID:2503389
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C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 30-May-1997
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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A;Residues: 1-112 <PEN>
A;Cross-references: UNIPARC:UPI0000176ESF; EMBL:X53343
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-112 <PRN>
A;Residues: 1-112 <PRN>
A;Croses-references: UNIPARC:UPI0000176900; EMBL:X53338
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <!MM>
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6.4;
                                                                                                                                                                                                                                                                                            DB 2;
6.4;
                                                                                                                                                                                                                                                                                       Query Match 62.1%; Score 41; DB Best Local Similarity 100.0%; Pred. No. 6.4 Matches 6; Conservative 0; Mismatches
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A;Title: Aino acid sequence of homogeneous antibodies to dextran and DNA rearrangements A;Reference number: A26242; MUID:80078170; PMID:6765983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Note: the sequences of 10 hybridoma proteins that also bind dextran differ from that s C;Comment: This protein binds dextran.
C;Comment: This protein binds dextran.
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; hybridoma; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;22-96/Disulfide bonds: #status predicted
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C,Accession: D3656
T, Derry, J.; Flaherty, D.; Dunnick, W.
J. Immunol. 138, 3060-3068, 1987
A;Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced wit A;Reference number: A30556; MUID:87196439; PMID:3106498
A;Accession: D30556
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region (J558) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V region (5G4) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Feb-1989 #sequence_revision 23-Feb-1989 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig heavy chain V region (5-1E4) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Nov-1988 #sequence_revision 03-Aug-1992 #text_change 16-Aug-1996
                                               Gaps
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A;Note: the sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;13-98/Domain: immunoglobulin homology < IMM>
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                                               Indels
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100.0%; Pred. No. 6.9;
ive 0; Mismatches
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R;Schilling, J.; Clevinger, B.; Davie, J.M.; Hood,
Nature 283, 35-40, 1980
                                            Mismatches
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               Pred. No.
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               100.08;
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Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
                                            Conservative
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                                                                                                                                             102 YWYFDV 107
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         Best Local Similarity
Matches 6; Conserv
                                                                                                 6 YWYFDV 11
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Ig heavy chain V region (clone 178.130) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Dacession: PH1018
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B C
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Resension: PH1018
A;Reterence number: H018
A;Reserences: UNIPARC:UPI0000176CEA
A;Residues: 1-113 <TIL>
A;Coss-references: UNIPARC:UPI0000176CEA
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer: immunoglobulin homology <IMM>F;15-99/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Igheavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 813694
C;Accession: 813694
A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to clarke feccession: 813694
A;Accession: 813694
A;Residues: 1-115 <PEN>
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A, Residues: 1-116 < PEN.
A, Residues: 1-116 < PEN.
A, Residues: 1-116 < PEN.
A, Cross-references: UNIPARC: UPI0000113773; EMBL: X53344; NID: G55235; PIDN: CAA37430.1; PIC
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology < IMM.>
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Ig heavy chain V region - mouse (fragment)

Ig heavy chain V region - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Accession: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: 813691

R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.

A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl

A;Reference number: $13685; MuID:89338557; PMID:2503389

A;Accession: $13691.
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100.0%; Pred. No. 6.4;
tive 0; Mismatches
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 6; Conservative
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Query Match

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107 YWYFDV 112
                Query Match
Best Local Similarity
Matches 6; Conserv
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Ig heavy chain V region (HPCG13) - mouse

C.Species: Mus musculus (house mouse)

C.Species: Mus musculus (house mouse)

C.Accession: F93256

R.Seathart, P.J.; Johnson, N.D.; Douglas, R.; Hood, L.

R.Fleathart, P.J.; Johnson, N.D.; Douglas, R.; Hood, L.

Nature 291, 29-34, 1981

A;Title: IgG antibodies to phosphorylcholine exhibit more diversity than their IgM count
A;Reference number: A93256, MUID:81197602; PMID:7231520

A;Recession: F93256

A;Molecule type: protein
A;Residues: 1-123 - GEBA

A;Residues: 1-123 - GEBA

A;Residues: L-123 - GEBA

A;Resid
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AVMSH8
Ig heavy chain V region (HPCG8) - mouse
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C.Accession: E93256
R.Gearlart, P.J.; Johnson, N.D.; Douglas, R.; Hood, L.
Nature 291, 29-34, 1981
A.Title: IgG antibodies to phosphorylcholine exhibit more diversity than their IgM count A;Reference number: A93256, MUID:81197602; PMID:7231520
A.Molecule type: protein
A.Residues: 1-123 -GEA>
A.Molecule type: protein
A.Residues: UNPROT:P01792; UNIPARC:UPI0000027115
A.Mote: the possibility that some of the diversity seen in sequences of phosphorylcholine.
C.Comment: This hybridoma protein binds phosphorylcholine.
C.Comment: This hybridoma protein binds phosphorylcholine.
C.Superfamily: immunoglobulin v region; immunoglobulin homology
C.Keywords: heterotetramer; hybridoma; immunoglobulin homology < IMM>
F:15-100/Domain: immunoglobulin homology < IMM>
F:22-98/Disulfide bonds: #status predicted
R; Feeney, A.J.; Clarke, S.H.; Mosier, D.E.
J. Immunol. 141, 1267-1272, 1988
J. Immunol. 141, 1267-1272, 1988
J. Title: Specific H chain junctional diversity may be required for non-T15 antibodies to A; Reference number: A30515; MUID:88285740; PMID:3135325
A; Accession: B30515
A; Conserved type: mRNA
A; Residues: 1-122 < FEE>
A; Conserved type: mRNA
A; Residues: 1-122 < FEE>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 14-99/Domain: immunoglobulin homology < IMM>
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Pred. No. 6.9;
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100.0%; Pred. No. ...
0; Mismatches
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Best Local Similarity luv...
6; Conservative
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YWYFDV 111
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: O1-Sep-1981 #sequence revision 01-Sep-1981 #text change 09-Jul-2004
C;Accession: A93804; A90795; A94449; A93256; C30539; I30539; B30539; A02070; A90.
R;Rudikoff, S;Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 73, 2109-2112, 1976
A;Title: Size differences among immunoglobulin heavy chains from phosphorylcholine-bindin A;Reference number: A93804; WUID:76222762; PMID:819932
A;Contents: TEPC 15
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A,Residues: 1-123 <RUD>
A,Cross-references: UNIPARC: UNIPARC: UDI000002710F
A,Cross-references: UNIPARC: UNIPARC: UDI000002710F
B,Early, P.; Huang, H.; Davis, M.; Calame, K.; Hood, L.
Cell 19, 981-992, 1980
A,Title: An immunoglobulin heavy chain variable region gene is generated from three segme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-101 < EAR>
A; Cross-references: UNIPARC: UPI0000173733
A; Note: sequence determined from the germline H107 gene
R; Rudikoff, S.; Barstad, P.; Potter, M.; Hood, L.
unpublished results, cited by Hood, L., Campbell, J.H., and Elgin, S.C.R., Annu. Rev. Gerl
A; Reference number: A94474
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A,Accession: A9474
A,Molecule type: protein
A,Residues: 1-123 <RU2>
A;Cross-references: UNIPARC:UPI000002710F
R,Barstad, P.
B,Barstad, P.
A,Reference number: A94449
A,Reference number: A94449
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A; Residues: 1-104, 'B', 106-123 < BAR>
A; Residues: 1-104, 'B', 106-123 < BAR>
A; Carsh-references: UNIPPARC:UPI0000027110
R; Gazhart, P.J.; Johnson, N.D.; Douglas, R.; Hood, L.
Nature 291, 29-34, 1981
Nature 291, 29-34, 1981
A; Title: 1gG antibodies to phosphorylcholine exhibit more diversity than their IgM counter
A; Reference number: A93256; WUID:81197602; PMID:7231520
A; Accession: A93256
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2. Immunol. 141, 4012-4019, 1988
A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneum
A;Reference number: A30534; MUID:89035545; PMID:3141511
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A;Residues: 1-123 <CL2>
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                                                                           Gaps
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1; Length 123;
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A;Residues: 1-123 <GRA>
A;Cross-references: UNIPARC:UPI000002710F
A;Experimental source: hybridoma proteins HPCM1, HPCM2, HPCM3
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A;Cross-references: UNIPARC:UP1000002710F
A;Experimental source: hybridoma proteins 224.288, 224.2G3
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h 62.1%; Score 41; DB Similarity 100.0%; Pred. No. 7; 6; Conservative 0; Mismatches
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Conservative

Best Local Similarity Matches 6; Conserv

Query Match

107 YWYFDV 112

g à

6 YWYFDV 11

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Ig heavy chain V region (2B2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 3.2-Feb-1989 #sequence_revision 23-Feb-1989 #text_change 16-Aug-1996
C;Accession: B30556
R;Claflin, J.L.; Berry, J.; Flaherty, D.; Dunnick, W.
A;Tltle: Somatic evolution of diversity among anti-phosphocholine antibodies induced wit A;Reference number: A30556; MUID:87196439; PMID:3106498
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C;Species: Mus musculus (house mouse)
C;Accession: D30339
R;Claflin, J.L.; Berry, J.
A) Immunol. 141, 4012-4019, 198
A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pnew A;Reference number: A30534; MUID:89035545; PMID:3141511
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A;Molecule type: mRNA
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C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 23-Jul-1999
C;Accession: B30566
C;Accession: T.; Kabat, E.A.
J. Immunol. 142, 863-870, 1989
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-123 «CLLA»
A;Cross-references: UNIPARC:UPI0000176C3C
A;Cross-references was determined from the differentiated gene
C;Superfamily: Immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology «IMM»
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                                          Indels
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100.0%; Pred. No. .,
... 0; Mismatches
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               ed. No. 7;
Mismatches
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      Best Local Similarity 100.0%;
Matches 6; Conservative 0
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Best Local Similarity 100.
Matches 6; Conservative
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107 YWYFDV 112
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B30556
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: PL0017
R;Chien, N.C.; Pollock, R.R.; Desaymard, C.; Scharff, M.D.
J. Exp. Med. 167, 954-973, 1988
A;Title: Point mutations cause the somatic diversification of IgM and IgG2a antiphosphor A;Reference number: JL0029; MUID:88171315; PMID:3127529
A;Accession: PL0017
A;Residues: I-123 <CHI>A;Residues: UNIPARC:UPI0000176C41
C;Superfemily: immunoglobulin y region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-101/Domain: immunoglobulin homology 
A;Cross-references: UNIPARC:UPI00002710F
A;Experimental source: hybridoma proteins 252.5E11, 253.12G5
A;Accession: B30539
A;Accession: B30539
A;Accession: B30539
A;Residues: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-121 < CL3>
A;Access-references: UNIPARC:UPI0000173734
A;Cross-references: UNIPARC:UPI0000173734
A;Cross-references: UNIPARC:UPI0000173734
A;Experimental source: hybridoma protein 174.2E11
C;Comment: These chains were isolated from myeloma and hybridoma proteins that bind phos C;Superfamaily: immunoglobulin jmmunoglobulin homology
C;Keywords: heterotetramer; hybridoma; immunoglobulin homology ciMH>
F;15-100/Domain: immunoglobulin homology ciMH>
F;2-98/Disulfide bonds: #status predicted
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A;Molecule type: mRNA
A;Residues: 1-123 <CLAA
A;Cross-rences: UNIPARC:UPI0000176D24
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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Ig heavy chain V region (253.15D10) - mouse (fragment)

Species: Nus musculus (house mouse)

C;Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 16-Aug-1996

C;Accession: B30540

R;Clafflin, J.L.; Berry, J.

J. Immunol. 141, 4012-4019, 1988

A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneu A;Reference number: A30534; MUID:89035545; PMID:3141511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Filo2-106/Domain: D region <DRE>
F;107-123/Domain: J region (fragment) <JRE>
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Conservative

Local Similarity

Query Match Best Local S Matches 6

9

107 YWYFDV 112

A; Accession: B30540

Query Match

6 YWYFDV 11

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7.32 . 3.4.4

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6; Conservative
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|121 YWYFDV 126
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             Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                       6 YWYFDV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-181 < FEA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 VPYWYP 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-284 <DEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 VFYWYF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 VFYWYF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: G22848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics:
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G22848
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503326
Ig heavy chain precursor V-D-J region (clone pCP12) - mouse (fragment)
C; Species: Wus musculus (house mouse)
C; Species: Wus musculus (house mouse)
C; Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 23-Jul-1999
C; Accession: 503326
R; Reininger, L; Kaushik, A; Izui, S; Jaton, J.C.
Eur. J. Immunol. 18, 1521-1526, 1988
A; Title: A member of a new V(H) gene family encodes antibromelinized mouse red blood cell A; Reference number: 503326; MUD: 89052754; PMID: 2903828
A; Molecule type: mRNA
A; Residues: 1-137 < REI-
A; Ccession: 503326
A; Molecule type: mRNA
A; Residues: 1-137 < REI-
A; Cross-references: UNIPARC: UPIO000115093; EMBL: X00743; NID: 952483; PIDN: CAA68712.1; PIT
C; Superfamily: immunoglobulin v region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin newlogy
C; Keywords: heterotetramer; immunoglobulin homology cited <SIG>
F; 20-117/Ponduct: Ig heavy claim v region pCPL2 #status predicted <MAT>
F; 118-120/Domain: immunoglobulin homology <IMM>
F; 118-120/Domain: J region #status predicted <ARE>
F; 121-137/Domain: J region #status predicted <ARE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Igh heavy chain V region (M511) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: B93857
R;Robinson, E.A.; Appella, E.
Proc. Natl. Acad. Sci. U.S.A. 77, 4909-4913, 1980
A;Title: Complete amino acid sequence of mouse immunoglobulin alpha chain (MOPC 511).
A;Reference number: A93857; MUID:81054880; PMID:6776528
A;Accession: B93857
A;Molecule type: protein
A;Accession: B93857
A;Molecule type: protein
A;Accession: B93857
C;Comment: Tile myeloma protein binds phosphorylcholine.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology <br/>C;Superfamily: immunoglobulin homology <br/>C;Superfamily: immunoglobulin homology <br/>F;22-98/Disulfide bonds: #status predicted
A;Title: Variable region cDNA sequences and antigen binding specificity of mouse monocld
                                                                                                       A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-123 «MAT»
A/Fesidues: 1-123 «MAT»
A/Cross-references: UNIPARC:UPI0000114E20; GB:M24269; NID:g195619; PIDN:AAA38373.1; PID:C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                 Score 41; DB 2; Length 123;
                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                           A;Reference number: A30560; MUID:89110062; PMID:2464028
A;Accession: B30560
                                                                                                                                                                                                                                                                                                              62.1%; Score ___ 100.0%; Pred. No. 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. No.
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Best Local Similarity 100.
Matches 6; Conservative
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YWYFDV 113
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Best Local Similarity
Matches 6; Conserv
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cytochrome-c oxidase (EC 1.9.3.1) chain III - Trypanosoma brucei mitochondrion (fragment)
C;Species: mitochondrion Trypanosoma brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: A28782
R;Feagin, J.E.; Abraham, J.M.; Stuart, K.
Eell 53, 413-422, 1988
A;Title: Extensive editing of the cytochrome c oxidase III transcript in Trypanosoma bruk A;Reference number: A28782; MUID:88210466; PMID:2452697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Genome: mitochondrion
A;Genetic code: SGC6
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytochrome-c oxidase (EC 1.9.3.1) chain III - Leishmania tarentolae mitochondrion Cytochromes: mitochondrion Leishmania tarentolae Cybecies: mitochondrion Leishmania tarentolae Cybecies: mitochondrion Leishmania tarentolae Cybecesion: G22848

Ride la Cruz, V.E.; Neckelmann, N.; Simpson, L.
J. Biol. Chem. 259, 15136-15147, 1984
A;Fitle: Sequences of six genes and several open reading frames in the kinetoplast maxic;
A;Reference number: A22848; MUID:85079995; PMID:6096360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Genome: mitochondrion
A;Genetic code: SGC6
C;Superfamily: cytochrome-c oxidase chain III
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytochrome-c oxidase (EC 1.9.3.1) chain III - Crithidia fasciculata mitochondrion (fragme C;Species: mitochondrion Crithidia fasciculata C;Species: mitochondrion Crithidia fasciculata C;Date: 19-Jan-1988 #sequence_revision 19-Jan-1988 #text_change 07-Dec-1999 C;Accession: A25877
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A;Note: the authors translated the codon TGT for residues 131 and 140 as Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 31-Dec-2004
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Length 137;
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                                                                       0; Indels
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   DB 2;
. 7.8;
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Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches
62.1%; Score 41; DB 100.0%; Pred. No. 7.8 ive 0; Mismatches
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62.1%; Score 41; DB 2; 100.0%; Pred. No. 16; ive 0; Mismatches

6; Conservative

Query Match Best Local Similarity Matches 6; Conserv

|||||| 138 VFYWYF 143

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RESULT 45

4 VPYWYP

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C; Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
C; Accession: A25941; JH0666
R; Brueggemann, M: Free, J: Diamond, A: Howard, J: Cobbold, S: Waldmann, H.
Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986
A; Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse antibod A; Reference number: A25941; MUID:86287397; PMID:3016742
A; Accession: A25941
A; Molecule type: DNA
A; Residues: 1-18 <BRU>
A; Cross-references: UNIPARC:UP10000114C27; GB:M13798; NID:g204707; PIDN:AA41371.1; PID: R; Lang, P: Mocikat, R.
Gene 102, 261-264, 1991
A; Title: Immunoglobulin heavy-chain joining genes in the rat: comparison with mouse and A; Reference number: JH0666; MUID:91340162; PMID:1908401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conserved hypothetical protein Atu5299 [imported] - Agrobacterium tumefaciens (strain CS C,Species: Agrobacterium tumefaciens C,Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 02-Jun-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CjAccession: AE3196
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. Rage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:013689; UNIPARC:UPI000013AA46; EMBL:Z98595; PIDN:CAB11189.2; A;Experimental source: strain 972h-; cosmid c11E3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ster, B.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CSB.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
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T37538
hypothetical protein SPAC11E3.10 - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37538
R;Murphy, L; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
A;Reference number: Z21721
A;Reference number: Z21721
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A;Residues: 1-18 <LAN>
A;Cross-references: UNIPARC:UP10000114C27; EMBL:X56791
A;Cross-references: UNIPARC:UP10000114C27; EMBL:X56791
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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A;Molecule type: DNA
A;Residues: 1-162 <MUR>
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Pred. No. 1.6;
1; Mismatches
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Matches 5; Conservative
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1 YYWYFD 6
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A; The sequence sequence of the plant pathogen Xylella fastidiosa.
A; Reference number: A82515; MUID:20365717; PMID:10910347 #Spiz28 below
A; Residues: Dealiminary
A; Residues: 1-415 cSIM>
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A; Romes: L.: Remper: E.: Ritajima: J.: R
              Risloof, P.; van den Burg, J.; Voogd, A.; Benne, R.
Nucleic Acids Res. 15, 51-65, 1997
A.7title: The nucleotide sequence of a 3.2 kb segment of mitochondrial maxicircle DNA fro ytochrome b gene and a possible frameshift gene; further evidence for the use of unusual A.Reference number: A25877
A.Accession: 
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Pred. No. 24;
1; Mismatches 0; Indels
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A;Gene: XF0087 C;Superfamily: citrate utilization determinant

Similarity 85.7%; 6; Conservative 1

Local Similarity

Matches

Query Match

||||:|| ETVFFWY 409

403

RESULT 46

2 ETVFYWY 8

8 요 A25941 Ig heavy chain J-H1 region - rat (fragment) C;Species: Rattus norvegicus (Norway rat)

Gaps

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Indels

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Best Local Similarity 85.7%; Pred. No. 35; Matches 6; Conservative 0; Mismatches
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G89009
protein ROBFIL: [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: G89009
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:99851916
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: G89009
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1.381 <5TO>
A;Coss-references: UNIPROT:001888; UNIPARC:UPI00000805EF; GB:chr_V; PIDN:AAB54247.1; PI
C;Generics:
A;Gene: R08F11.5
A;Map position: 5
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A, Molecule type: DNA
A, Residues: 1-432 <STO>
A, Residues: 1-432 <STO>
A, Cross-references: UNIPROT: Q916Q9; UNIPARC: UP100000C4FAC; GB: AE004461; GB: AE004091; NIC
A, Experimental source: strain PAO1
C; Genetics:
A;Accession: AE3196
A;Status: preliminary
A;Aolecule type: DNA
A;Residues: 1-364 «KUR»
A;Cross-references: UNIPARC:UPI0000D158A; GB:AE008687; PIDN:AAL45987.1; PID:g17743741;
A;Experimental source: strain C58 (Dupont)
A;Genetics:
A;Genetics: Atu5299
A;Genome: plasmid
C;Superfamily: uncharacterized conserved protein
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Pred. No. 29;
1; Mismatches 0; Indels
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66.7%; Pred. No. 31;
iive 1; Mismatches 2; Indels
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C;Superfamily: citrate utilization determinant
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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44 YWYFDI 49
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1.5 165 2 Q8ММС9_РГАРА Q8mwc9	1.5 166 2 QBWMCF PLARA QBWWCF 1.5 166 2 QBWWCT PLARA QBWWCT 1.5 166 2 QBWWDO_PLARA QBWWDO	1.5 166 2 Q8MWD1_PLAFA Q8mwd1 1.5 167 2 Q9PQ67_UREPA Q9pg67	1.5 168 2 Q8VDC9_MOUSE Q8vdc9 1.5 171 2 Q8MWC5_PLAFA Q8mwc5	1.5 172 2 QSHUF9_CAMJR QShuf9	1.5 1/2 2 Q6RVH2_PLAFA Q6rvh2 1.5 173 2 Q6RVH2_PLAFA	1.5 173 2 Q4T3M7 TETNG Q4t3m7	1.5 176 2 Q51J85_MAGGR Q51J85	1.5 176 2 Q4LLMO_9BURK Q41lm0	1.5 1/9 2 Q819/2 FLAFA Q819/2 1.5 181 1 TBX35 CAEEL 009376	1.5 181 2 Q7N616_PHOLL Q7n616	1.5 181 2 0983A1 RHILO 0983A1	1.5 188 2 Q60CP0_METCA Q60Cp0 1.5 189 2 O9NSH0_HTMAN O9nsh0	1.5 189 2 Q8MVV3_PLAFA Q8mvv3	1.5 189 2 Q8MVV5_PLAFA Q8mvv5	1.5 189 2 Q8MVV6 PLAFA Q8mvv6	1.5 189 2 ORMVW3 PI.APA ORMVW3	1.5 189 2 Q767F6 PACTO Q767£6	1.5 192 2 QBT4L1_BRUMA QBt4l1	1.5 193 2 Q73YD3 MYCPA Q73yd3	1.5 199 2 O6PAO3 MOUSE O6pad3	1.5 200 2 QSWGRO_BACSK QSwgro	1.5 200 2 Q88CR6_PSEPK Q88cr6	1.5 201 2 GSL2H2 GEOKA 0512h2	1.5 202 1 ADHR DROER P28485	1.5 202 2 Q54CA3 DICDI Q54ca3	1.5 202 2 QSDB14_SCHOA 1.5 205 2 OBRBZ1_THETN	1.5 207 2 QBPTI3 METMA QBpti3	1.5 207 2 Q8PJK4_XANAC Q8pjk4	1.5 209 2 Q9ZURO_ARATH Q9ZURO	L.S 209 Z GRIU4S KALSO GRYU4S	1.5 210 2 Q4L778 STAHJ Q41778	1.5 210 2 QSKW44_GEOKA QSkw44	1.5 210 2 Q5WEB5 BACSK Q5web5	1.5 210 2 Q81KS4 BACAN Q81k84	1.5 210 2 Q6G8J3_STAAS Q6G8j3	1.5 210 2 OSHP40 STAAK Q691X4 1.5 210 2 OSHP40 STAAC OShF40	1.5 210 2 Q7A534 STAAN Q7a534	1.5 210 2 Q8NW35_STAAW Q8nw35	1.5 210 2 QYYTDU STAAM QYYTGU	1.5 210 2 Q65G33_BACLD Q65G33	1.5 211 2 Q73QD9_TREDE Q73qd9	1.5 214 2 Q72Z67_BACC1 Q72Z67	1.5 214 2 Q81629_BACCR Q81629	1.5 214 2 Q633C7_BACCZ Q633C7 1.5 217 2 O8CXA4_OCEIH O8cxa4	1.5 220 2 Q60ZY9 CAEBR Q60ZY9	1.5 226 2 Q93IB2_STAAU Q93ib2	1.5 226 2 QSI998 SIAAU QSI998	1.5 229 2 Q7VF22 HELHP Q7vF22	1.5 231 2 Q6TDNO_9VIRU Q6tdn0	1.5 237 2 09VC84 DROME 09vc84	1.5 239 2 003133_TROAR 003133	1.5 240 2 Q6WMX1_DROER Q6wmx1	
4 51.5 165 2 Q8MWC9_PLAFA Q8mwc9	166 2 QBMWGC PLAFA QBmwcS 166 2 QBMWDO_PLAFA QBmwdO 166 2 QBMWDO_PLAFA QBmwdO	4 51.5 166 2 Q8MWD1_PLAFA Q8mwd1 4 51.5 167 2 Q9PQ67_UREPA Q9pg67	4 51.5 168 2 Q8VDC9 MOUSE Q8vdc9 4 51.5 171 2 Q8MWC5 PLARA Q8mwc5	4 51.5 172 2 QSHUF9_CAMJR QShuf9	4 51.5 173 2 Q6RVH2_PLAFA Q6rvh2	4 51.5 173 2 Q4T3M7 TETNG Q4t3m7 4 51 5 174 2 O80C50 DBATA	4 51.5 176 2 Q51J85_MAGGR Q51J85	4 51.5 176 2 Q4LLMO 9BURK Q41lm0	4 51.5 1/9 2 Q819/2 FLAFA Q819/2 4 51.5 181 1 TBX35 CAEEL 009376	4 51.5 181 2 Q7N616_PHOLL Q7n616	4 51.5 181 2 Q983A1_RHILO Q983a1	4 51.5 188 2 Q6OCPO METCA Q6OCDO 4 51.5 189 2 O9NSHO HIMAN O9nsho	4 51.5 189 2 Q8MVV3_PLAFA Q8mvv3	4 51.5 189 2 Q8MVV5_PLAFA Q8mvv5	4 51.5 189 2 Q8MVV6 PLAFA Q8mvv6	4 51.5 189 2 COMMW2 DLAPA COMMW3	4 51.5 189 2 Q767F6 9ACTO Q767E6	4 51.5 192 2 Q8T4L1_BRUMA Q8t4l1	4 51.5 193 2 Q73YD3 MYCPA Q73yd3	4 51.5 199 2 06PAÖ3 MOUSE 06pag3	4 51.5 200 2 QSWGRO_BACSK QSwgro	4 51.5 200 2 Q88CR6_PSEPK Q88cr6	4 51.5 201 2 QSKFU3_FONFI QSKTU3 4 51.5 201 2 QSL2H2_GEOKA O512h2	4 51.5 202 1 ADHR DROER P28485	4 51.5 202 2 Q54CA3 DICDI Q54CA3	4 51.5 205 2 QSBSI_THETN	4 51.5 207 2 QBPTI3 METMA QBpti3	4 51.5 207 2 Q8PJK4_XANAC Q8pjk4	4 51.5 209 2 Q9ZURO ARATH Q9ZURO	4 51.5 209 2 Qaio45 KADSO Qay045	4 51.5 210 2 Q4L778 STAHJ Q41778	4 51.5 210 2 Q5KW44_GEOKA Q5kw44	4 51.5 210 2 QSWEB5 BACSK Q5web5	4 51.5 210 2 Q81KS4_BACAN Q81k84	4 51.5 210 2 Q6G8J3_STAAS Q6g8j3	4 51.5 210 2 OSHP40 STAAK Q5DEX4	4 51.5 210 2 Q7A534 STAAN Q7a534	4 51.5 210 2 QBNW35_STAAW QBNW35	4 51.5 210 2 Q99TDU STAAM Q99EQ0	4 51.5 210 2 Q65G33_BACLD Q65G33	4 51.5 211 2 Q73QD9 TREDE Q73Qd9	4 51.5 214 2 Q72Z67_BACC1 Q72Z67	4 51.5 214 2 Q816Z9_BACCR Q816Z9	4 51.5 214 2 Q633C7_BACCZ Q633C7 4 51.5 217 2 O8CXA4_OCEIH O8Cxa4	4 51.5 220 2 Q60ZY9_CAEBR Q60ZY9	4 51.5 226 2 Q93IB2_STAAU Q931b2	4 51.5 226 2 Q51998 SIAAU Q51998 4 51.5 226 2 ORCH53 STARD ORCH53	4 51.5 229 2 Q7VF22_HELHP Q7vF22	4 51.5 231 2 Q6TDNO_9VIRU Q6tdn0	4 51.5 237 2 09VC84 DROME 09vC84	4 51.5 239 2 003133_TROAR 003133	4 51.5 240 2 Q6WMX1_DROER Q6wmx1	•
34 51.5 165 2 QBMWC9_PLAFA QBmwc9	4 51.5 166 2 QBMWCC PLARRA QBMWCR 4 51.5 166 2 QBWWC7 PLARRA QBMWC7 4 51.5 166 2 QBWWD0 PLARRA QBMWD0 PLARRA	34 51.5 166 2 Q8MWD1_PLAFA Q8mwd1 34 51.5 167 2 Q9PQ67_UREPA Q9PQ67	34 51.5 168 2 Q8VDC9_MOUSE Q8vdc9 34 51.5 171 2 Q8MWC5_PLAFA Q8mwc5	34 51.5 172 2 Q5HUF9_CAMJR Q5huf9	34 51.5 173 2 Q6RVH2_PLAFA Q6rvh2 Q6rvh2	34 51.5 173 2 Q4T3M7_TETNG Q4t3m7 34 51 5 174 2 CMSCFG BDAIA CMSCFG	34 51.5 176 2 Q51J85_MAGGR Q51J85 Q51J85	34 51.5 176 2 Q4LLMO_9BURK Q411m0	34 51.5 1/9 2 QBI9/2 34 51.5 181 1 TBX35 CAREL 009376	34 51.5 181 2 Q7N616_PHOLL Q7n616	34 51.5 181 2 0983A1_RHILO 0983A1	34 51.5 189 2 Q60CPO_METCA Q60CpO	34 51.5 189 2 Q8MVV3_PLAFA Q8mvv3	34 51.5 189 2 Q8MVV5_PLAFA Q8mvv5	34 51.5 189 2 QBMVV6 PLAFA QBmvv6 34 51.5 189 2 QBMVV6	34 51.5 189 2 QOMVW2 PIAPA ORMVW3	34 51.5 189 2 Q767F6 PACTO Q767£6	34 51.5 192 2 Q8T4L1_BRUMA Q8t4l1	34 51.5 193 2 Q73YD3 MYCPA Q73Yd3	34 51.5 199 2 06PAÖ3 MOUSE 06pad3	34 51.5 200 2 Q5WGRO_BACSK Q5wgro	34 51.5 200 2 Q88CR6 PSEPK Q88cr6	34 51.5 201 2 OSL2H2 GEOKA OS12h2	34 51.5 202 1 ADHR DROER P28485	34 51.5 202 2 Q54CA3 DICDI Q54ca3	34 51.5 205 2 08RBZ1 THETN 08rbz1	34 51.5 207 2 QBPTI3 METWA QBpti3	34 51.5 207 2 QBPJK4_XANAC QBpjk4	34 51.5 209 2 Q9ZURO_ARATH Q9zuro	34 51 5 210 1 ACTA RACSIT D29065	34 51.5 210 2 Q4L778 STAHJ Q41778	34 51.5 210 2 Q5KW44 GEOKA Q5kw44	34 51.5 210 2 Q5WEB5_BACSK Q5web5	34 51.5 210 2 Q81KS4 BACAN Q81ks4	34 51.5 210 2 Q6G8J3_STAAS Q6G8J3	34 51.5 210 2 QBGFA4_STAAK QBGFX4 34 51.5 210 2 Q5HP40_STAAC Q5hf40	34 51.5 210 2 Q7A534_STAAN Q7a534	34 51.5 210 2 QBNW35_STAAW QBnw35	34 51.5 210 2 Q99TDU_STAAM Q99TQU 34 51.5 210 2 O9K7X2_RACHD O9K7X3	34 51.5 210 2 Q65G33_BACLD Q65g33	34 51.5 211 2 Q73QD9_TREDE Q73Qd9	34 51.5 214 2 Q72Z67_BACC1 Q72Z67	34 51.5 214 2 Q816Z9_BACCR Q816Z9	34 51.5 214 2 Q633C7_BACCZ Q633C7 34 51.5 217 2 O8CXA4_OCEIH O8CXA4	34 51.5 220 2 Q60ZY9 CAEBR Q60ZY9	34 51.5 226 2 Q93IB2_STAAU Q93IB2	34 51.5 226 2 USLYSB STAMU QSLYSB	34 51.5 229 2 Q7VF22_HELHP Q7vF22	34 51.5 231 2 Q6TDNO_9VIRU Q6tdn0	34 51.5 237 2 09VC84 DROME 09vC84	34 51.5 239 2 003133_TROAR 003133	34 51.5 240 2 Q6WMX1_DROER Q6wmx1	-

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Archinerry B., Nusbaum C., Abouelleil A., Allen N., Anderson S., Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L., Burken B., Nusbaum C., Calvo S.B., Gamazata J., Chang J., Chang J., Chang J., Chang J., Chang J., Chang J., Chang J., Chang J., Chang J., Chang J., Chang J., Chang J., Elkins T., Elkins T., Engels R., Erickson J., Faros S., Ferreira P., Fliederald M., Gage D., Galagan J., Bardyna S., Graham L., Grand-Pierre N., Hafez N., Hagos B., Hall J., Horton L., Hulme W., Illev I., Andfeb D., Johnson R., Jones C., Mand-Pierre N., Hafez N., Andfeb C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A., Mathews C., Maucell E., McCarthy M., Meldrim J., Meneus L., Manning J., Mitchews C., Maucell E., McCarthy M., Meldrim J., Meneus L., Micol R., Norbu C., O'Connor T., O'Donnell P., O'Neil D., Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S., Schupbac K., Schupbac K., Seaman S., Severy P., Smirnov S., Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M., Talamas J., Tesfaye S., Theodore J., Topham K., Travers M., Vassiliev H., Vonkataraman V.S., Viel R., Vo A., Wang S., Wilson B., Minder E., Stange-T., Stander E., Zimmer A., Zimmer A., Zody M., Lender E., Eller E., Minder E., Zimmer A., Zimmer A., Zody M., Lender E., Eller E., Zimmer A., Zimmer A., Zody M., Lender E., Eller E., Zimmer A., Zody M., Lender E., Eller E., Zimmer A., Zody M., Lender E., Zimmer A., Zody M., Lender E., Eller E., Zimmer A., Zody M., Lender E., Zimmer A., Zody M., Lender E., Eller E., Zimmer A., Zody M., Lender E., Zody M., Lender E., Zody M., Lender E., Zody M., Zimper E., Zimmer A., Zody M., Lender E., Zody M., Zimper E., Zody M., Zody M., Zimpe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Hypocreomycetidae, Hypocreales, Nectriaceae, Gibberella.
                          0580ms
0494v4
0494v6
09hnp6
05kcy6
08mvu5
08mvu7
08mvu7
08mvu7
073xb5
073xb5
077587
077587
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Q6wmw8
Q6wmx0
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Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              635 AA
                                                                                                TRUA HALSA
OSKCZG CRYNB
OBMVU4 PLARA
OBMVU5 PLARA
OBMVU6 PLARA
OBMVU7 PLARA
OBMVU8 PLARA
OGISA9 CABBR
OTSKB5 WARDA
                          Q5SOM5_PLAVI
Q4G4V4_PLAVI
Q4G4T6_PLAVI
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Q6WMW8 DROEU
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ADHR DROMA
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13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
Hypothetical protein.
OKFNammes=FG00645.1,
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Q4IQ63;
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STRAIN=PH-1;
  GIBZE
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68.2%; Score 45; DB 2; Length 635;

Query Match

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                Gaps
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                                                                                                                                                                                                                                                                 Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
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"Annotation of the draft genome assembly of Arthrobacter sp. "Annotation of the draft genome assembly of Arthrobacter sp. Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arthrobacter sp. FB24.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Pred. No. 17;
1; Mismatches 1; Indels
               Indels
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Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AY517480; AA746501.1; -; Genomic_DNA.
Hypothetical protein; Plasmid.
SEQUENCE 108 AA; 12360 MW; C12448875911B87F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 197 AA; 22370 MW; 6A2F0A103C31FB7E CRC64;
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Last annotation update)
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EMBL; AAHG01000003; EAL97058.1; -; Genomic_DNA
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                                                                                                                                                108 AA
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 Pred. No. 68;
2; Mismatches
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US DOE Joint Genome Institute (PGF-ORNL);
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Best Local Similarity 75.0%;
Matches 6; Conservative
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13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
Hypochetical protein.
ORFNames=ArthDRAFT_2925;
Similarity 75.0%;
6; Conservative
                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, Hypothetical protein.
                                                                                                                                                                                                                                       Sulfolobus tengchongensis.
                                                                                                                                              QEH025 9CREN PRELIMINARY;
QEH025;
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543 TLFFWYFD 550
                                            3 TVFYWYFD 10
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Sulfolobus.
Best Local
Matches
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Q4NJB2 9MICC
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Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CS7BL/6J; TISSUE=Cerebellum;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marmey P., Bothner B., Jacquot E., de Kochko A., Ong C.A., Yot P., Siuzdak G., Beachy R.N., Fauquet C.M.;
Rice tungro baciliform virus open reading frame 3 encodes a single Virology 253:319-326(1999).

Wirology 253:319-326(1999).
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
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QBN922.
QBN922.
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:9630050K02 product:weatly similar to
HEPATOCELLULAR CARCINOMA-ASSOCIATED ANTIGEN 112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE=99119505; PubMed=9918890; DOI=10.1006/viro.1998.9519;
Marmey P., Bothner B., Jacquot E., de Kochko A., Ong C.A., Yot
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Pred. No. 51;
   DB 2; Length 197
                                                              0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update) Hypothetical protein.
Vice tungro bacilliform virus.
Viruses; Retroid viruses; Caulimoviridae; Tungrovirus.
                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 08, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                   222 AA
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
Score 44; DB 2
Pred. No. 31;
5; Mismatches
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66.78;
                               50.08;
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Matches 6; Conservative
                                                              5; Conservative
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132 RDSIFYWHFN 141
                                                                                                                         1 RETVFYWYFD 10
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222 AA; 26
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Mus musculus (Mouse)
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                            Best Local Similarity
Matches 5; Conserv
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Q08BV92 MC
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STRAIN-CSTBL/GST TISSUE-Cerebellum;
Adachi J. Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Rukuda S., Furuno M., Hangaki T., Haracka T., Hirozane T.,
Angashida K., Hayatsu N., Hirandco K., Hiracka T., Hirozane T.,
Antorani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
Antihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
A Saitoh H., Sataoh H., Sakai C., Sakazume N., Sanon H.,
Asasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (ARR-2002) to the EmBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CS7BL/6J; TISSUE=Cerebellum; MEDILIBE=20499314; PubMed=11042199; DOI=10.1101/gr.145100; MEDILIBE=20499314; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayateu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; proprinciple and subtraction of cap-trapper-selected cDNAs to prepare full-length CDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubil P., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Frunno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Rietcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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STRAIN=C57BL/6J; TISSUB=Cerebellum;
MEDLINE=2530913 PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=2530913 PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=2530913 PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=2530913 PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=2530913 PubMed=11076861; Riteunal T., Tashiro H., Itoh M., Sumin N., Ishiro H., Itoh M., Ishin Y., Nakamura S., Hazama M., Nishine T., Rashiwagi R., Yamamoto R., Mataunuto H., Sakaguchi S., Ikagami T., Kashiwagi R., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Oxazaki Y., Muramatsu M., Iloue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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Ensembl; ENSWUSG0000023367; Mus musculus.
MGI; MGI:1913308; 0610011104Rik.
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The FANTOM Consortium,
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PANTHER; PTHR15756; LR8;
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Length 244;

DB 2; 56;

Score 43; Pred. No.

65.2%;

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KEARIN-CSTBL/60; TISSUB-Kidney;

KEARIN-CSTBL/60; TISSUB-Kidney;

KEARIN-CSTBL/60; TISSUB-Kidney;

A Arakawa T., Shinata A., Yoshino M., Ishii Y.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Salto T., Okazaki Y., Gojobori T., Bono H., Kaukawa T., Salto R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T.,

Richt D., Lewis S., Matsuo Y., Nikaido I., Peeole G., Quackenbush J.,

Kuchil P., Lewis S., Matsuo Y., Nikaido I., Peeole G., Quackenbush J.,

Sakai K., Okido T., Puruno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Iyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamtoo N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

A Wynshaw-Booris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayashirat.
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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayaten N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
[Genome Res. 10:1617-1630(2000).
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STRAIN-ECTSBL/G01 TISSUE=Kidney;
The FANTOM CONSORTIUM.
The RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUB=Kidney;
MEDLINE=99279553; PLDMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
  Gaps
                                                                                                                   OBJOCSI MOUSE PRELIMINARY; PRT; 244 AA.

OBJOCSI OBK4TO;

OL-JUN-2001 (TrEMBLrel. 17, Last sequence update)

13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

Mus musculus adult male kidney cDNA, RIKEN full-length enriched

library, clone:0610011104 product:weakly similar to HEPATOCELLULAR

CARCINOWA-ASSOCIATED ANTIGEN 112 (0610011104Rik protein) (Kidney

expressed gene 2 product) (RIKEN cDNA 0610011104).
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Mismatches
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7; Conservative
                                                    145 RELNFYWYF 153
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                                                                                                                                                                                                                                                              Mus musculus (Mouse).
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Carbaile Seguence:

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

REDINE=2238827; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RAIschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

RAB Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Dokins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RAB S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rabersie, M., Touchman J.W., Green E.D., Dickson M.C.,

Rodiguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodiguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

Redereation and initial analysis of more than 15,000 full-length human
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STRAIN-ESPEND.6J. TISSUE-Kidney;
A Arakawa T., Arai A., Aono H.,
A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayateu N., Hiramcto K., Hiraoka T., Hori F.,
A Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
A Kawai J., Koina Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ebert L., Muenstermann B., Schatten R., Henze S., Bohn B.,
Mollenhauer J., Wiemann S., Schick M., Korn B.;
"Cloning of mouse full open reading frames in Gateway(R) system entry
                                   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RIKEN integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
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Strainsberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AK002546; BAB22177.2; -; mRNA.
EMBL; AT010190; CAJN8198.1; -; mRNA.
EMBL; AB063313; BAB97230.1; -; mRNA.
EMBL; AB063313; BAB97230.1; -; mRNA.
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Nakajima H., Takenaka M., Kaimori J., Imai E., Hori M.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
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STRAIN=C57BL/6J; TISSUE=Kidney;
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sequence of the plant pathogen Ralstonia solanacearum.";
                                       Nature 415:497-502(2002)
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Best Local Similarity
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Name=LOC314521;
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Burkholderiaceae; Ralstonia.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
PUTATIVE ALPHA-KTOCLUTARATE PERMEASE TRANSMEMBRANE PROTEIN.
Name=kgtPl; OrderedLocusNames=RSp0075; ORFNames=RS05546;
Ralstonia solanacearum (Pseudomonas solanacearum).
                                                                                                                                                                                                                                                                         65.2%; Score 43; DB 2; Length 244; 77.8%; Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 2; Length 251;
Pred. No. 83;
0; Mismatches 2; Indels
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB047676; BAB12184.1; -; Genomic_RNA.
                                                                                                                                                                 Pfam; PF06077; LR8; 1.
SEQUENCE 244 AA; 26596 MW; 515A398BA6243CCA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 251
251 AA; 28785 MW; BFE79D3A26134F18 CRC64;
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Last annotation update)
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                                   MGI; MGI:1913308; 0610011104Rik.
GO; GO:0016021; C:integral to membrane; TAS
                                                                                                                                                                                                                                                                                                                                             0; Mismatches
Ensembl; ENSMUSG0000023367; Mus musculus.
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                                                                                             InterPro; IPR009281; LRB.
PANTHER; PTHR15756; LRB; 1.
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Best Local Similarity 77.00,
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Q9ENN7;
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Qextni;
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|145 RELNFYWYF 153
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STRAIN=A712;
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NCBI_TaxID=12092;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; MEDLINE G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Mand=1 G.D., Ma
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Nature 415:497-502 (2002).

1-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

1-2 SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

1-3 GO: 0016021; Cantegral to membrane; IEA.

1-3 GO: 0016021; Cintegral to membrane; IEA.

1-4 GO: 0016021; Cintegral to membrane; IEA.

1-5 GO: 0016021; Firansporter activity; IEA.

1-6 GO: 0016021; Firansporter activity; IEA.

1-7 GO: 0016010; Piransporter activity; IEA.

1-8 GO: 0016010; Piransporter activity; IEA.

1-8 GO: 0016011; Firansporter activity; IEA.
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Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC092586; AAH92586.1; -; mRNA.
GO; GO:0003823; F:antigen binding; IEA.
                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00083; Sugar_tr; 1.
TIGRRAMS; TIGR00883; ZA0106; 1.
PROSITE; PS50850; MFS; 1.
PROSITE; PS00217; SUGAR TRANSPORT 2; 1.
Complete proceome; Plasmid; Transmembrane.
SEQUENCE 437 AA; 47326 MW; 619FD527C73A9C7D CRC64;
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Last annotation update)
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Query Match
Best Local Similarity
Matches 6; Conserv
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Matches 6; Conserv
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P01757;
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HV13 MOUSE
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OS-JUL-2004 (TrEMBLrel. 27, Last sequence update)
OS-JUL-2004 (TrEMBLrel. 27, Last annotation update)
OS-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Cytochrome c oxidase III (Fragment).
Trypanosoma brucei.
Trypanosoma brucei.
Bukaryota, Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5691;
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Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
James K., Rutherford K., Harris B., Churcher C.,
James K., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
Bidwell S.L., Rajandream M.A., Carucci D.J. Yates J.R., Kafatos F.C.,
"A comprehensive survey of the Plasmodium life cycle by genomic,
transcriptomic, and proteomic analyses.";
Science 307:82-86(2055).
FIREL/Genbark/DDBJ whole genome shotgun (WGS) entry which is
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04XGUG_PLACH PRELIMINARY; PRT; 34 AA.
04XGUG_FLACH
04XGUG;
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
14)Pothetical protein.
0KPNames=PC401639.00.0;
Plasmodium chabaudi.
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                       Score 42; DB 2; Length 617;
Pred. No. 2e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41; DB 2; Length 34;
Pred. No. 17;
3; Mismatches 1; Indels
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5943B1AFDD14C460 CRC64;
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SEQUENCE 34 AA; 4233 MW; 5D6964BAB37D8AD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary data.
                                                                                                                                                                                   PROSITE; PS50815; IG LIKE; 5.
PROSITE; PS00290; IG MHC; UNKNOWN
SEQUENCE 617 AA; 68362 MW; 594
                                    InterPro; IPR003597; Ig_cl.
InterPro; IPR003065; Ig_MHC.
InterPro; IPR003065; Ig_V.
Pfam; PP07654; Cl.set; 4.
SWART; SM00409; IG; 2.
SWART; SM00407; IGcl; 4.
                   InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                          63.6%;
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Best Local Similarity 75...
6. Conservative
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Q7GHK8;
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InterPro; IPR003599; Ig.
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17 KNVFYFYFDI 26
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TGYYWYFD 129
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchoncoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                Gaps
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-I- MISCELLANEOUS: This protein binds dextran.
-I- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
STRAIN=EATRO 164;
MEDLINE-89003064; PubMed=2844415; DOI=10.1016/0092-8674(88)90049-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-80078170; PubMed-6765983; Schilling J., Clevinger B., Davie J.M., Hood L.; Schilling J., Clevinger B., Davie J.M., Hood L.; Amino acid sequence of homogeneous antibodies to dextran and DNA rearrangements in heavy chain V-region gene segments."; Nature 283:35-40(1980).
                                                     Abraham J.M., Feagin J.E., Stuart K.;
"Characterization of cytochrome c oxidase III transcripts that edited only in the 3' region.";
Cell 55:267-272(1988).
EMBL; M22662; AAA63541.; -; mRNA.
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                                                                                                                                                                                                                                                                                        DB 2; Length 111;
54;
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                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                      SEQUENCE 111 AA; 13581 MW; 21C3265699917280 CRC64;
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PROSITE; PSS6883; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 AA
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100.0%; Pred. No. 54;
ive 0; Mismatches
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By similarity.
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HSSP; P01751; 1M0B.
SMR; P01757; 1-117.
InterPro; IPR001110; Ig-like.
InterPro; IPR003596; Ig-v.
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"IgG antibodies to phosphorylcholine exhibit more diversity than their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clafilin J.L., Berry J.;
"Genetics of the phosphocholine-specific antibody response to
Streptococcus pneumoniae. Germ-line but not mutated T15 antibodies are
dominantly selected.";
                                                          NUCLEOTIDE SEQUENCE (H107).

MEDLINE=80199926; PubMed=6769593; DOI=10.1016/0092-8674(80)90089-6;

Early P., Huang H., Davis M., Calame K., Hood L.;

"An immunoglobulin heavy chain variable region gene is generated from three segments of DNA, VH, D and JH.";

Cell 19:981-992(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Immunol. 141:4012-4019(1988).
-!- MISCELLANEOUS: All those sequence appears to be identical.
-!- MISCELLANEOUS: These chains were isolated from myeloma and hybridoma proteins that bind phosphorylcholine.
-!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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InterPro; IPR003596; Ig-v.
SMART; SMO046; IG-v. 1.
PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Hybridoma; Immunoglobulin domain;
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phosphorylcholine-binding proteins.";
Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
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01, Last sequence update)
47, Last annotation update)
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SMR; P01787; 1-123.
Ensembl; ENSMUSG0000021155; Mus musculus.
                                                                                                                                                                                                                                             DOI=10.1146/annurev.ge.09.120175.001513;
Rudikoff S., Barstad P., Potter M., Hood I
Unpublished results, cited by:
Hood L., Campbell J.H., Elgin S.C.R.;
Annu. Rev. Genet. 9:305-353(1975).
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MEDLINE=89035545; PubMed=3141511;
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                                                                                                                                                                                                          PROTEIN SEQUENCE (S107).
MEDLINE=76110488; PubMed=813561;
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123 AA;
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Matches 6, Conserv
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21-JUL-1986
10-MAY-2005
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HV19_MOUSE
ID HV19 MC
AC P01788 in 21-JUL-
DT 21-JUL-
DT 10-MAY-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 77:4909-4913(1980).
--- MISCELLANBOUS: This chain was isolated from a myeloma protein that binds phosphorylcholine.
--- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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21-JUL-1986 (Rel. 01, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
Mus musculus (Mouse).

Bukaryota; Mctazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euzrchontcoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Mus.
                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                   Robinson E.A., Appella E.; "Complete amino acid sequence of a mouse immunoglobulin alpha chain (MOPC 511).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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Rudikoff S., Potter M.;
"Size differences among immunoglobulin heavy chains from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 AA; 13652 MW; 9F4837731EA50207 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.
                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-VMX-2005 (Rel. 47, Last annotation update)
Ig heavy chain V region M511.
                                                                                                     122 AA
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SMR; P01790; 1-122.
Ensembl; ENSMUSG0000021155; Mus musculus.
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                                                                                                     PRT;
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MEDLINE=81054880; PubMed=6776528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
PROSITE; PS50815; IG_LIKE; 1.
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101 YWYFDV 106
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Best Local Similarity
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P01787;
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"IgG antibodies to phosphorylcholine exhibit more diversity than their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 291:29-34(1981).
--- MISCELLANEOUS: This chain was isolated from a myeloma protein that binds phosphorylcholine.
--- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                    InterPro; IPR007110; 1g-like.
InterPro; IPR003596; 1g_v.
SMART; SM0406; IGv.
InterPro; IPR03596; 1g_v.
SMART; PS50835; IG_LIKE; 1.
Direct protein sequencing; Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Pheavy chain V region HPCG13.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 AA.
HSSP; P01789; 1Mcr.
SMR; P01792; 1-123.
Ensembl; ENSMUSG0000021155; Mus musculus.
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HSSP; PO1799; IMCP.
SMR; PO1793; 1-123.
Ensembl; ENSMUSG0000021155; Mus musculus.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; I.
PROSITE; PS50835; IG_LIKE; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
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SEQUENCE
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-!- MISCELLANBOUS: This chain was isolated from a myeloma protein that binds phosphorylcholine.

-!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.

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Barstad P.;

Thesis (1975), California Institute of Technology, United States.

-!- MISCELLANEOUS: This chain was isolated from a myeloma protein that binds phosphorylcholine.

-!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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"IgG antibodies to phosphorylcholine exhibit more diversity than their
IgM counterparts.";
Ig heavy chain V region H8.

Mus musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchoncoglires; Glires; Rodentia; Sciurognathi;

Muroidea; Murinae; Mus.
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21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
1g heavy chain V region HPGG8.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buzrohotoglires; Giires; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus.
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Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
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InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
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SMR; P01788; 1-123.
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P01792;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=85079995; PubMed=6096360; de la Cruz V.F., Neckelmann N., Simpson L.; sequences of faix genes and several open reading frames in the "Sequences of faix genes and several open reading frames in the Kinetoplast maxicircle DNA of Leishmania tarentolae."; J. Biol. Chem. 259:15136-15147(1984).
-i- FUNCTION: Subunits I, II and III form the functional core of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 3 family.
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Mitochondrion.
Ebkaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania;
lizard Leishmania.
                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania,
lizard Leishmania.
                                                                                                                                                                                01-JAN-1990 (Rel. 13, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Cytochrome c oxidase subunit 3 (EC 1.9.3.1) (Cytochrome c oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; G22848; G22848.
InterPro; IPR001298; CytC_oxdse_III.
PANTHER; PTHR114012 CytC_oxdse_III; 2.
PROSTTE; PS50253; COX3; 1.
Kinetoplast; Mitochondrion; Oxidoreductase; Transmembrane.
SEQUENCE 284 AA; 34152 MW; EA52C947C71CF6CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.1%; Score 41; DB 1; Length 284; 100.0%; Pred. No. 1.4e+02; ive 0; Mismatches 0; Indels
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                          Leishmania tarentolae (Sauroleishmania tarentolae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          287 AA.
                                                                                                                            284 AA.
                                                                                                                            PRT;
                                                                                                                                                                             01-JAN-1990 (Rel. 13, Created)
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01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q34935_LEITA PRELIMINARY;
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                                                                                                                            STANDARD;
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271 VFYWYF 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enzyme complex.
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                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=5689;
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                                                                                                                       COX3 LEITA
P14546;
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Q34935_LE
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                                                                         RESULT 20
                                                                                                                          THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SE
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                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Ankara isolate clone C9;
Pain A., Renauld H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
Hall N., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kozono Y., Kozono H., Azuma T.;
Submitted (AUG-2010) to the EMBL/GenBank/DDBJ databases.
EMBL; AB06920; BAB63936.1; -; mRNA.
PIR; PH1137; PH1137.
PIR; S26744; S26744.
HSSP; P01751; 1A6W.
SWR; Q924P5; 1-1135.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR007110; Ig-11ke.
SWART; SM00406; IGV;
SWART; SM00406; IGV;
PNOSTIE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The chromosome 3 genome sequence of Theileria annulata."; Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases. EMBL; CR940152; CA175907.1; -; Genomic_DNA. Hypothetical proctein. SEQUENCE 276 AA; 32517 MW; EE4AS4AF2118AE0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.1%; Score 41; DB 2; Length 144; 100.0%; Pred. No. 70; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.1%; Score 41; DB 2; Length 276; 100.0%; Pred. No. 1.3e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DCT-2003 (TrEMBLrel. 25, Last annotation update)
VH186.2-5-J-C mu protein (Fragment).
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Last annotation update)
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13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
Hypochetical protein.
ORFNames=TA17745;
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Best Local Similarity 100.0
Local 6; Conservative
                                                                                            Q924P5 MOUSE PRELIMINARY;
Q924P5;
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Q4UB94_THEAN PRELIMINARY;
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CS7BL/6;
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                                        Matches
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PUDMED-1546720; DOI=10.1038/ng1447;
PubMed-1546720; DOI=10.1038/ng1447;
PubMed-1546720; DOI=10.1038/ng1447;
PubMed-1546720;
Cazalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L., Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F., Etienne J., Glaser P., Buchrieser C.;
Etienne J., Glaser P., Buchrieser C.;
Etienne J., Glaser P., Buchrieser C.;
Etienne J., Glaser P., Buchrieser C.;
It is a promised to the Legional parametric promised to the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the cont
                                                                                                                                                                                                                                                                                                                                                                             Mitochondrion.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=88210466; PubMed=2452697; DOI=10.1016/0092-8674(88)90161-4;
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Legichist; lpp3441; ...
Legichist; lpp3441; ...
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:000986; P:methionine biosynthesis; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR00119; LysR. subst.
Pfam; PF00126; HTH 1; I.
Pfam; PF00126; HTH 1; I.
Pfam; PF00126; LysR_substrate; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Feagin J.E., Abraham J.M., Stuart K.D.; "Extensive editing of the cytochrome c oxidase III transcript in Tryvanosoma brucei "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
OrderedLocusNames=1pp2441;
Legionella pneumophlia (strain Paris).
Bacteria, Proteobacteria; Gammaproteobacteria; Legionellales;
Legionallaceae; Legionella.
NCBI_TAXID=297246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.1%; Score 41; DB 2; Length 288; 100.0%; Pred. No. 1.4e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005739; C:mitochondrion; IEA.
GO; GO:0006419; F:cytochrome-c oxidase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
FINETEPRO; IPR000299; CytC_oxdse_III.
FROSITE; PS03053; CytC_oxdse_III.
SRQUENCE 288 AA; 34689 MW; 47CA8B3F88B5D6E8 CRC64;
                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                 288 AA
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                                                                                                                                                           Created)
                                                                                 PRT;
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PIR; A28782; A28782.
                               993_9TRYP

035993_9TRYP PRELIMINARY;

025993; 026739;

01-NOV-1996 (TEMBLEL: 01, CX

01-NOV-1996 (TEMBLE: 01, LA

01-MAR-2004 (TEMBLE: 26, La
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QSX2F2 LEGPA
ID Q5X2F2 LEGPA PRELIMINARY;
AC Q5X2F2;
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Best Local Similarity 100...
Grand 6; Conservative
                                                                                                                                                                                                                                                                    Cytochrome c oxidase III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trypanosoma brucei.";
Cell 53:413-422(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
STRAIN=EATRO 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 VFYWYF 144
                                                                                                                                                                                                                                                                                                                                      Trypanosoma brucei
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                                                                                                                                                                                                                                                                                                           Name=COIII;
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                                                                                                                                                                                                          A de la Cruz V.F., Neckelmann N., Simpson L.;

"Sequences of six genes and several open reading frames in the kinetoplast maxiciatel DNA of Leishmania tarentolae.";

I Sequences of six genes and several open reading frames in the kinetoplast maxiciatel DNA of Leishmania tarentolae.";

I Siol. Chem. 259:15136-15147(1984).

R GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016020; C:integral to membrane; IEA.

R GO; GO:0005739; C:integral to membrane; IEA.

R GO; GO:0005139; F:cytochromerc oxidase activity; IEA.

R GO; GO:0006118; P:electron transport; IEA.

R GO; GO:0006118; P:electron transport; IEA.

R RROSITE; PS50253; COX3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maslov D.A., Avila H.A., Lake J.A., Simpson L.;
"Evolution of RNA editing in kinetoplastid protozoa: pan-editing preceded 5'-editing.";
Nature 368:345-348(1994).
EMBL; U05814; AAA73419.1; -; Unassigned DNA.
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100.0%; Pred. No. 1.4e+02;
live 0; Mismatches 0; Indels
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Blastocrithidia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94173338; PubMed=8127370; DOI=10.1038/368345a0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34174 MW; CC5F69B18DFB54C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0X3; 1.
33994 MW; 3F670C5AE053D127 CRC64;
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GO; GO:0016020; C:membrane; IEA.
GO; GO:001539; C:mitochondrion; IEA.
GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
InterPro; IPRO0298; CytC_oxdse_III.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                           STRAIN=UC;
MEDLINE=85079995; PubMed=6096360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q33549 9TRYP PRELIMINARY;
Q33549;
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
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SEQUENCE 288 AA; 33994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blastocrithidia culicis.
                               Cell 53:401-411(1988).
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                                                                                                 NUCLEOTIDE SEQUENCE
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   287 AA;
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codons.";
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=GSS1 / DSM 4299 / JCM 9571;

MEDLINE=20570466; PubMad=11121031; DOI=10.1073/pnas.97.26.14257;

MEDLINE=20570466; PubMad=11121031; DOI=10.1073/pnas.97.26.14257;

Rawashima T., Amano N., Kolke H., Makino S.-I., Higuchi S., Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T., Runoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;

"Archaeal adaptation to higher temperatures revealed by genomic sequence of Thermoplasma volcanium.";

"Archaeal adaptation to higher temperatures revealed by genomic sequence of Thermoplasma volcanium.";

"Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).

-!- CATALYTIC ACTIVITY: ATP + L-asparagine + tRNA(Asn) = AMP + Gliphosphate + L-asparaginyl-tRNA(Asn).

-!- Gliphosphate + L-asparaginyl-tRNA(Asn).

-!- SIBCELLULAR LOCATION: Cycoplasmic.

-!- SIBCELLULAR LOCATION: Cycoplasmic.
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MEDLINE=22421331; PubMed=12533478;
MEDLINE=22421331; PubMed=1026.2003;
DOI=10.1128/JB.185.3.1018-1026.2003;
Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B., Moon D.H., Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H., Takita M.A., Lemos B.G.M., Machado M.A., Ferro M.I.T., da Silva F.R., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M., Carrer H., Carraro D.M., de Oliveira R.C., Numes L.R., Siqueira W.J., Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO1042; TRNASYNTHASP.
TIGREAMS; TIGRO0457; asnS; 1.
PROSITE; PSS0862; AA TRNA LIGASE II; 1.
Aminoacyl-trNA synthetase; ATP-binding; Complete proteome; Ligase;
Nucleotide-binding; Protein biosynthesis.
SEQUENCE 429 AA; 49893 MW; 92ACE28F75CEDE87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales,
Xanthomonadaceae; Xylella.
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50.0%; Pred. No. 2.18+02;
ive 3; Mismatches 2; Indels
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Alpha-ketoglutarate permease symporter.
Name-kett. OrderedLocusNames=PD0064;
Xylella fastidiosa (strain Temeculal / ATCC 700964)
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InterPro; IPR004522; AsnS.
InterPro; IPR004355; OB tRNA NA bd.
InterPro; IPR004364; tRNA-synt 2.
InterPro; IPR002312; tRNA-synt asp.
InterPro; IPR005312; tRNA-igase_II.
Pfam; PF00152; tRNA-synt 2; 1.
Pfam; PF01336; tRNA-anti; 1.
         Thermoplasmataceae; Thermoplasma
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Best Local Similarity 50.vv,
5; Conservative
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                             NCBI_TaxID=50339,
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Chien M., Morozova I., Shi S., Sheng H., Chen J., Gomez S.M.,
Asamani G., Hill K., Nuara J., Feder M., Rineer J., Greenberg J.J.,
Steshenko V., Park S.H., Zhao B., Teplitskaya E., Edwards J.R.,
Pampou S., Georghiou A., Chou I.-C., Iannuccilli W., Ulz M.E.,
Kim D.H., Geringer-Sameth A., Goldsberry C., Morozov P., Fischer S.G.,
Segal G., Ou X., Rzhetsky A., Zhang P., Cayanis B., De Jong P.J.,
Ju J., Kalachikov S., Shuman H.A., Russo J.J.;
"The genomic sequence of the accidental pathogen Legionella
                                                                                                                                               Gaps
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B-PFBB-2003 (Rel. 41, Last sequence update)
13-5EP-2005 (Rel. 48, Last annotation update)
Asparaginyl-tRNA synthetase (EC 6.1.1.22) (Asparagine--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 / ATCC 33152).
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GO; GO:0003700; F:transcription factor_activity; IEA.
GO; GO:0009086; P:methionine biosynthesis; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001947; HTH_LYSR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Proteobacteria, Gammaproteobacteria, Legionellales,
Legionellaceae, Legionella.
                                                                                               62.1%; Score 41; DB 2; Length 305; 80.0%; Pred. No. 1.5e+02; ive 0; Mismatches 2; Indels
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Archaea; Buryarchaeota; Thermoplasmata, Thermoplasmatales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.1%; Score 41; DB 2; Length 305
80.0%; Pred. No. 1.5e+02;
...marrhes 2; Indels
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PROSITE; PS50931; HTH LYSR; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 305 AA; 34885 MW; 4AD291961B9C9B94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        305 AA; 34907 MW; 8CDA907F8D6B2DEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Transcriptional regulator, LysR family.
                                                                                                                                                                                                                                                                                                                                                         305 AA
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                                                                      Ouery Match
Best Local Similarity 80.v.
8, Conservative
                                                                                                                                                                                                                                                                                                                                                     QSZSZO LEGPH PRELIMINARY;
QSZSZO;
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1.2 J. Bacteriol. 185:1018-1026(2003).
1.3 EMBLIA ABOUTEDIAR LOCATION: Integral membrane protein (By similarity).
1.4 EMBLIA ABOUTEDIA AAOZTOS4.1; — J. Genomic_DNA.
1.5 GO:0016021; Cintegral to membrane; IEA.
1.6 GO:0016020; C:membrane; IEA.
1.7 GO:000521; Fitransporter activity; IEA.
1.8 GO:0006810; P:transporter activity; IEA.
1.8 InterPro; IPR005828; Sub_transporter.
1.8 InterPro; IPR005828; Sub_transporter.
1.8 InterPro; IPR005828; Sug_transporter.
1.8 InterPro; IPR005828; Sug_transporter.
1.9 FROSITE; PS006820; Sug_transporter.
1.0 RPOSITE; PS00217; SUGAR_TRANSPORT_2; 1.
1.0 RPOSITE; PS00217; SUGAR_TRANSPORT_2; 1.
1.0 Complete protecome; Transmembrane.
1.5 GOUENCE 435 AA; 47918 MW; 03181910C660E5B5 CRC64;
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Marino C.L., Giglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M., Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V., da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri B.F., Kishi L.T., Leoni S.G., Oliveira A.R., Rous V.E. Jr., Sassaki F.T., Sena J.A.D., de Souza A.A., Truffi D., Taukumo F., Yanai G.M., Zaros L.G., Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                   Kitalima J.P.; "Comparative analyses of the complete genome sequences of Pierce's disease and citrus variegated chlorosis strains of Kylella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xylella fastidiosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
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Pred. No. 2.1e+02;
1; Mismatches 0; Indels
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0MR-2004 (TrEMBLrel. 26, Last annotation update)
Alpha-ketoglutarate permasse symporter.
OrderedLocusNames=Xf0087;
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85.7%;
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Q9PH59;
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da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr., da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A., de Souza A.P., Ternati M.E., Truffi D., Tsai S.M., Tsuhako M.H., Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L., Zago M.A., Zatz M., Meldanis J., Setubal J.C.; m'The genome sequence of the plant pathogen Xylella fastidiosa."; Nature 406:151-159 (2000).

-i- SUBCELLULAR LOCATION: Integral membrane protein (By similarity). EMBL, AE003863; AAF82900.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vibrio parahaemolyticus.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.1%; Score 41; DB 2; Length 435; 85.7%; Pred. No. 2.1e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                     GO; GO:0016021; Ciintegral to membrane; IEA.
GO; GO:0016021; Ciintegral to membrane; IEA.
GO; GO:0016220; Cimembrane; IEA.
GO; GO:0006215; Fitransporter activity; IEA.
GO; GO:0006610; P:transport; IEA.
InterPro; IPR007114; MFS.
InterPro; IPR007114; MFS.
InterPro; IPR00829; Sug_transporter.
Ffam; PF0083; Sugar tr; 1.
RP0081TE; PS50850; MFS; 1.
RP0SITE; PS50810; MFS; 1.
RP0SITE; PS00217; SUGAR TRANSPORT_2; 1.
Complete proteome; Transmembrane.
SEQUENCE 435 AA; 47987 MW; 2663EAD5B8454CIC CRC64;
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PROSITE; PS00633; GLYCOSYL_HYDROL_F1_2; 1.
Complete protocome; Glycosylaae; Hydrolaae.
SEQUENCE 463 AA; 52993 MW; 4E39CFD9FD23342A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   463 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BA000032; BAC61523.1; -; Genomic_DNA. HSSP; P11546; 1PBG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel, 24, 01-JUN-2003 (TrEMBLrel, 24, 01-OCT-2003 (TrEMBLrel, 25, Phospho-beta-glucosidase B. OrderedLocusNames=VPA0180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q87JR8_VIBPA PRELIMINARY,
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Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pectobacterium.
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PubMed=15263089; DOI=10.1073/pnas.0402424101;
PubMed=15263089; DOI=10.1073/pnas.0402424101;
Bell K.S., Sebaihia M., Pritchard L., Holden M.T.G., Hyman L.J.,
Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
Ormond D., Price C., Hauser H., Jagels K., Moule S., Norbertczak H.,
Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
"Genome sequence of the enterobacterial phytopathogen Erwinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
PubMed=15564664; DOI=10.1271/bbb.68.2270;
An C.L., Lim W.J., Hong S.Y., Kim E.J., Shin E.C., Kim M.K., Lee J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pectobacterium carotovorum (subsp. carotovorum) (Erwinia carotovora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (subsp. carotovora)).
Bactéria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Pectobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).

REBL; BX950851; CAG73576_1; -; Genomic DNA.

GO; GO:0008706; F: 6-phospho-beta-glucosidase activity; IEA.

GO; GO:0004557; F: 6-phospho-beta-glucosidase activity; IEA.

GO; GO:0005975; F: hydrolase activity, hydrolysing O-glycosyl. .

RIGHTAPRO: IPRO01350; Glyco-hydro-l.

REAM: PPO0232; Glyco-hydro-l.

REAM: PRO0131; GLHYDRIANEI.

REAM: PRO0131; GLHYDRIANEI.

RESOITE; PS00572; GLYCOSYL HYDROL. Fl.1; 1.

RESOITE; PS006573; GLYCOSYL HYDROL. Fl.2; 1.

ROMDIETE protecome; Glycosidase; Hydrolase.

SEQUENCE 467 AA; 53622 MW; 24FD49FF7BD37E26 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.1%; Score 41; DB 2; Length 467
63.6%; Pred. No. 2.3e+02;
ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                     25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
6-phospho-beta-glucosidase (EC 3.2.1.86).
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA)
                                                                                                                                                                                                                                                                                            467 AA.
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   Mismatches
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D OGDSF4_ERWCT

D OGDSF4_ERWCT

DT 25-OCT-2004 (TrEMBLrel. 28,
DT 25-OCT-2004 (TrEMBLrel. 28,
DT 25-OCT-2004 (TREMBLrel. 28,
DT 25-OCT-2004 (TREMBLrel. 28,
DE 5-DORDSD-Deta-glucosidase
GN GreedLocusNames=ECA0662;
OC Bacteria, Proteobacteria; GE
ENTAINS-CRI 1043 / ATCC BAAR

RA PLANS-CRI 1043 / ATCC BAAR

RA PLANS-CRI 1043 / ATCC BAAR

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Best Local Similarity 63...
7; Conservative
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QGQGYS;
7; Conservative
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                                                                                                                             449 RKDSFYWYQDV 459
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                                                                1 RETVEYWYFDV 11
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   Matches
                                                                                                                                                                                                                     RESULT 32
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Kang J.M., Lee S.M., Yun H.D.;

A Cryptic beta-glucosidase Gene, casB, of Pectobacterium carotovorum subsp. carotovorum LY34.",

Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, PX866383, PANS7580.1; -; Genomic_DNA.

InterPro, IPR001366; Glyco_hydro_1.

PROMIST: PR00131; GLYCOSYL_HYDROL F1 1; 1.

PROSITE: PS00652; GLYCOSYL_HYDROL_F1_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania
NCBI_TaxID=5671;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reguera R.M., Ferez-Pertejo Y., Balana-Fouce R., Ordonez-Escudero Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF309637; AAG46031.1; -; Genomic_DNA.
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Enterobacteriaceae; Pectobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    467 AA; 53063 MW; E03D69A2EDF4F2EF CRC64;
                                                                                                                                                                                                                 01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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63.6%; Pred. No. 2.3e+02;
                                                                                                                                                              467 AA
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                                                                                                                                                                                                                                                                                                                   6-phospho-beta-glucosidase-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 63.6°
--^a 7; Conservative
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Q4VK76;
                                                                                                                                                        Q9GPU3_LEIIN PRELIMINARY;
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443 RKKSFYWYQDV
                                                                                                                                                                                                                                                                                                                                                                                       Leishmania infantum.
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Best Local Similarity
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Length 467;

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Gaps

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0; Indels

Length 470;

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The German cDNA Consortium;

The German cDNA Consortium;

Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,

Han M., Wiemann S.;

Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,

Han M., Wiemann S.;

Bandt G. And Consortium;

EMBL; BK640947; CAE45572.1; -; mRNA.

RAR; OsM206; 20-475.

RICEPPO; IPR001599; Ig.

InterPro; IPR001510; Ig-like.

RICEPPO; IPR001599; Ig.

RICEPPO; IPR001599; Ig.

RICEPPO; IPR001599; Ig.

RICEPPO; IPR001599; Ig.

RICEPPO; IPR001596; Ig.

RART; SM00409; IG. 2.

RART; SM00400; IG. 2.

RART; SM04000; IG. 2.

RART; SM00400; IG. 3.

RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART; RART;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
GO; GO:0003823; F:antigen binding; IEA.
InterPro; IPR00710; IG-like.
InterPro; IPR003006; IG-like.
InterPro; IPR003006; IG-like.
InterPro; IPR003006; IG-like.
InterPro; IPR003006; IG-like.
InterPro; IPR00306; IG-like.
InterPro; IPR00306; IG-like; 4.
PROSITE; PS00290; IG-like; 4.
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothei.cal protein DKFZp686G11190.
Name-DKFZp686G11190;
                                                                                                                                                                                                                                                                                                                                                                                             Query Match 62.1%; Score 41; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 2.3e+02;
:ive 0; Mismatches 0;
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ID Q91XE1 MOUSE PRELIMINARY;
AC Q91XE1 O1-08C-2001 (TEMBLEE1. 19
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Q6MZQ6;
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Best Local Similarity 100.v
Section 6; Conservative
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129 YWYFDV 134
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Q6MZQ6_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 36
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TISSUB-Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.

Expression driven by an MMTV-LTR enhancer.;

MEDINNE-2238825; PubMed-1247932; DOI=10.1073/pnas.242603899;

Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S. I., Wang J., Haleh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,

Brownstein M.J., Wadin T.B., Toshiyuki S., Carninci P., Prange C.,

Racha S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffaus G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schmerzh O.N., Marra M.A.;

"Green Exting and initial analysis of more than 15,000 full-length human
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                          "Analysis of bgl Operon Structure and Characterization of beta-
"Analysis of bgl Operon Structure and Characterization of beta-
Glucosidase from Pectobacterium carotovorum subsp. carotovorum LY34.";
Biosci. Biotechnem. 62700-2270-2270-2270-2270-2016.
GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . .; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IRR001360; Glyco_hydro_l.
PRINTS; PR00131; GLHYDRLASE1.
PRINTS; PR00131; GLHYDRLASE1.
PROSITE; PS000572; GLYCOSYL HYDROL_F1.1; 1.
PROSITE; PS000533; GLYCOSYL HYDROL_F1.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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Expression driven by an MMTV-LTR enhancer.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.1%; Score 41; DB 2; Length 468; 63.6%; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                        468 AA; 53494 MW; 4B08C2E31087293A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein Al324046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
   Park S.R., Woo J.G., Lim Y.P., Yun H.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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Submitted (AUG-2003) to the EMBL/Gen
EMBL; BC055910; AAH55910.1; -; mRNA.
HSSP; P01865; 1KBS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q7TWK1 MOUSE PRELIMINARY;
Q7TWK1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 63.6
les 7; Conservative
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Gaps

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Indels

Length 475;

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Burkholderiaceae; Burkholderia; pseudomallei group.
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Q62BC6_B
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                                                                                                                                      STRAIN=FVB/N; TISSUE=Colon;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;

Altschul S.P.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;

Altschul S.P.; Zeeberg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;

Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Haieh F.;

A stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;

B rownstein M.J.; Usdin T.B.; Toshiyuki S.; Carninci P.; Prange C.;

A Raha S.A.; McEwan P.J.; McKernan K.J.; Malled D.P.; Millahy S.J.;

B Bosak S.A.; McEwan P.J.; McKernan K.J.; Malled J.J.; Hulyk S.W.;

A Nilalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;

B Hakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;

B Niting M.; Madan A.; Young A.C.; Shevchenko Y.; Boulfard G.G.;

B Niting M.; Madan A.; Young A.C.; Shevchenko Y.; Boulfard G.G.;

B Niting M.; Madan A.; Young A.C.; Shevchenko Y.; Boulfard G.G.;

B Notterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smailus D.E.;

B Schnerch A.; Schein J.E.; Jones E.J.M.; Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
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                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative glycosyl transferase.
OrderedLocusNames-BPSS0735;
Burkholderia pseudomallei (Pseudomonas pseudomallei).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.1%; Score 41; DB 2; Length 480; 100.0%; Pred. No. 2.38+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC10798; AMH10798.1; -; MRNA.
HSSP; P01788; 1MCP.
SWR; O91XE1; 19-235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          480 AA; 51936 MW; 20B9234EEF2B41ED CRC64;
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
101-WAR-2004 (TrEMBLrel. 26, Last annotation update)
104-VJ558 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ensembl; ENSMUSGO000021155; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR0031597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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PROSITE; PS00290; IG MHC; UNKNOWN 2.
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STRAIN=FVB/N; TISSUE=Colon;
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Q63MC5;
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                                                                                         Muridae; Murinae; Mus
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Best Local Similarity
Matches 6; Conserv
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                                                                                                   NCBI_TaxID=10090;
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SEQUENCE
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PubMed=1537793; DOI=10.1073/pnas.0403306101;
PubMed=15377793; DOI=10.1073/pnas.0403306101;
Peldblyum T.V., DeShazer D. Kim H.S., Tettelin H., Nelson K.E.,
Peldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrow G., Dodson R.J.,
Madup R.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M.,
Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
Zafar N., Zhou L., Fraser C.M.;
"Structural flexibility in the Burkholderia mallei genome.";
Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
TIGR; BMBL; CP000011; AAU46463.1; -; Genomic_DNA.
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 655;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               655 AA; 72469 MW; 0961DFD6680B7826 CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last 'sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative cellulose synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0016020; C:membrane; IEA.
GO; GO:0016759; F:cellulose synthase activity; IEA.
GO; GO:0006011; P:UDP:glucose metabolism; IEA.
InterPro; IPR003919; Cell synth A.
InterPro; IPR001173; Glyco_trans_2.
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Best Local Similarity 62.5'
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NCBI_TaxID=28450;
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NUCLEOTIDE SEQUENCE.
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BMBL, BT011360; ARR96152.1; -; mRNA.
GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0007160; P:cell-matrix adhesion; IEA.
InterPro; IPR005533; AMOP.
InterPro; IPR005886; NIDO.
InterPro; IPR001886; NUDO.
InterPro; IPR001886; NUDO.
InterPro; IPR001886; WWP.D.
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                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41, DB 2; Length 1240,
Pred. No. 5.9e+02,
0; Mismatches 4; Indels
                                                   62.1%; Score 41; DB 2; Length 655; 62.5%; Pred. No. 3.2e+02; ive 2; Mismatches 1; Indels
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PSS0923; SUSHI; 1.
1240 AA; 141592 MW; 087A69CD17D9DCD3 CRC64;
                       Complete proteome.
SEQUENCE 655 AA; 72457 MW; BF28DFD6680B7FC0 CRC64;
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09040657
01-MAR-2000 (TYEMBLrel. 13, Created)
01-MAR-2003 (TYEMBLrel. 23, Last sequence update)
01-MAR-2004 (TYEMBLrel. 26, Last annotation update)
CG31004-PA, isoform A (CG31004-pb, isoform b).
Name=CG31004; ORFNames=CG31004;
                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                 PRT; 1240 AA.
                                                                                                                                                                                    Created)
Pfam; PF00535; Glycos transf 2; 1. PRINTS; PR01439; CELLSNTHASEA.
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QGNNDO;
                                                Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 60.0
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393 LLYWYFDI 400
                                                                                           4 VFYWYFDV 11
                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                             NCBI_TaxID=7227;
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                                                                                                                                                                                                                            Name=CG31004;
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Decephila and mogaster (Fruit fig).

Bukryota: Wetazoa Arkthopoda; Hexapoda; Insecta; Perryota; Wetazoa Arkthopoda; Hexapoda; Insecta; Perryota; Wetazoa Arkthopoda; Hexapoda; Insecta; Perryota; Wetazoa Arkthopoda; Perryota; Metazoa Arkthopoda; Perryota; Metazoa Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Decephilada; Dec
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STRAIN=SC5314;
bubdels1213810;
bDI=10.1073/pnae.0401648101;
Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
ORFNames=Cao19.10707;
Candida albicans SC5314.
Bukaryota; Pungi; Ascomycota; Saccharomyceties;
Saccharomycetales; mitosporic Saccharomycetales;
                                                                                                           Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium chabaudi.
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                 0; Indels
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GO; GO:0004806; F:triacylglycerol lipase activity; IEA. GO; GO:0006629; P:lipid metabolism; IEA. InterPro; IPR0C2921; Lipase 3. Pfam; PP01764; Lipase 3; 1. Pfam; PP01764; Lipase 3; 1. SEQUENCE 287 AA; 34119 MW; AC74943B9A5C42A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 62 AA; 7636 MW; 435D6FD70CF780BD CRC64;
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Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
                                                                                                          Score 40.5; DB 2;
Pred. No. 1.7e+02;
1; Mismatches 0;
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EMBL; CAAJ01003729; CAH80487.1; -; Genomic_DNA.
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Pred. No. 44;
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                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                           Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative 1
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13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
Hypothetical protein.
ORFNames=PC107290.00.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
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QS9YX1;
                                                                                                                                                                                                                                                                                                              Q4xrH5_PLACH PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=5825;
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Q4XRH5_PLA
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Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                        NUCLEOTIDE SEQUENCE.
Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith
                                                     Lewis S.E.; _{i} . "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genomic sequence of the Amsacta moorei entomopoxvirus: analysis and comparison with other poxviruses."; Virology 274:120-139(2000).
EMBL; AF250284; AAG02839.1; -; Genomic_DNA.
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MEDLINE=20396580; PubMed=10936094; DOI=10.1006/viro.2000.0449;
Bawden A.L., Glassberg K.J., Diggans J., Shaw R., Farmerie W.,
                                                                                                                                                                                                                                                                                                                                                                                              GO; GO: 0005578; C: extracellular matrix (sensu Metazoa); IEA.
GO; GO: 0016021; C: integral to membrane; IEA.
GO; GO: 0016020; C: membrane; IEA.
GO; GO: 0007160; P: cell-matrix adhesion; IEA.
InterPro; IPR003886; NIDO.
InterPro; IPR003886; NIDO.
InterPro; IPR00486; NWD.
Pfam; PF03782; AMOP; 1.
Pfam; PF03782; AMOP; 1.
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Pred. No. 6.9e+02;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1431 AA; 162377 MW; 7C7F4C01CC052DFC CRC64;
                                                                                                                                                                                                                                                                                                         FlyBase;
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003777; AAF57123.2; -; Genomic DNA.
Ensembl; CG31004; Drosophila melanogasTer.
FlyBase; FEGIN0051004; CG31004.
                                                                                                                                                                                                                  Yu C., Rubin G.;
"Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                        systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amsacta moorei entomopoxvirus (AmEPV).
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Pfam; PF00094; VWD; 1.
SWART; SW00723; AMOP; 1.
SWART; SW00323; CCP; 1.
SWART; SW00539; NIDD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50856; AMOP; 1
PROSITE; PS50923; SUSHI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9EMR6_AMEPV PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 60.0
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 RSNFMYWYFD 171
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                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
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NCBI_TaxID=28321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=AMV133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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RESULT 41
1096 AME
10 09 EWR
AC 09 EWR
DT 01 - WR
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED utstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                  RACALLE-2184401; PubMed=11859360; DOI=10.1038/nature724;

RACALLE-2184610; PubMed=11859360; DOI=10.1038/nature724;

RACOD V., Gwilliam R., Rajandream M.A., Lyne M.H., Lyne R., Stewart A.,

RACOD S., Gwilliam R., Brown S., Chillingworth T., Churcher C.M.,

RACOLLINS M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Gontles S., Goble A., Hamlin N., Harris D.E., Hiddlago J., Hodgeon G.,

RACONORY P., Moule S., Minghy T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

ANDOROY P., Moule S., Minghy T., Murphy L.D., Niblett D., Odell C.,

RACONORY P., Moule S., Minghall K.L., Murphy L.D., Niblett D., Odell C.,

RACONORY P., Moule S., Minghall K.L., Murphy L.D., Niblett D., Odell C.,

RACONORY P., Moule S., Minghall K.L., Murphy L.D., Niblett D., Odell C.,

RACONORY P., Moule S., Minghall K.L., Murphy L.D., Niblett D., Odell C.,

RACONORY P., Moule S., Minghall M.A., Rabbinowitsch E.,

RACHLON J., Simmonds M.N., Squares S., Stewens K.,

RACHON J., Simmonds M.N., Squares S., Stewens K.,

RACHON J., Simmonds M.N., Squares S., Stewers S.,

RACON J., Miner J., Simmermann W., Wedler H., Wambutt R., Purnelle B.,

RACON J., Squares S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

LUCAS M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

RACON J., Squares D., Armetrong J., Forsburg S.L.,

RACON J., Squares D., Shances D., Shances P.,

RACON J., Shances D., Shances D., Shances D.,

hances D.,

RACON J., Shances D., Shances D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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Pred. No. 1.1e+02;
1; Mismatches 1; Indels
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Pfam; PF04892; Vanz; 1.
Complete protecme; Hypothetical protein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18481 MW; 6E10E58EFE55131F CRC64;
                                                                                                                                                                        Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                      15-JUL-1998 (Rel. 36, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Hypothetical protein Cl1E3.10 in chromosome I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 AA.
                                                                                                                                               Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
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PIR; T37538; T37538.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q4KAS6_PSEFS PRELIMINARY;
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                                                                                                                         ORFNames=SPACI1E3.10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 VEYWYFDV 11
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                                                                                                                                                                                                                           Schizosaccharomyces.
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70
97 1
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                                                                                                                                                                                                                                                  NCBI_TaxID=4896;
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Q4KAS6 PSE
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MEDLINE=22855698; PubMed=12917642; DOI=10.1038/nature01947;
Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
Webb E.A., Zinser E.R., Chisholm S.W.;
"Genome divergence in two Prochlorococcus ecotypes reflects oceanic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4). astoria; Cyanobacteria; Prochlorales; Prochlorococcaceae; Prochlorococcus.
                                                                                                                                        Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O., Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W., Jones T., Scherer S., Agabian N.;
"Annotation of the Genome of Candida albicans.";
Submitted (ARR-2004) to the BML/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 2; Length 127;
Pred. No. 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.6%; Score 40; DB 2; Length 133; 85.7%; Pred. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                                                                                                                                                                                              preliminary data.

EMBL; AACQ01000097; EAK95700.1; -; Genomic_DNA.

Hypochetical protein.

SEQUENCE 127 AA; 15222 MW; B625A49643EF2BCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome; Endonuclease.
SEQUENCE 133 AA; 15449 MW; BDA7A95D647B2FC0 CRC64;
                      "The diploid genome sequence of Candida albicans."; Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BX572093; CAE19862.1; -; Genomic_DNA.
GO; GO:0004519; F:endonuclease activity; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
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InterPro; IPR003615; HNH_nuc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.78;
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Q7V077;
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hes 6; Conservative
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Davis R.W., Scherer S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01844; HNH; 1.
SMART; SM00507; HNHC;
                 The diploid genome
                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 TVFYWY 100
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YDYA_SCHPO
ID _YDYA_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Q4WV37 A
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CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) + H(2)O = 2 3-phospho-D-glycerate.

CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + O(2) = 3-phospho-D-glycerate + 2-phosphoglycolate.

SUBNIT: 8 large chains + 8 small chains (By similarity).

SUBCELLULAR LOCATION: Chloroplast (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chloroplast.
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Asparagales, Amaryllidaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                         Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S., Mavrodi D., DeBoy R.T., Sebhadri R., Ren Q., Madupu R., Dodson R.J., Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M., Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K., Khouri H.M., Pierson B., Plerson L. III, Thomashow L., Loper J.; "Complete genome sequence of the plant commensal Pseudomonas fluorescens PF_S.";
                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 24, Last amnotation update)
01-0TN-2003 (TrEMBLrel. 24, Last annotation update)
Ribulose 1,5-bisphosphate carboxylase large subunit (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.6%; Score 40; DB 2; Length 213; 85.7%; Pred. No. 1.5e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nat. Biotechnol. 23.873-878 (2005).
EMBL; CP000076; AAY92821.1; -; Genomic DNA.
SEQUENCE 213 AA; 24433 MW; 9961C6935D9F8221 CRC64;
                    13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Transcriptional regulator, Tetk family.
                                                                                                                     ORFNames=PFL 3554;
Pseudomonas fluorescens (strain Pf-5)
                                                                                                                                                                                                                                                                                                                  PubMed=15980861; DOI=10.1038/nbt1110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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Best Local Similarity 85.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 9ASPA
Q9MT27 9ASPA PRELIMINARY;
Q9MT27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apodolirion lanceolatum.
                                                                                                                                                                                                                                               [1]NUCLEOTIDE SEQUENCE.
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                                                                          GO: GO: 0009573; C: chloroplast; IEA.
GO: GO: 0009573; C: chloroplast; IEA.
GO; GO: 0009573; C: cribulose bisphosphate carboxylase complex (. . .; IEA.
GO; GO: 00016829; F: lyase activity; IEA.
GO; GO: 0016984; F: ribulose-bisphosphate carboxylase activity; IEA.
GO; GO: 0015977; P: carbon utilization by fixation of carbon di. .; IEA.
GO; GO: 0015977; P: proarbon utilization JEA.
GO; GO: 0015979; P: photosynthesis; IEA.
InterPro; IFR000665; RubisCO_large.
Ffam; PF0016; RubisCO_large; I.
Ffam; PF0016; RubisCO_large; N; I.
FROSITE; PS00157; RUBISCO_large; N; I.
Carbon dioxide fixation; Chloroplast; Lyase; Moncoxygenase;
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EMBL; ABO16968; AAP56780.1; -; Genomic_DNA.

GO; GO:0005354; C:nucleus; IEA.

GO; GO:0003570; F:transcription factor activity; IEA.

GO; GO:0005355; P:regulation of transcription, DNA-dependent; IEA.

Complete proteome; Hypothetical protein.

SEQUENCE 231 AA; 28093 MW; 2BBABD9846320C4 CRC64;
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Bacteria, Firmicutes, Mollicutes, Mycoplasmataceae, Mycoplasma.
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-!- SIMILARITY: Belongs to the RuBisCO large chain family. EMBL; AF116944; AAF97638.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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54.5%; Pred. No. 1.6e+02;
.ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 AA; 26300 MW; 2794B15706B8A35F CRC64;
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01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oxidoreductase; Photorespiration; Photosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.6%; Score 40; DB 2; I
71.4%; Pred. No. 1.6e+02;
ive 1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 71.4%;
Matches 5; Conservative
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Q4WV37;
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Query Match
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A Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
Bowyer P., Chen D., Collins M., Coulsen R., Davies R., Dyer P.S.,
Barman M., Fedorova N., Fedbolyum T.V., Fischer R.,
Fosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
Goldman G.H., Gomit K., Griffith-Jones S., Gwilliam R., Haas B.,
Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
Mangai T., Lafton A., Latge J.P., Li W., Lord A., Lu C.,
Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
Penalva M.A., Perrea M., Price C., Pritchard B.L., Quail M.A.,
Rabbinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
Renauld H., Robson G.D., Rodriguez Cordoba S., Rodriguez-Pena J.M.,
Anning C.M., Rutter S., Salzberg S.L., Sanchez M.,
Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
Takeuchi M., Tekaia F., Turner G., Vazquez de Aldana C.R., Weidman J.,
Mhite O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
Machida M., Hall N., Barrell B., Denning D.W.;
Agenomic sequence of the pathogenic filamentous fungus
Responding tungatus ";
Agengerilus fungatus ";
Anning C.M., Anning R.M., Anning D.W.;
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MEDLINE=91133195; PubMed=2013564;
MEDLINE=91133195; PubMed=2013564;
MEDLINE=91133195; PubMed=2013564;
Structural Omplexity of the symbiotic plasmid of Rhizobium leguminosarum bv. phaseeli.";
J. Bacteriol. 173:2411-2419(1991).
                                                                                                                    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.6%; Score 40; DB 2; Length 348; 55.6%; Pred. No. 2.4e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypochetical protein.
SEQUENCE 348 AA; 41230 MW; 72310A91FEDD985B CRC64;
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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Last annotation update)
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; AAHF01000003; EAL91539.1; -; Genomic_DNA.
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                             Hypothetical protein.
ORFNames=Afu5g10670;
Aspergillus fumigatus Af293.
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01-0CT-2002 (TrEMBLEE). 22,
01-MAR-2004 (TrEMBLEE). 26,
Hypothetical protein yp091.
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Q8KKU1;
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24 TVFHWFYEV 32
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[2]
NUCLEOTIDE SEQUENCE.
STRAIN=CFN42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
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                                                                                                                                                                          NCBI_TaxID=330879;
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                                                                                                                                                                                                                                                                   STRAIN=Af293;
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                                                                                   "Sequence, localization and characteristics of the replicator region
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Gonzalez V., Bustos P., Medrano-Soto A., Ramirez-Romero M.A.,
Romero D., Salgado H., Hernandez-Gonzalez I., Hernandez-Celis J.C.,
Quintero V., Girard L.L., Rodriguez O., Flores M., Cevallos M.A.,
Collado-Vides J., Davilla G.,
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                       Quintero V., Cevallos M.A., Davila G.;
"A site-specific recombinase (Ring) is required to exert incompatibility towards the symbiotic plasmid of Rhizobium etli.";
Mol. Microbiol. 46:1023-1032(2002).
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Ramirez M.A., Bustos P., Girard L., Rodriguez O., Cevallos M.A.,
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                         Ramirez-Romero M.A., Bustos P., Girard L., Rodriguez O.,
Cevallos M.A., Davila G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CFN42;
Quintero V., Bustos P., Davila G.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; UR6028; AAM55039.1; -; Genomic_DNA.
INTERPY: IPRO9213; UCP031854.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quintero V., Bustos P., Davila G.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Plasmid.
SEQUENCE 364 AA; 40120 MW; 20964670BB9D8F48 CRC64;
                                                                                                                   of the symbiotic plasmid of Rhizobium etli."; Microbiology 143:2825-2831(1997).
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MEDLINE=97419521; PubMed=9274036;
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